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).
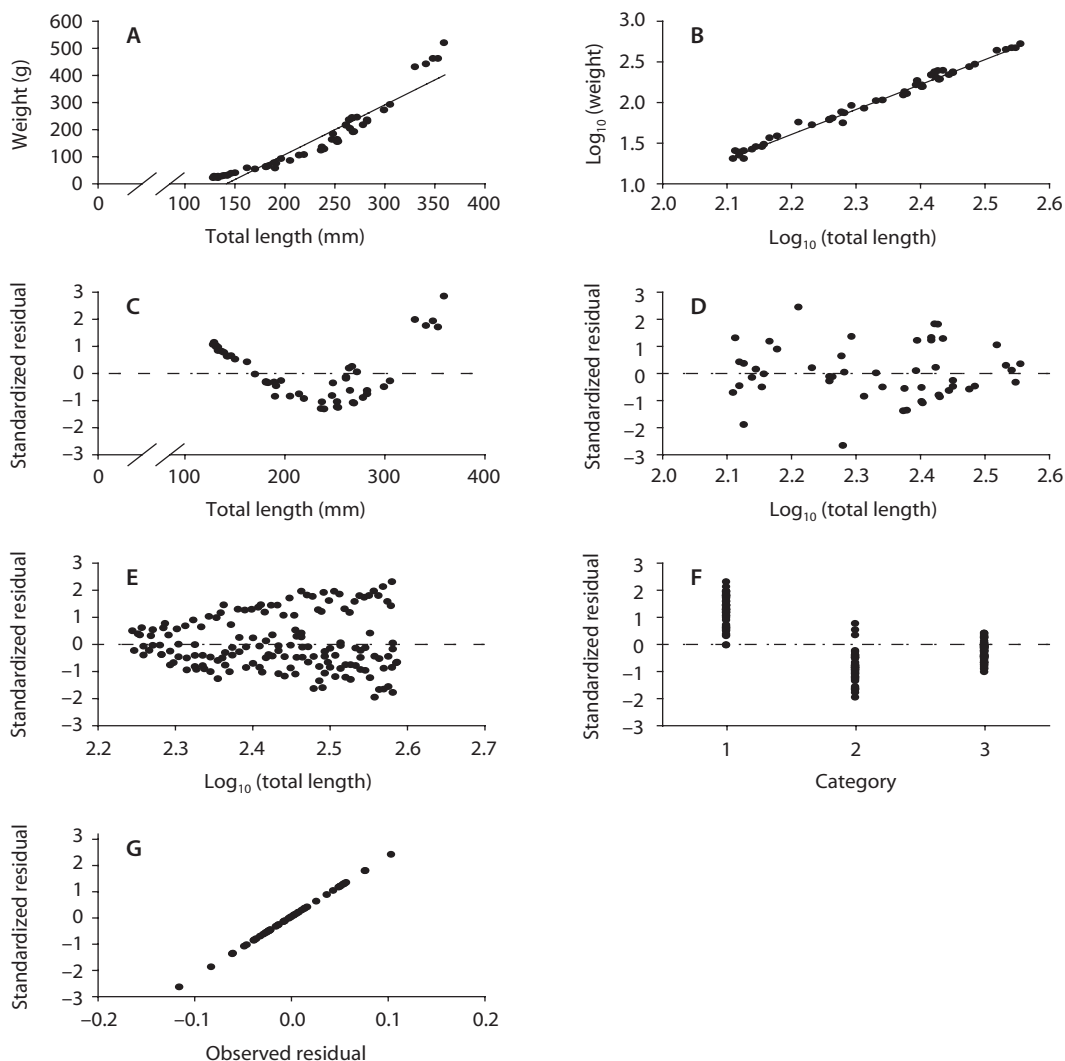
Figure 10.1   Graphical depiction of the curvilinear relationship of (A) untransformed length–weight data from the low-elevation stream Yellowstone cutthroat trout population described in Box 10.1 versus (B) the linear nature of the same data after log_{10} transformation. (C) A typical diagnostic residual 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.

Box 10.1   Transformation and Regression Analyses of Weight–Length Data—Comparing the Condition of Two Populations

Table   Presented are total length (TL; mm), weight (WT; g), and body fat as a percentage of overall wet weight for samples of Yellowstone cutthroat trout collected in midsummer from three locations that could influence individual weight at length: a lower-elevation stream (1,810 m elevation), a lower-elevation lake (1,785 m), and a higher-elevation lake (2,610 m). Fat values were randomly generated for example only. Fish samples were collected via electroshocking, gill nets, and angling.

Low-elevation stream (A)			Low-elevation lake (B)			High-elevation lake (C)		
TL	WT	Fat (%)	TL	WT	Fat (%)	TL	WT	Fat (%)
129	20	5.91	254	181	10.59	180	63	8.32
130	25	12.88	262	186	9.08	191	77	4.78
132	22	7.67	272	136	1.38	198	54	0.6
132	24	11.29	274	191	2.64	203	73	2.63
134	20	2.27	282	245	7.32	231	100	0.99
134	25	11.57	287	236	6.68	234	104	1.21
138	26	6.63	290	168	1.39	236	109	5.91
140	28	11.04	297	263	6.81	239	118	2.55
143	28	9.45	302	290	9.1	239	127	5.37
144	30	9.86	305	290	7.97	241	127	2.87
147	36	8.79	328	327	5.9	244	141	4.97
151	38	13.78	330	354	2.47	244	141	5.51
163	56	11.69	333	363	5.16	244	154	8.21
171	52	6.46	333	390	9.29	246	141	4.37
182	60	8.83	338	372	3.64	246	150	6.27
182	61	8.93	340	417	12.98	246	168	8.44
184	63	8.97	340	417	9.92	249	145	2.34
190	75	11.71	343	399	5.36	249	145	4.51
191	55	4.73	345	408	5.39	249	154	6.44
192	73	7.35	345	445	10.37	249	159	7.88
197	90	12.88	351	463	10.24	251	145	2.99
206	83	4.52	353	390	5.78	251	145	3.04
215	103	9.1	353	390	1.75	251	145	3.57
220	105	6.41	356	467	8.51	254	150	7.98
237	121	3.06	356	472	8.66	254	150	3.64
238	133	6.52	358	408	1.87	254	154	4.63
240	126	3.42	361	545	1.99	254	159	2.95
248	161	9.81	361	472	9.61	254	163	5.94
249	182	12.24	363	481	6.19	257	154	3.73
253	153	7.34	363	508	8.87	257	159	3.11
253	161	11.11	366	481	4.62	257	168	5.98
254	154	4.25	368	476	2.69	257	172	7.38
262	213	12.33	373	544	11.45	257	172	7.83
262	215	12.53	378	526	4.29	259	154	1.23
265	234	12.9	381	535	3.12	259	159	3.93
266	202	10.44	381	535	3.37	259	159	4
268	242	13.04	384	608	9.99	259	172	6.19
269	189	4.27	386	572	5.84	259	181	7.9
270	190	4.29	389	562	7.05	262	181	7.25
273	243	12.66	391	590	4.86	262	181	6.31
279	215	9.63	394	635	3.9	264	159	1.87

(Box continues)

Box 10.1   *(continued)*

Table (*continued*)

Low-elevation stream (A)			Low-elevation lake (B)			High-elevation lake (C)		
TL	WT	Fat (%)	TL	WT	Fat (%)	TL	WT	Fat (%)
283	228	6.83	396	590	2.48	267	191	6.74
283	233	8.62	399	581	2.43	269	136	3.45
300	270	5.45	401	603	2.43	272	163	0.73
306	290	7.62	406	703	7.24	282	195	2.28
331	429	11.87	411	703	6.36	284	231	9.7
342	440	10.71	414	676	2.51	284	245	10.89
349	460	9.82	425	752	4.33	290	231	4.8
354	460	7.63	433	780	3.05	290	231	4.81
360	518	10.77	462	1170	9.99	290	240	5.74

Program

The following SAS program is configured to provide two regression analyses—linear regression of the weight–length data after $\log_{10}$ transformation on sample data from both the low-elevation stream (A) and lake (B) Yellowstone cutthroat trout populations and nonlinear regression of the untransformed data from the stream (A) sample. Only output relevant to the following discussion is provided. Hereinafter, all references to weight–length data transformations refer to a $\log_{10}$ transformation.

```
OPTIONS PS=54 LS=75;
DATA TROUT;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
CARDS;
A    129    20
B    254    181
[Input complete data set];
PROC SORT; BY POP;
PROC REG; BY POP; MODEL LOGWT=LOGTL/CLB;
PROC NLIN; BY POP; PARMS A=0.000001 B=3; MODEL WT=A*(TL**B);
RUN;
```

Output

Table Linear regression of transformed weight–length data for population A. The dependent variable is $\log_{10}$WT (LOGWT). Abbreviations are sum of squares (SS), coefficient of variation (CV), mean square error (MSE), and $\log_{10}$TL (LOGTL).

		Analysis of Variance			
Source	*df*	SS	Mean square	*F*-value	*P* > *F*
Model	1	8.54267	8.54267	4545.72	<0.0001
Error	48	0.09021	0.00188		
Corrected total	49	8.63287			
r^2	0.9896	Root MSE	0.04335		
Adjusted r^2	0.9893	Dependent mean	2.01073		
CV	2.15597				

Parameter Estimates

Variable	df	Parameter estimate	SE	t-value	P > |t|
Intercept	1	−5.14432	0.10630	−48.39	<0.0001
LOGTL	1	3.06874	0.04552	67.42	<0.0001

Variable	df	95% Confidence limits	
Intercept	1	−5.35805	−4.93059
LOGTL	1	2.97722	3.16025

Table   Nonlinear regression of weight–length data for population A. The dependent variable is WT, which is modeled as a constant (A) times TL raised to a power (B). The convergence criterion was met. An intercept was not specified for this model.

Iteration	A	B	SS
0	$1·10^{-6}$	3.0000	1656903
1	$1.832·10^{-6}$	3.2801	58540.3
2	$2.141·10^{-6}$	3.2545	53615.7
3	$2.686·10^{-6}$	3.2164	49075.3
4	$3.413·10^{-6}$	3.1775	41355.6
5	$4.911·10^{-6}$	3.1183	31198.0
6	$5.801·10^{-6}$	3.1049	11611.2
7	$5.868·10^{-6}$	3.1056	11159.7
8	$5.869·10^{-6}$	3.1056	11159.7

Estimation Summary

Method	Gauss-Newton
Iterations	8
Subiterations	7
Average Subiterations	0.875
R	$2.223·10^{-7}$
PPC(A)	$6.674·10^{-8}$
RPC(A)	0.000045
Object	$5.848·10^{-8}$
Objective	11159.7
Observations Read	50
Observations Used	50
Observations Missing	0

Regression Model

Source	df	SS	Mean square	F-value	Approximate P > F
Regression	2	2001114	1000557	4303.59	<0.0001
Residual	48	11159.7	232.5		
Uncorrected total	50	2012274			
Corrected Total	49	838762			

(Box continues)

Box 10.1   *(continued)*

Table *(continued)*

		Parameter Estimates		
Variable	*df*	Approximate SE	Approximate 95% confidence limits	
A	$5.869 \cdot 10^{-6}$	$2.215 \cdot 10^{-6}$	$1.416 \cdot 10^{-6}$	0.000010
B	3.1056	0.0659	2.9731	3.2381

Approximate Correlation Matrix		
	A	B
A	1.0000000	−0.9995920
B	−0.9995920	1.0000000

Table   Linear regression of transformed weight–length data for population B. The dependent variable is $\log_{10}$WT.

		Analysis of Variance			
Source	*df*	SS	Mean square	*F*-value	*P* > *F*
Model	1	1.66271	1.66271	914.86	<0.0001
Error	48	0.08724	0.00182		
Corrected total	49	1.74995			
r^2	0.9501	Root MSE	0.04263		
Adjusted r^2	0.9491	Dependent mean	2.63145		
CV	1.62008				

		Parameter Estimates			
Variable	*df*	Parameter estimate	SE	*t*-value	*P* > |*t*|
Intercept	1	−5.36936	0.26459	−20.29	<0.0001
LOGTL	1	3.14307	0.10391	30.25	<0.0001

Variable	*df*	95% confidence limits	
Intercept	1	−5.90135	−4.83737
LOGTL	1	2.93413	3.35200

Interpretation
Regression of the transformed weight–length data from sample (A) shows a highly significant relationship ($P < 0.0001$) that explains 99% of the variation in weight (r^2). Regression of the transformed data provides a more precise estimation of fish weight than can be obtained by linear regression of the untransformed data and is a useful tool for inferring changes in overall condition (weight) temporally within or spatially across populations. Often a linear equation fitted to the entire range of untransformed data predicts that a fish must be of substantial size before the

weight exceeds zero, overestimates weights for mid-length fish, and underestimates the weight of larger fish—thus, the equation is not biologically relevant. Here, the transformed equation ($\log_{10}WT = -5.144 + 3.069\log_{10}TL$) estimates that individuals incrementally gain mass once they exceed 1 mm in length and demonstrates a strong linear relationship between weight and length.

The nonlinear regression of the untransformed data (equation [10.1]) provides the power function $WT = 0.000005869(TL)^{3.1056}$ and predicts weights very similar to the linear regression (equation [10.2]) based on the transformed data (e.g., a 300-mm cutthroat trout is predicted to weigh 287 g with the transformed equation and 289 g with the power function). In fact, equations (10.1) and (10.2) are the exact same model ($b_{equation\ [10.1]} = b_{equation\ [10.2]}$ and $a_{equation\ [10.1]} = 10^{a\ equation\ [10.2]}$). In our example, the coefficients have slightly different values and they provide slightly different predictions because the power function assumed homoscedastic error variances when, in reality, the larger fish had more variance in weight than did the smaller ones. Even with these similarities, interpretation and comparison among populations based on nonlinear regression is intuitively and statistically more difficult, and transformation to a linear equation is the preferred approach.

Often a primary question is whether differences in condition exist between or within specific populations or groups of fish across space and time. Comparisons of the regression coefficients associated with a given set of weight–length data can be used to determine whether a population (or group) of fish is significantly heavier and, by extension, in better condition at a given length. An interesting comparison might be whether Yellowstone cutthroat trout from a lake habitat are better conditioned than are stream-dwelling individuals found at similar elevations because a lake environment could be perceived as energetically favorable (e.g., no current or warmer). The estimated slope and intercept for the sample of transformed weight–length data from the stream population (A) are, respectively, 3.069 and –5.144 compared with 3.143 and –5.369 for the lake population (B). These equations suggest that average fish of 250 mm and 450 mm in length would weigh 164 g and 997 g, respectively, in the stream environment and 147 g and 933 g, respectively, in the lake environment. The regression results seem to indicate that stream fish are heavier at a given length than are their lake counterparts, at least in the sampled locations. However, in order to make meaningful statements regarding this relationship, we need to determine whether these populations are significantly different, given natural variation in weight at length.

Confidence intervals (CIs) around the estimated parameter (slope in this example) can be used as an initial assessment of differences in condition, if any, between populations. Using equation (10.2) (or the values provided by the SAS output) one can calculate the CIs around the parameter estimates. For example, the 95% CI around the estimated slopes (the actual parameter estimate is parenthetically enclosed) are 2.977–(3.069)–3.160 for stream fish and 2.934–(3.143)–3.352 for the lake population. These CIs overlap almost completely, and at least one interval encompasses the slope estimate of the other (in this case both intervals encompass the other slope estimate—the slope of the stream fish falls within the CI for the lake fish, and vice versa), indicating that the slopes are not significantly different, or that weight gain as the fish grows (body form) is similar between these two sites. Similar analyses show that the intercepts of these two populations are not significantly different. Thus we conclude that although the respective transformed equations predict different average weights, neither population is significantly heavier or better conditioned than is the other, contrary to our a prior expectation. If the CIs for the two slope estimates had not overlapped, it would have been an indication that the two values were indeed significantly different.

(Box continues)

Box 10.1   *(continued)*

A clearer comparison that provides a relevant level of precision, and one that must be performed if intervals overlap but neither one encloses the slope estimate of the other, is a CI around the difference between the slopes. For example suppose there are two populations with slopes 3.6 (SE = 0.2) and 3.0 (SE = 0.15). Based on a sample of 62 (60 df) individuals from each and a 95% confidence level, intervals for these slopes overlap but do not encompass the other slope estimate. The SE of the difference between these two slope values is

$$\sqrt{SE_1^2 + SE_2^2} = \sqrt{0.2^2 + 0.15^2} = 0.25,$$

and the CI for the difference is 0.6 ± 1.98(0.25), where 0.6 is the difference between the slopes of the two populations and 1.98 is the *t*-value for an $\alpha = 0.05$ with 120 df (equation [10.4]). This interval does not include zero, which is indicative of significantly different slopes. Completing this calculation for the Yellowstone cutthroat trout example above reveals that the CI around the differences in slopes (0.074 ± 2.013[0.113], based on 48 df) includes zero, which indicates that the slopes are not different (as was previously concluded).

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).

Differences in weight–length regression lines can be cursorily assessed by comparing confidence interval (CI) overlap around the coefficients generated by the regression analysis. However, more precise statistical contrast includes determining the CI around the difference between two like coefficients or conducting analysis of covariance (ANCOVA). A CI, or the range of values within which the

regression coefficient is likely to fall over $1 - \alpha$ percent of all samples from the population of interest, is calculated by

$$g \pm t_{(1 - \alpha/2;\, n - 2)} \bullet s(g), \tag{10.3}$$

where g is the coefficient estimate, $s(g)$ is the standard error of g, and t is the t-value for a given confidence level (α) and df ($n - 2$). A quick assessment, with no relevant statistical precision, is to calculate interval overlap. If CIs around two linear regression slopes (or some other coefficient) developed from independent samples do not overlap, then they are significantly different. Furthermore, if the CI from one slope encloses the estimated value of the other then the two are not significantly different. A comparison that does provide statistical precision, and one that is required if CIs overlap (but neither encloses the estimated slope of the other), is determination of whether the interval around the difference in slopes contains zero; if so, the difference between the two estimated coefficients is statistically nonsignificant. The interval around the difference in slopes is given by

$$(\mathrm{RS}_1 - \mathrm{RS}_2) \pm t_{(1 - \alpha/2;\, df)} \bullet \sqrt{\mathrm{SE}_1^2 + \mathrm{SE}_2^2}, \tag{10.4}$$

where RS_1 is the first regression slope, RS_2 is the second regression slope, SE_1 is the standard error of the first slope, and SE_2 is the standard error of the second slope. The df is equal to the sum of ($n_1 - 2$) and ($n_2 - 2$). Box 10.1 compares CIs of regression coefficients from samples of lake and stream Yellowstone cutthroat trout populations, where one might expect differences in population condition resulting from environmental influences. Interval analyses are relatively simplistic tests of regression line differences but are adequate for contrasting samples where sample size *(n)* and distribution (length categories of individuals captured) are similar, especially if the latter approach of testing the difference between co-efficients is employed, or for preliminary analyses for general discussion purposes (interval overlap comparison). When the size-ranges of fish captured become uneven (e.g., larger fish in one sample but not the other), a test such as ANCOVA (section 10.2.2) that controls for size differences across time or habitat is more appropriate.

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 regression 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., elevation) 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

$$W_i = \beta_0 + \beta_1 L_i + \beta_2 X_i + \beta_3 L_i X_i + \varepsilon_i, \qquad (10.5)$$

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.

10.2.3   Weight–Length Regression Line Residual Analyses

Most commonly weight–length regression coefficients are used to describe the relationship between length and weight or to compare differences in body form (condition) at a population level. However, Fechhelm et al. (1995) and Sutton et al. (2000) used magnitude and sign of the individual residuals as an indicator of fish condition (a larger negative residual indicated poorer relative condition) to summarize seasonal and sex-related patterns in condition. This type of analysis is synonymous with condition indices but can overcome some of the limitations associated with testing ratio data.

Box 10.2   Analysis of Covariance (ANCOVA)

The ANCOVA can be used to test for differences between regression parameters (i.e., slopes and intercepts) and is especially appropriate when the length ranges sampled in the populations to be compared are generally unequal. Here, the following SAS program provides results for both the complete (equation [10.5]) and reduced (equation [10.6]) models used to analyze differences in the log_{10} transformed weight–length regression equations from the low-elevation stream (A) and low-elevation lake (B) Yellowstone cutthroat trout populations presented in Box 10.1.

Program

```
OPTIONS PS=54 LS=75;
DATA TROUT;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
CARDS;
A   129    20
B   254    181
[Input complete data set];
PROC SORT; BY POP;
PROC GLM; CLASS POP; MODEL LOGWT=POP|LOGTL/SS3;
PROC GLM; CLASS POP; MODEL LOGWT=POP LOGTL/SS3 SOLUTION;
RUN;
```

Output

Table   The ANCOVA to test for slope differences ($n = 100$). The dependent variable is LOGWT for the two populations (POP).

Source	df	SS	Mean square	*F*-value	*P* > *F*
Model	3	19.83785325	6.61261775	3577.54	<0.0001
Error	96	0.17744331	0.00184837		
Corrected total	99	20.01529656			
R^2	0.991135	Root MSE	0.042993		
CV	1.852261	LOGWT mean	2.321090		

Source	df	Type III SS	Mean square	*F*-value	*P* > *F*
POP	1	0.00113727	0.00113727	0.62	0.4347
LOGTL	1	5.47809028	5.47809028	2963.74	<0.0001
LOGTL*POP	1	0.00078440	0.00078440	0.42	0.5163

Table   The ANCOVA to test for intercept differences. The dependent variable is LOGWT ($n = 100$).

Class Level Information		
Class	Levels	Values
POP	2	A B

Analysis of Covariance					
Source	df	SS	Mean square	F-value	P > F
Model	2	19.83706885	9.91853443	5398.14	<0.0001
Error	97	0.17822771	0.00183740		
Corrected total	99	20.01529656			
R^2	0.991095	Root MSE	0.042865		
CV	1.846757	LOGWT mean	2.321090		

Source	df	Type III SS	Mean square	F-value	P > F
POP	1	0.01778497	0.01778497	9.68	0.0024
LOGTL	1	10.20459461	10.20459461	5553.83	<0.0001

Parameter Estimates				
Variable	Estimate[a]	SE	t-value	P > |t|
Intercept	–5.209761011 z	0.10539178	–49.43	<0.0001
POP A	0.038319477 z	0.01231671	3.11	0.0024
POP B	0.000000000 z			
LOGTL	3.080368006	0.04133391	74.52	<0.0001

[a] The X'X matrix has been found to be singular, and a generalized inverse was used to solve the normal equations. Terms whose estimates are followed by the letter z are not uniquely estimable.

Interpretation
For modeling purposes, the dummy variable (treatment variable POP) value for each fish from the stream and lake samples was 1 and 0, respectively, and the interaction term was calculated as LOGTL times the dummy variable. Thus the interaction term is equal to LOGTL (dummy code * LOGTL) for stream fish and zero for the lake samples. The LOGWT was then regressed against all the independent variables in the complete model (dummy POP, covariate LOGTL, and interaction LOGTL*POP). Of interest is the significance of the interaction term, which indicates whether or not the slopes of the two populations, when controlling for length, are significantly different—in this case they are not (interaction $P = 0.516$). If the slopes had been different, we would have concluded that these two populations had different trends in weight (condition) relative to length (i.e., incremental weight gain for a given increase in length is different) and we would have stopped with our analysis. Further, if we had found a difference between slopes, it would be appropriate to model LOGWT as a function of POP and LOGTL(POP) (length nested in populations).

(Box continues)

Box 10.2 *(continued)*

Because the slopes were not different, we remove the interaction term from the model and regress LOGWT against the remaining independent variables (POP and LOGTL). In this example the adjustment for the dummy or treatment (POP) variable is significantly different from 0 ($P = 0.002$), and we conclude that the intercepts are different. Overall these results suggest that the two populations gain weight incrementally in a similar fashion, but trout in population A are consistently heavier at a given length than are trout in population B.

In the output from the reduced model (i.e., interaction term removed), the coefficient for the dummy variable (POP) is 0.0383. This value represents the magnitude of the difference in intercepts of the linear regressions for the transformed data. Because the lake sample was coded as 0, the population is represented by slope 3.080 for the parameter estimate for LOGTL and intercept −5.210 (see reduced model output), whereas the stream population is represented by slope 3.080 and intercept (−5.2097 + 0.0383) or −5.171.

The residualized weights are the error terms associated with equation (10.2) and can be calculated as the observed transformed weight of an individual fish minus the predicted transformed weight, or

$$e_i = \log_{10}(W_i) - \log_{10}(a) - b\log_{10}(L_i), \tag{10.7}$$

where e_i is the residual value and can be negative; W_i is the weight of fish i; L_i is the length of fish i; and a and b are the regression parameter values for the equation developed from the group of fish of interest (population).

Residual condition uses the weight–length relationship of a discrete, sampled population; thus inferences regarding any individual or group of individuals from that population are relative only to other individuals within the overall sample used to develop the weight–length regression. Larger-scale comparisons of population level residual condition variation would require a single equation developed from all populations under consideration, with the assumption that all individual population weight–length relationships have similar slopes (Jakob et al. 1996; Sutton et al. 2000).

Residual analysis is very similar to the condition indices discussed in the following section (10.3), and the two are often highly correlated, but Fechhelm et al. (1995) suggested that in some cases residuals can be normally distributed in data sets in which condition indices are not, or vice versa. Thus, this technique can provide parametric options that might not otherwise be available with condition indices. Patterson (1992) suggested that in comparing condition to other variables it is inappropriate to use the residuals from a weight–length regression as an index to condition because the residuals are not unbiased estimators of the underlying error of a regression model. Rather, a more complete regression model including all factors that might affect weight should be fitted prior to analyzing residuals (see equation [10.12]).

Raw or standardized residuals can be generated by most statistical software. For example, SAS (SAS Institute 1998) calculates residuals for regression analysis; these values are stored in the variable name RESIDUAL and can be treated like any other SAS variable. Adding the SAS command PLOT RESIDUAL*TL (within the regression procedure command [PROC REG]) to the weight–length regression exercise will produce a plot of residuals as a function of total length (TL); an evident trend in residuals may suggest a lack of fit of the regression model. The residuals can also be used as variables in other common statistical tests, such as mean comparisons, to assess condition level and trends.

■ 10.3   CONDITION INDICES

Condition indices are widely used to assess many facets of fish populations, including the general health of fish stocks, the effects of management actions, community structure, or environmental influences (Bolger and Connolly 1989; Ney 1993; Neumann and Willis 1995; Ward and Zimmerman 1999; Blackwell et al. 2000). Condition indices are intended to estimate physiological condition (e.g., lipid stores) indirectly based on the premise that a fish of a given species and length should weigh as much as a standard or average for its length, and variations from the standard are taken as an indication of the relative wellness of an individual. Measures of fish condition based on a standard weight have been available since the early 1900s and have undergone an evolution in methodology (Murphy et al. 1991) as well as rigorous reviews regarding their correlation with physiological parameters and statistical merit (e.g., Bolger and Connolly 1989; Patterson 1992; Blackwell et al. 2000; Vila-Gispert and Moreno-Amich 2001; Brenden et al. 2003). They remain popular tools because they are simplistic and noninvasive (only weight–length data needed) and are more easily compared than are the regression parameters in weight–length relationships. Murphy et al. (1990) indicated that an ideal condition index should be consistent, that is, maintain similar statistical properties and meaning across length and species; tractable, that is, analyzable by standard statistics; robust, that is, insensitive to data collection and analysis variations; and efficient, that is, provide precision from relatively small sample sizes. Anderson and Neumann (1996) and Blackwell et al. (2000) provided thorough reviews of the history of condition factors, and here we only briefly describe their history and development.

10.3.1   Fulton's Condition Factor

Traditionally, one of the ways to relate fish length to weight was simply to cube the length of the fish (Spencer 1898; Wootton 1990). However, this basic equation is imprecise because it fails to account for allometric growth (i.e., $b \neq 3$; equation [10.1]; Fulton 1904; Martin 1949). Nonetheless, this basic physical principle has been used extensively in fisheries science and is still used today (e.g., Ratz and Lloret 2003; Stone et al. 2003). For example, Fulton's condition factor (Anderson

and Neumann 1996) is calculated as the ratio between observed and expected weight for a fish of given length:

$$K = (W/L^3) \bullet 100{,}000, \qquad (10.8)$$

where W is the weight (g), L is length (mm), and 100,000 is a scaling constant. In application, body form changes with length ($b > 3$) and species ($b_1 \neq b_2$), which results in condition factors that are often length and species dependent (Murphy et al. 1991; Jakob et al. 1996; Blackwell et al. 2000). Thus K increases with increasing length, limiting its application to fish of similar length within the same species.

10.3.2   Relative Condition Factor

Le Cren (1951) attempted to solve the deficiencies of K by comparing the actual weight to a standard predicted by the weight–length regression based on the population from which the fish was sampled. Relative condition is calculated as

$$K_n = (W/W') \bullet 100, \qquad (10.9)$$

where W is individual fish weight and W' is the predicted length-specific weight based on $\log_{10}$ transformed data. Average fish of all lengths and species have an average K_n value of 100; however, because weight–length relationships can vary among populations and geographic sites, comparisons of K_n must be confined to those populations with homogenous weight–length parameters. Swingle and Shell (1971) indicated that K_n could be useful as an indicator of physiological stress on a population and expanded the concept by establishing species-specific weight–length relationships across a broader geographical range, which allowed comparisons of condition across populations. This broadened application of condition analyses from a population level to regional scale; however, regional differences still existed, making comparison and communication difficult.

10.3.3   Relative Weight

Relative weight (W_r) was proposed by Wege and Anderson (1978) as a condition analysis tool for largemouth bass and represents further evolution of the K_n concept by allowing comparisons of condition across the geographical occurrence of a species, as well as among species. The W_r index is calculated as

$$W_r = (W/W_s) \bullet 100, \qquad (10.10)$$

where W is individual fish weight and W_s is a length-specific standard weight predicted from a weight–length regression developed to represent the body form of the species across its geographical range (see Blackwell et al. 2000 for a list of developed standard weight equations). The W_r index uses 100 (or a range, 95–105) as a benchmark for a fish in good condition—a readily identifiable standard

for fisheries scientists. Fish greater than the target are considered in relatively better condition than a standard fish, whereas those less than the target are considered in worse condition with severity depending on the distance from the benchmark. For example, condition values exceeding 105 may indicate abundant prey and favorable environmental conditions (e.g., Marwitz and Hubert 1997; Porath and Peters 1997).

The estimation of a and b in the standard weight equation (note equation [10.2]),

$$\log_{10}(W_s) = a + b(\log_{10}L), \tag{10.11}$$

has undergone several iterations and review of statistical validity (see Anderson and Neumann 1996). The currently accepted technique for development of W_s equations is the 75th regression-line–percentile (RLP) technique proposed by Murphy et al. (1990), which has consistently provided W_s equations with little or no length-related biases, allowing for comparisons within and across species. Gerow et al. (2004), however, suggested this bias has been incorrectly assessed in the past and may be greater than originally reported for most standard W_s equations. Because standard weight equations are developed based on weight–length relationships across the range of the species, comparison and communications of condition analyses are consistent across the species range. Herein lays the value of W_r relative to other condition indices. Whereas a single W_s equation for each species has generally proven adequate, and is preferred for simplicity, differences in body forms between broad habitat types (e.g., lotic versus lentic habitats) has required maintaining multiple standard weight equations or target goals (i.e., something other than 100) for some species (e.g., burbot, Fisher et al. 1996; inland cutthroat trout, Kruse and Hubert 1997).

It is logical that both environmental and genetic factors influence body form and weight, and, by extension, condition as well. Furthermore, it is possible for an individual to increase energetic fitness without a change in body weight (Booth and Keast 1986). Thus, questions remain whether W_r, or any weight to length ratio, is both a valid and interpretable indicator of the physiological condition in fish or a metric sensitive and relevant enough to assess the effects of changed management or environment on fish condition. Numerous studies have investigated the practical limits in the application of W_r. Liao et al. (1995) and Gutreuter and Childress (1990) found W_r a weak indicator of growth, a relationship that seems intuitive based on the assumption that a fish in better condition can devote more energy to growth. Conversely, Brown and Murphy (1991) and Neumann and Murphy (1992) found W_r was correlated with fat composition in the body, an indication that W_r can be a relative measure of individual energy stores. Blackwell et al. (2000) provided excellent discussion regarding the relationships, or in some cases the lack thereof, between W_r and body composition, growth, and reproductive potential, among other things. Brenden et al. (2003) suggested that the lack of clear relationships in some studies attempting to relate W_r to variables that seem intuitively related to individual condition might be the result of an index

that, in most cases, does not satisfy the theoretical assumptions on which the statistical test is founded.

Most analyses of W_r are either mean comparisons among different populations or length categories (e.g., *t*-test, ANOVA, or nonparametric equivalents) or an assessment of the correlation and regression relationship among condition and other independent variables that might influence fitness (e.g., prey density as a good predictor of condition for a given population or size-class of fish). Sections 10.3.4 and 10.6 describe some of the common statistical procedures used to analyze and compare individual and population level condition as measured by an index.

10.3.4   Application and Common Statistical Analysis of Relative Weight

10.3.4.1   Statistical Analysis of Relative Weight Data

The application of W_r has increased over the last decade and is now commonly used as a condition assessment tool in the majority of the USA (Blackwell et al. 2000); thus, we focus our discussion of statistical analyses on W_r. The appropriateness of W_r, which is a ratio, as a variable in statistical testing has been the subject of several reviews. Numerous authors have recommended against the use of ratios to scale biological data because analyses of ratios may point to treatment effects that do not exist or they may fail to detect major differences that do exist (e.g., Tanner 1949; Atchley et al. 1976; Anderson and Lydic 1977; Atchley 1978; Atchley and Anderson 1978; Reist 1985; Packard and Boardman 1988). Bolgor and Connolly (1989) indicated that the potential for greater variability and nonnormal distributions of ratio data such as W_r might make parametric testing of W_r inappropriate. Furthermore, they indicated that ratio data commonly exhibit heteroscedasticity, skewness, and leptokurtosis (a taller distribution with fatter tails as compared with normal), all of which violate the assumptions of common statistical tests (e.g., regression and ANOVA) and weaken the power of these comparisons. Thus, Hyatt and Hubert (2001) concluded that normality for W_r data cannot be assumed and should be assessed before applying parametric tests. Murphy et al. (1990), when evaluating W_r frequencies in walleye populations, suggested that the use of parametric tests to compare differences in W_r data yields conservative results, which Blackwell et al. (2000) interpreted as a greater probability of type II error (failure to reject the null hypothesis when the alternative is true). Contrarily, Bolger and Connolly (1989) stated that while skewness has minimal effect on significance or power, significant leptokurtosis could lead to greater nominal significance values. Sokal and Rohlf (1981) indicated that a nonnormal distribution is only a minor violation of the assumptions for parametric statistics, thus parametric mean-comparison tests are generally robust to departures from normality. If there is concern over violation of assumptions for parametric tests, an alternative is to use a nonparametric test such as Wilcoxon's rank-sum test or Kruskal–Wallis test for comparison.

Patterson (1992) also recognized the problems of skewed distributions of ratios and suggested, as summarized in section 10.2.3, that it is inappropriate to use

weight–length regression residuals because they are biased estimators of regression error. Likewise, Jakob et al. (1996) noted that residuals from the residual index for condition are not comparable across populations. This is germane because individual values of W_r are essentially the de-transformed residuals. As a solution, Patterson (1992) proposed that all variables assumed to affect weight be directly included in the analyses at the same time as length and the coefficient of each parameter used to assess its effect on condition. For example, when testing for mean monthly differences in condition, include month as a variable in the model:

$$\log_{10}(W_i) = \beta(0) + \beta(m) + \beta_1[\log_{10}(L_i)] + e_i, \tag{10.12}$$

where $\beta(0)$ is the overall intercept and $\beta(m)$ are monthly adjustments to the overall intercept. Each parameter coefficient is used to measure the effect on fish condition. This is essentially an extension of the ANCOVA analysis.

More recently, based on a derivation of the statistical properties of the index, Brenden et al. (2003) argued that W_r data are not independent and identically distributed, as required by both parametric and nonparametric tests, because the properties are conditionally dependent on fish length. Conventional tests that assume independence and identical distributions increase the likelihood of a type I error (rejecting the null hypothesis when there is no difference) when applied to W_r data. To alleviate this risk, they proposed an R-test as the most appropriate and conservative way to test relative weight data (see Brenden et al. [2003] for a more thorough discussion). Of concern is the relative difficulty of computing the R-statistic and its associated significance value, especially when the improvement in testing power is moderate. The application of this recently proposed test is probably greatest for researchers attempting to make definitive conclusions regarding patterns in condition but of less utility for management decisions that might include condition as only one component in a decision-making process.

Given these arguments, it is apparent that care should be taken when statistically analyzing W_r values, and the data should be analyzed to ensure that the assumptions of a chosen statistical test are not violated or that the test is robust enough to handle a violation of the assumptions. Transformations to normalize W_r data and homogenize the variances (e.g., Box–Cox transformation; Box and Cox 1964) have generally proven to be of little value (Murphy et al. 1990; Brenden et al. 2003). Alternatively, nonparametric tests can be used if the data will result in misapplication of parametric tests. However, as mentioned, Brenden et al. (2003) argue that their R-test is the most appropriate for testing W_r data. Undoubtedly the statistical merit of W_r comparisons will continue to be debated, leading to a better understanding of the statistical properties of this index, as well as a clearer picture of the potential shortcomings and strengths of using established parametric and nonparametric tests and alternative tests for comparisons. We suggest that mean comparisons (t-test, ANOVA, Mann–Whitney, and Kruskal–Wallis) and regression relationships can continue to be adequate methods for testing W_r data, as long as the discussion of comparative results includes reference to the potential

shortcomings of the test in relation to the distribution of the data. Results likely can be clarified and strengthened by comparing the results of multiple tests.

10.3.4.2   *Length-Related Patterns in Relative Weight Data*

Because environmentally dependent trends in condition across lengths can be averaged out, mean population condition should not be compared unless it can be demonstrated that length-related patterns or differences are absent in the population. Plotting individual or length-group mean W_r values allows a visual assessment of potential or important patterns such as size-related condition trends resulting from, for example, differences in prey availability, gonad maturity, or density. Murphy et al. (1991) suggested that condition data should be summarized by length-group based on Gabelhouse's (1984) five-cell model (stock-, quality-, preferred-, memorable- and trophy-length fish); others have suggested that this model may not be ecologically relevant depending on the relationship being explored and have summarized W_r differently (e.g., 50-cm length-groups; Porath and Peters 1997). Once W_r values have been classified in a fashion relevant to the question of interest (note that this does not preclude the use of individual fish condition as the unit of interest), individuals or groups can be compared with each other to determine whether one is poorer conditioned than another or whether condition as measured by W_r (as the dependent variable) is statistically related to another variable or suite of variables, such as a habitat attribute. Box 10.3 provides examples of tests comparing W_r among multiple populations.

10.3.4.3   *Relationship of Relative Weight to Physiological and Environmental Measures*

As surrogate indicators of physiological well being, condition index values such as W_r should reflect proximate body composition of individual fish (e.g., lipid content, protein content, or caloric content; Murphy et al. 1991). Strange and Pelton (1987) found a weak relationship between mean condition factor *(K)* and fat percentage in composite samples of prey fishes. However, more recent physiological assessments of W_r have found correlations between W_r and tissue energy content in walleye (Rose 1989), white crappie (Neumann and Murphy 1991), and striped bass and hybrid striped bass (Brown and Murphy 1991). Brown and Murphy (1991) suggested that W_r provided a better estimate of reserve energy than did measures such as the liver–somatic index. Thus, W_r appears to be a reliable index of energy reserves in these species and, as such, might be a good indicator of short-term growth potential or potential for resistance to nutritional stress (Murphy et al. 1991). However, complications such as volume replacement of lipid (fat) reserves by water may confound the relationship between W_r and proximate components (Novinger and Martinez Del Rio 1999).

On the other hand, assessments of relationships between W_r and characteristics that would seem a logical expression of energy use, such as growth, which represents the ultimate expression of individual fitness (Bolger and Connolly 1989), have had mixed results. A common notion is that W_r and other condition indices can be used as indicators of growth: poor condition indicates poor growth and vice versa (e.g., Busacker et al. 1990; Ney 1993). Positive correlations between W_r

Box 10.3   Comparisons of Mean Relative Weight

Murphy et al. (1990) provided a formula for computation of the 95% CI around a mean relative weight ($\overline{W}_r$) value:

$$CI = \overline{W}_r \pm t \cdot (SD/\sqrt{n}), \tag{10.13}$$

where t is the t-value that corresponds to an α-value (usually 0.05) with $n - 1$ df and $\overline{W}_r$ is the mean measure of condition for a specific group (population). The overlap in CIs for mean values from different populations or length-groups can be compared to determine whether they are statistically similar or not. For example, a simple mean calculation for the stream population of Yellowstone cutthroat trout presented in Box 10.1 provides a $\overline{W}_r$ of 94.7 (SD = 9.47), whereas the low-elevation lake population has a $\overline{W}_r$ of 92.9 (SD = 8.45). Thus, the respective CIs would be 94.7 ± 2.69 and 92.9 ± 2.32. Both intervals include the mean value of the other population (see discussion in Box 10.1), indicating that individuals in these two populations are similarly conditioned, but this tells us little about whether there are length-specific differences between populations.

Mean comparison tests such as the two-sample t-test (or the nonparametric equivalent, Mann–Whitney test) or multiple-comparison tests such as ANOVA (or the nonparametric Kruskal–Wallis test) can be used to examine length-related or inter-population trends in W_r. Herein, we discuss how one might test for difference in condition, as indexed by W_r, among length-groups from the same population or among populations. For the Yellowstone cutthroat trout data presented in Box 10.1 the question of interest is whether macro-scale habitat type (stream versus lake and low versus high elevation) has any significant influence on fish condition.

Relative weights were calculated for the three populations described in Box 10.1 based on the lotic ($\log_{10}W_s = -5.189 + 3.099 \cdot \log_{10}[TL]$) and lentic ($\log_{10}W_s = -5.192 + 3.086 \cdot \log_{10}[TL]$) standard-weight equations for cutthroat trout (Kruse and Hubert 1997). An important first step is to assess the distribution of the W_r data to determine whether a parametric or nonparametric test is more appropriate. This can be completed with typical assessments of normality, such as a histogram or box-plot of the data (not shown). In this case, the data appears generally normal, but there is some skewness and outliers for all three populations. It is important to assess whether the outliers (or individuals with extreme values when compared to the mean) are biologically relevant or errors due to measurement or data entry. We retained the outliers in this assessment.

Prior to comparing overall population means, it is prudent to check for length-related patterns in condition within each population (Murphy et al. 1990, 1991; Blackwell et al. 2000). For example, changes in W_r with increasing length for cutthroat trout from the low-elevation stream population can be assessed by grouping cutthroat trout in 50-mm length categories (e.g., group one is 100–149-mm fish and group five is 300–349-mm fish plus the two largest fish). Another way to group the fish is to use the five-cell model (Gabelhouse 1984) for stock- to trophy-length fish (see cutthroat trout length categories in Anderson and Neumann [1996]). The following SAS program calculates W_r values for individual fish and assigns each fish to a length-group for testing differences in $\overline{W}_r$ among length-groups by means of ANOVA, a test that is robust to small departures from normality.

Box 10.3   *(continued)*

Program

```
OPTIONS PS=54 LS=75;
DATA TROUT;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.189+(3.099*LOGTL));
WR=(WT/WS)*100;
IF TL>99 AND TL<150 THEN GRP=1;
IF TL>149 AND TL<200 THEN GRP=2;
IF TL>199 AND TL<250 THEN GRP=3;
IF TL>249 AND TL<300 THEN GRP=4;
IF TL>299 THEN GRP=5;
CARDS;
A    129    20
A    130    25
[Input complete data set];
PROC ANOVA; CLASS GRP; MODEL WR=GRP;
RUN;
```

Output

Table   The ANOVA procedure for comparing differences in $\overline{W}_r$ among length-groups (GRP) in a population of low-elevation stream-dwelling Yellowstone cutthroat trout ($n = 50$).

Class Level Information					
Class	Levels		Values		
GRP	5		1 2 3 4 5		
Analysis of Variance					
Source	df	SS	Mean square	F-value	P > F
Model	4	254.915000	63.728750	0.69	0.6005
Error	45	4136.534097	91.922980		
Corrected total	49	4391.449097			
R^2	0.058048	Root MSE	9.587647		
CV	10.12727	$\overline{W}_r$	94.67155		
Source	df	SS	Mean square	F-value	P > F
Group	4	254.9150003	63.7287501	0.69	0.6005

Interpretation
It does appear, if one calculates the means of each 50-mm length-group, that there are some differences in condition. For example, 150–199-mm fish have an average W_r value of 97.5, whereas 200–249-mm fish average only 90.3. This might indicate that the smaller fish have a better prey base than do larger individuals who may be using another food source. However, given the variability in W_r values among individuals within each group, and the differences in sample sizes,

are these mean values significantly different? The test of equality of $\overline{W}_r$ values in each 50-mm length-group (i.e., no differences in means among groups would indicate no length-related patterns) is based on a comparison of two types of variability—within groups (variability of individuals in each category around the mean for that category) and between groups (variability of the mean of each category around the overall mean for the population). The *F*-test value reported in the SAS output is based on the ratio of the variability between groups to the variability within groups. Mean W_r values among length-groups were not different. Thus, there does not appear to be an environmental influence such as prey or habitat selection differentially influencing the condition of Yellowstone cutthroat trout in this population, at least on a length-dependent basis (based on the length-groups we selected). Thus, it may be appropriate to calculate a population-wide $\overline{W}_r$ value for this Yellowstone cutthroat trout population.

For comparison sake, and because the data were somewhat nonnormal, we also provide the SAS program and output for a Kruskal–Wallis test.

Program

```
OPTIONS PS=54 LS=75;
DATA TROUT;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.189+(3.099*LOGTL));
WR=(WT/WS)*100;
IF TL>99 AND TL<150 THEN GRP=1;
IF TL>149 AND TL<200 THEN GRP=2;
IF TL>199 AND TL<250 THEN GRP=3;
IF TL>249 AND TL<300 THEN GRP=4;
IF TL>299 THEN GRP=5;
CARDS;
A    129    20
A    130    25
[Input complete data set];
PROC NPAR1WAY WILCOXON; CLASS GRP; VAR WR;
RUN;
```

Output

Table   The NPAR1WAY procedure of SAS for Wilcoxon scores (rank sums) for the variable $\overline{W}_r$ classified by length-group.

Group	N	Sum of scores	Expected under H_0	SD under H_0	Mean score
1	11	314.0	280.50	42.699532	28.545455
2	10	307.0	255.00	41.231056	30.700000
3	8	142.0	204.00	37.788887	17.750000
4	14	342.0	357.00	46.281746	24.428571
5	7	170.0	178.50	35.766605	24.285714

(Box continues)

Box 10.3   *(continued)*

Kruskal–Wallis Test

Chi-square	4.1380
df	4
P > chi-square	0.3877

Interpretation
The Kruskal–Wallis test indicates similar results as the ANOVA. The mean ranks suggest that the 150–199-mm fish are slightly better conditioned than are the other length-categories, and the 200–249-mm fish are poorer conditioned; however, the test for differences among length categories is nonsignificant (*P* = 0.39).

Similar to the stream population, there were no length-related patterns in W_r in either of the two lake Yellowstone cutthroat trout populations (results not shown); thus, we can use an ANOVA to determine if there are any differences in fish condition among populations.

Program

```
OPTIONS PS=54 LS=75;
DATA TROUTA;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.189+(3.099*LOGTL));
WR=(WT/WS)*100;
CARDS;
A    129    20
A    130    25
[Input complete data set for population A];

DATA TROUTB;
INPUT POP $ TL WT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.192+(3.086*LOGTL));
WR=(WT/WS)*100;
CARDS;
B    254    181
B    262    186
[Input complete data set for populations B and C];

DATA TROUT; SET TROUTA TROUTB;
PROC SORT; BY POP;
PROC ANOVA; CLASS POP; MODEL WR=POP; MEANS POP;
RUN;
```

Output

Table   The ANOVA procedure to compare $\overline{W}_r$ for three populations of Yellowstone cutthroat trout ($n = 150$).

Class Level Information		
Class	Levels	Values
POP	3	A B C

Analysis of Variance				
Source	*df*	SS	Mean square	*F*-value	*P > F*
Model	2	276.39380	138.19690	1.75	0.1773
Error	147	11604.08875	78.93938		
Corrected total	149	11880.48255			
R^2	0.023265	Root MSE	8.884784		
CV	9.542586	$\overline{W}_r$	93.10667		

Source	*df*	SS	Mean square	*F*-value	*P > F*
POP	2	276.3938029	138.1969014	1.75	0.1773

Population Estimates			
		Relative weight	
Population	*N*	Mean	SD
A	50	94.6715459	9.46685852
B	50	93.2871930	8.45707184
C	50	91.3612615	8.69911855

Interpretation
Mean W_r values for Yellowstone cutthroat trout in the low-elevation stream population (A), the low-elevation lake (B), and the high-elevation lake (C) were 94.7, 93.3, and 91.4, respectively. Even though we might have expected differences either on an elevation gradient or by habitat type, there was no significant difference in $\overline{W}_r$ for these three populations ($P = 0.18$). Thus, on average an individual fish of a given length from these three populations appears to be similarly conditioned. A Kruskal–Wallis test on these data provides similar results ($P = 0.35$). It is important to note that this example included fish from only one of each habitat type; thus, it is inappropriate to conclude that Yellowstone cutthroat trout condition does not vary as a function of elevation or habitat type. To explore the relationship between condition and elevation or habitat type, a different design is needed (i.e., samples of fish are required from multiple low-elevation streams, low-elevation lakes, and high-elevation lakes) because individual water bodies would be the experimental unit of interest, not individual fish within a water body.

and growth have been reported for largemouth bass (Wege and Anderson 1978), northern pike (Willis 1989), yellow perch (Willis et al. 1991), and juvenile striped bass and hybrid striped bass (Brown and Murphy 1991). However, other evidence contradicts the notion that W_r is consistently correlated with growth (Gutreuter and Childress 1990; Gabelhouse 1991). Furthermore, Liao et al. (1995) found no evidence that growth and W_r were correlated for pumpkinseed or golden shiner. Relative weight may reflect growth of some species under certain circumstances, but uncritical use of W_r as a predictor of growth could lead to substantial errors in population assessments.

Another factor commonly linked with W_r is prey availability (Anderson and Gutreuter 1983; Busacker et al. 1990; Flickinger and Bulow 1993; Ney 1993). Poor condition is assumed to reflect prey scarcity, whereas good condition is assumed to reflect an abundance of prey, and both these patterns can be found among size-classes of fish within the same population. Kohler and Kelly (1991) indicated that a quick and cost-effective method for evaluating prey supply was to assess condition of their predators. Porath and Peters (1997) believed that walleye W_r values from standardized fall surveys offer a cost-effective method of detecting prey deficiencies in reservoirs. Small W_r values were reported for lake trout in oligotrophic Wyoming lakes with sparse zooplankton; larger W_r values were found for lake trout in two Wyoming mesotrophic lakes, and the largest W_r values were reported from Flaming Gorge Reservoir, the most productive reservoir in the study (Hubert et al. 1994). Prey availability and W_r values were correlated for pumpkin-seed but not for golden shiner; differences in these two species may be related to differences in food habits, with golden shiner having a more flexible and omnivorous diet (Liao et al. 1995). Relative weight may be a good predictor of prey availability especially for species with relatively narrow or specialized diets.

Most of these relationships have been examined through the use of group mean comparisons, bivariate correlations, or linear regression analyses. In Box 10.4 some of these common techniques are applied to the relationship between Yellowstone cutthroat trout W_r and whole-body fat composition.

■ 10.4 PHYSIOLOGICAL MEASURES OF CONDITION

Whereas condition indices attempt to approximate indirectly energetic well-being based on individual whole-body mass, other measures of condition relate directly to the physiological composition of body tissues, thereby providing a more precise measure of actual fitness in terms of stored energy. Physiological measures of condition have used either an index (ratio) of tissue weights or direct measures of tissues such as lipid or protein content. These include the liver–somatic index (hepatosomatic index or ratio of liver weight to body weight minus gonads), body water content, visceral–somatic index, percent composition of body tissues (e.g., percent lipid or fat), and RNA/DNA ratios (Elliott 1976; Heidinger and Crawford 1977; Jensen 1979; Bulow et al. 1981; Adams and McLean 1985; Håkanson 1989; Shackley et al. 1994). These types of measures are typically invasive, lethal, and more costly and time consuming than are indices based on weight–length

information, which has typically been the impetus for developing indexes such as W_r. Statistical procedures and limitations associated with the use of physiological measures of condition are similar to those described above for weight–length relationships and W_r. Physiological information summarized in ratio form (e.g., liver–somatic index) has the same problems of nonnormality, nonindependence, and heteroscedasticity as does W_r. Measures of tissues composition based on percentage body weight vary in synchrony (colinearity or highly related independent variables) by their very nature. For example, if the percentage of fat based on overall body weight increases, than the percentage of another tissue component (e.g., protein or water) must decrease because the total cannot exceed 100%.

Many fisheries scientists simply use these measures in a graphical form to describe the trend in fish condition as measured by tissue weight or composition over time. Others have used simple correlation analysis to relate one measure to another or to some environmental variable. Adams and McLean (1985) used the liver–somatic index as a variable in a regression analysis to predict largemouth bass growth, whereas Delahunty and de Vlaming (1980) determined the organ weight–body weight relationship of goldfish by means of linear regression, tested the seasonal variation of the relationship using ANCOVA, and used ANOVA to determine if lipid values varied by month (see Box 10.4).

■ 10.5 ADDITIONAL MORPHOMETRIC MEASURES OF CONDITION

Morphometric assessments of condition estimate individual fitness based on measurement of body form. Condition indices are a type of morphometric index that measure body form along a single axis, which is used to calculate an average or standard weight for a given length. Instead of the progression of condition indices from K to K_n to W_r, as described in section 10.3, Jones et al. (1999) proposed an alternative condition factor (B) based on two dimensions of fish body form, length and height, in association with weight (building on equation [10.8]) in an attempt to eliminate some of the length and species-related biases associated with Fulton's condition factor (K):

$$B = M/(H \bullet L^2), \tag{10.14}$$

where M is body mass or weight, H represents body height, and L is body length. The premise is that mass is related to body density and form in three dimensions (length, height, and thickness). Jones et al. (1999) suggested that the third dimension, thickness or girth, could be reasonably approximated by length (i.e., thickness is linearly related to length) and reduce regression variability while eliminating substantial handling and measurement time required to assess girth or thickness. Richter et al. (2000) argued that the assumption of a linear relationship between thickness and length was false in most cases and that the effects of allometric growth could be better minimized by the equation

$$B' = M/(H^2 \bullet L). \tag{10.15}$$

Box 10.4   Analysis of Fat Composition Data

In Box 10.3, we tested for differences in W_r within and among populations. Here we examine whether those W_r values are related to whole-body fat content in individual fish and then test whether population mean fat content differs among populations. Fat composition, a direct measure of individual wellness or energy stores, was estimated for the Yellowstone cutthroat trout sampled in stream and lake habitats (see Box 10.1 for data). We compared fat composition to W_r by means of correlation and regression analyses. The question of interest is whether W_r is a good indicator of individual physiological fitness as referenced by tissue fat content. Additionally, we want to know if using fat as the indicator of individual fitness results in a different conclusion regarding the population-level effects that elevation (a surrogate for environmental conditions such as temperature, growing season, and food supply) might have on fish condition. Please note that in this example we did not check for length-related biases (e.g., potential differences among length categories) within each population. The following SAS program regresses wet weight fat percentage against individual W_r (all populations combined into one data set) and compares mean percent fat composition among the three Yellowstone cutthroat trout populations by means of ANOVA.

Program

```
OPTIONS PS=54 LS=75;
DATA TROUTA;
INPUT POP $ TL WT FAT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.189+(3.099*LOGTL));
WR=(WT/WS)*100;
CARDS;
A    129    20    5.91
A    130    25    12.88
[Input complete data set for population A];
DATA TROUTB;
INPUT POP $ TL WT FAT;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
WS=10**(-5.192+(3.086*LOGTL));
WR=(WT/WS)*100;
CARDS;
B    254    181    10.59
B    262    186    9.08
[Input complete data set for populations B and C];
DATA TROUT; SET TROUTA TROUTB;
PROC SORT; BY POP;
PROC REG; MODEL FAT=WR;
PROC ANOVA; CLASS POP; MODEL FAT=POP; MEANS POP/TUKEY;
RUN;
```

Output

Table   Linear regression of wet weight fat percentage against individual W_r.

Analysis of Variance					
Source	*df*	SS	Mean square	*F*-value	*P* > F
Model	1	857.46498	857.46498	158.72	<0.0001
Error	148	799.53931	5.40229		
Corrected total	149	1657.00428			
r^2	0.5175	Root MSE	2.32428		
Adjusted r^2	0.5142	Dependent mean	6.57033		
CV	35.37542				

Parameter Estimates					
Variable	*df*	Parameter estimate	SE	*t*-value	*P* > |t|
Intercept	1	−18.44302	1.99447	−9.25	<0.0001
Relative weight	1	0.26865	0.02132	12.60	<0.0001

Interpretation

Fat composition and W_r are significantly correlated with each other ($r = 0.719$, $P < 0.001$) and the regression F-test ($P < 0.0001$) indicates that the slope (0.27) of the relationship between these variables is significantly greater than zero. Thus, it is apparent that W_r does reflect whole-body fat content (as a percentage of whole body weight) in individual fish to some degree. However, the coefficient of determination (r^2), or the proportion of the variability in percent fat explained by the linear relationship with W_r, is 0.52, suggesting only moderate explanatory power and providing evidence that other factors are influencing the weight and ultimately W_r of individual Yellowstone cutthroat trout.

Additional Output

Table   Comparison of percent fat among populations ($n = 150$). The Tukey's studentized range (HSD) test controls the type I experimentwise error rate, but it generally has a higher type II error rate than the Ryan–Einot–Gabriel–Welsch multiple-range test.

Class Level Information		
Class	Levels	Values
POP	3	A B C

Analysis of Variance					
Source	*df*	SS	Mean square	*F*-value	*P* > F
Model	2	414.859585	207.429793	24.55	<0.0001
Error	147	1242.144698	8.449964		
Corrected total	149	1657.004283			
R^2	0.250367	Root MSE	2.906882		
CV	44.24254	Fat mean	6.570333		

(Box continues)

Box 10.4   *(continued)*

Source	df	SS	Mean square	F-value	P > F
POP	2	414.8595853	207.4297927	24.55	<0.0001

Tukey's Studentized Range (HSD) Test for Fat

Alpha	0.05
Error *df*	147
Error mean square	8.449964
Critical value of studentized range	3.34848
Minimum significant difference	1.3765

Tukey grouping[a]	Mean fat	N	Population
A	8.8376	50	A
B	5.9782	50	B
B	4.8952	50	C

[a] Means with the same letter are not significantly different.

Interpretation
When comparing percent fat scores among populations, the *F*-test for the ANOVA was significant (*P* < 0.0001), indicating that at least one of the populations had significantly different overall mean percent fat. However, the ANOVA does not provide information regarding which or how many populations are significantly different; thus, a post hoc multiple-comparisons test is needed. There are several post hoc multiple comparisons that can be used to determine which group mean(s) are statistically different, such as Tukey's studentized range test, Duncan's multiple-range test, least significant differences, and Scheffé's statistic. Carmer and Swanson (1973) provide a good decision tree regarding which multiple-comparison test is most appropriate.

In this case, we used Tukey's test to determine which populations were different. The Tukey's grouping shows that Yellowstone cutthroat trout in both lake populations (B and C) had significantly lower percent body fat than did Yellowstone cutthroat trout in the low-elevation stream population (A). Further, percent body fat for Yellowstone cutthroat trout in the two lakes are not significantly different from each other (either there are no real differences or there was enough uncertainty or variance in the percent fat values that the multiple-comparison test could not differentiate B from C). These results seem different than those of the similar ANOVA we ran in Box 10.3, which indicated that mean population condition as measured by W_r was not statistically different among populations. However, we must remember that W_r estimates were calculated using different W_s equations, which were designed to account for general body-form differences between cutthroat trout in lotic and lentic systems. Even so, there is some question, as illustrated by both the linear regression relationship between W_r and fat in this example and the ANOVA in the previous example (Box 10.3), as to whether W_r provides a true reflection of fish condition in these Yellowstone cutthroat trout populations, at least as measured by fat reserves in the body.

Both B and B' provide improvement over K when comparing the regression relationship between actual body mass and the body mass back-calculated from the condition factors (Jones et al. 1999; Richter et al. 2000). These are an appropriate modification to the condition factor concept, allowing broader condition comparisons across size ranges and populations, especially for those species for which W_s equations have not been developed. Statistical tests similar to those discussed for condition indices in section 10.3 can be applied to B or B' to provide rigorous comparisons.

Similarly, measurements of body form dimensions other than length, such as distances between anatomical landmarks, can be used in lieu of weight to assess condition. This approach may be especially useful when individual measurements of weight are highly imprecise, such as with small fish. Box 10.5 describes an example of condition assessment in juvenile largemouth bass based on body depth (height) and length in an ANCOVA. The use of one or two anatomical distances to assess condition is a simplistic form of truss analysis.

Truss analysis has been in use for several decades (Humphries et al. 1981; Strauss and Bookstein 1982) but primarily for morphometric comparisons of differences in body form among different types or stocks of fish. This type of analysis involves systematic measurement between multiple pairs of landmarks across the body in order to differentiate body shapes computationally. These measurements, often based on discrete juxtapositions such as fin insertion points (Fitzgerald et al. 2002), form polygons across the body, which give rise to the term truss analysis. Fitzgerald et al. (2002) applied truss analysis to quantify changes in fish condition by using a 10-point truss system to assess the effect of differing feed rations. Eigenvector coefficients from principle component analysis (PCA), a multivariate data reduction technique, were successful in demonstrating that key truss measurements change as condition changes and can be used to describe differences in body form between groups of better- and lesser-conditioned fish. The PCA approach is a common analytical tool for truss comparisons (Toline and Baker 1993; Moore and Bronte 2001).

Truss analysis can be used to compare the condition of fish among groups (populations), habitats, or sampling time. Fitzgerald et al. (2002) argued that although truss measurements may currently be more time and cost consuming than traditional condition indices, they provide a much clearer picture of the effect condition, or lack thereof, has on body form and allow for precise comparisons over time. Truss comparisons may prove to be more ecologically, morphologically, genetically, and physiologically revealing than are more popular and traditional numerical constructs of fish condition. As digital imaging techniques and computer analytical software continue to evolve and advance, truss analysis likely will become a common technique for analyzing fish condition.

■ 10.6   FACTORS AFFECTING CONDITION DATA

Seasonal changes occur in fish condition due to changes in fish behavior and physiology that are influenced by many factors (e.g., changes in temperature,

Box 10.5   Morphological Assessment of Juvenile Condition

The following data are used to assess effects of starvation on body condition of largemouth bass juveniles. For most fishes, standard condition indices (e.g., W_r) are applicable to only adults and large juveniles because weight measurements are imprecise for small fish. A controlled experiment was conducted to determine if simple morphological measurements could be used to determine condition of juvenile largemouth bass (partial data set from Smith et al. [2005]). Hatchery-reared largemouth bass were raised until completion of fin development and then divided into two experimental groups of fed and unfed fish. Differences in body morphology existed after only 3 d of food deprivation, and a simple bivariate ratio of body depth at the anus to standard length was almost as efficient and robust at classifying fed and unfed largemouth bass as a multivariate index based on 23 morphometric characters. Here we provide an assessment of differences in the body depth after 6 d of food deprivation.

Table   Standard length (SL; mm) and body depth (BD; mm) of juvenile largemouth bass. Fed largemouth bass were provided brine shrimp; unfed largemouth bass were deprived food for 6 d.

Fed		Unfed	
SL	BD	SL	BD
9.237	1.706	11.934	2.427
9.267	1.730	10.482	2.164
9.500	1.895	10.605	1.907
9.291	1.811	10.604	1.903
9.291	1.814	13.024	2.811
12.296	2.680	12.215	2.390
12.575	2.585	12.660	2.324
12.296	2.388	12.984	2.419
12.707	2.495	11.047	1.875
11.329	2.328	11.853	2.259
12.659	2.489	11.531	2.296
9.842	2.148	12.136	2.390
10.237	1.981	11.651	2.196
8.818	1.791	11.167	2.032
8.500	1.707	12.216	2.358
10.105	2.129	12.054	2.229
11.344	2.530	12.821	2.290
8.053	1.454	12.581	2.194
8.474	1.621	11.653	1.969
9.503	2.105	12.342	2.196
10.422	2.127	11.540	2.103
9.212	1.961	13.638	2.583
10.848	2.425	11.168	1.872
8.369	1.537	11.490	2.003
10.925	2.316	11.651	1.907
12.448	2.674	11.697	2.097

Program

The following SAS program tests for differences among the body depth of fed and unfed large-mouth bass by means of ANCOVA to remove the confounding effect of fish size.

```
OPTIONS PS=54 LS=75;
DATA LMB;INPUT FOOD $ SL BD @@;CARDS;
F    9.237   1.706      U11.9342.427
F    9.267   1.730      U10.4822.164
[Input complete data set];
PROC SORT; BY FOOD;
PROC GLM; CLASS FOOD; MODEL BD=FOOD|SL/SS3;PROC GLM; CLASS FOOD; MODEL
BD=FOOD SL/SS3 SOLUTION;RUN;
```

Output

Table   An ANCOVA to test for slope differences in body depth (BD) of fed and unfed fish ($n = 52$).

Source	df	SS	Mean square	*F*-value	*P* > *F*
Model	3	4.06177300	1.35392433	73.52	<0.0001
Error	48	0.88395183	0.01841566		
Corrected total	51	4.94572483			
R^2	0.821270	Root MSE	0.135704		
CV	6.321951	BD mean	2.146558		

Source	df	Type III SS	Mean square	*F*-value	*P* > *F*
FOOD	1	0.00498644	0.00498644	0.27	0.6052
SL	1	2.64331777	2.64331777	143.54	<0.0001
SL*FOOD	1	0.00007687	0.00007687	0.00	0.9488

Table   An ANCOVA to test for intercept differences in BD of fed and unfed fish ($n = 52$).

Class Level Information		
Class	**Levels**	**Values**
Food	2	F U

Analysis of Variance					
Source	**df**	**SS**	**Mean square**	**F-value**	**P > F**
Model	2	4.06169612	2.03084806	112.57	<0.0001
Error	49	0.88402870	0.01804140		
Corrected total	51	4.94572483			
R^2	0.821254	Root MSE	0.134318		
CV	6.257381	BD mean	2.146558		

(Box continues)

Box 10.5   *(continued)*

Source	df	Type III SS	Mean square	*F*-value	*P* > *F*
FOOD	1	0.61792239	0.61792239	34.25	<0.0001
SL	1	3.91445980	3.91445980	216.97	<0.0001

Parameter Estimates

Variable	Estimate[a]	SE	*t*-value	*P* > |*t*|
Intercept	−0.5671680765 z	0.18968254	−2.99	0.0044
FOOD-FED	0.2627719497 z	0.04490009	5.85	<0.0001
FOOD-UNFED	0.0000000000 z			
SL	0.2330097751	0.01581879	14.73	<0.0001

[a] The X′X matrix has been found to be singular, and a generalized inverse was used to solve the normal equations. Terms whose estimates are followed by the letter z are not uniquely estimable.

Interpretation
Differences existed in the body depth between fed and unfed largemouth bass (slopes were not different [*P* = 0.95]; intercepts were different [*P* < 0.0001]; see discussion in Box 10.2), with greater body depth for fed fish (see figure below). Thus, body morphology is related to nutritional status in juvenile largemouth bass. Therefore, distances between anatomical landmarks or trusses (see Strauss and Bookstein [1982] for a discussion of trusses) may be used in some instances to quantify fish condition. This approach may be especially useful for assessing condition of larval and juvenile fishes; however, careful consideration must be given to ontogenetic stage, size, and species (Suthers 1992; Ferron and Leggett 1994). In addition, changes in fish condition in response to changes in food availability is likely greatest at intermediate abundances of prey (Ferron and Leggett 1994). That is, no change in condition will occur with an increase in prey abundance if a larval fish is already consuming the biological maximum amount of food (i.e., food intake is limited by handling and digestion). Likewise, little change in condition is expected for a starved larval fish that is provided a small amount of food, especially if the fish is near the threshold for irreversible starvation (also called the point-of-no-return). Thus, our statistical ability to detect differences in fish condition will vary as a function of food abundance and period of assessment.

turbidity, food supplies, and photoperiod; Pope and Willis 1996). Condition is a short-term indicator of fish health status and is primarily influenced by resource availability and gonadal growth. Typically with spring spawners, fish condition is greatest in the spring just before spawning, declines immediately after spawning, and then increases through the summer and into the fall. Obviously, the seasonal trend in condition for fish species that spawn in the summer (e.g., bluegill) or fall (e.g., brook and brown trout) should be different than spring spawners. Furthermore, differences in gonadal development between males and females may show gender differences in seasonal condition trends. Finally, fish size may also affect the seasonal trend in fish condition (see Pope and Willis 1996 for detailed examples of related studies). Le Cren (1951) noted that seasonal changes in condition of mature fish are often due to changes in gonad weight. However,
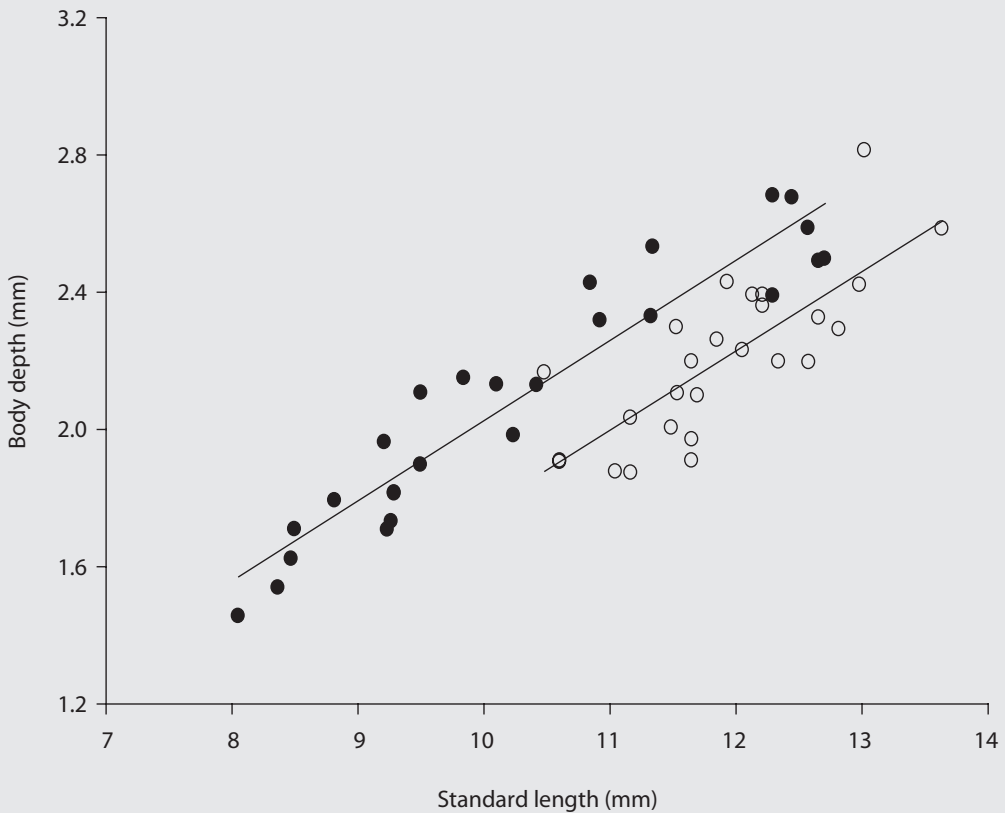
Figure   Body depth (mm) as a function of size (standard length; mm) for fed (solid circles) and unfed (open circles) juvenile largemouth bass.

seasonal changes in the condition of immature fish may be attributable to feeding conditions throughout the winter and spring. For example, Brown (1993) reported that smaller (125–300-mm TL) largemouth bass in Aquilla Lake, Texas, came out of the winter with a low W_r (i.e., 85), and condition remained low until late spring–early summer, when W_r increased (i.e., 105). Gabelhouse (1991) found that small white crappies (130–199-mm TL) in Melvern Reservoir, Kansas, exhibited the greatest W_r in July and that W_r continued to decline throughout the fall and winter. He speculated that the summer peak condition of small white crappies reflected the feeding conditions associated with peak spawning of gizzard shad in mid to late May. Thus, it is inappropriate to combine condition data across seasons. Furthermore, condition data should be reported separately for mature and immature fish and may need to be separated by gender for mature individuals. Generally, W_s

equations are reported for combined sexes; however, Neumann and Willis (1994) provided separate W_s equations for male and female muskellunge (slopes of these two equations were different).

Although general seasonal trends in condition of fish are observed, more specific spatial and temporal patterns of variation in W_r also exist. For example, Liao et al. (1995) observed spatial and temporal differences among lakes for pumpkinseed and golden shiner. Temporal variations in condition have been reported for black crappie (Gabelhouse 1991; Guy and Willis 1991), burbot (Pulliainen and Korhonen 1990), northern pike (Guy and Willis 1991), walleye (Guy and Willis 1991), and yellow perch (Le Cren 1951; Guy and Willis 1991). Many of these studies have resulted in the common practice of sampling during "standard" periods for assessing condition of fishes. However, the temporal asynchrony of pumpkinseed and golden shiner W_r suggests that standard sampling periods might not be as comparable among lakes or among years as previously believed (Liao et al. 1995). This temporal asynchrony illustrates some of the biotic and abiotic variability that fisheries scientists must deal with when assessing fisheries.

Fisheries scientists primarily use condition assessments as a measure of the quality of fish populations, ideally with respect to local environmental and climatic conditions and species potential, and as a means of measuring changes in population quality resulting from management practices (Childress 1991). Thus, comparisons of condition are made on many different scales. Comparisons can be made within populations to assess differences across length-groups or to conduct spatiotemporal comparisons. Theoretically, data on the condition of various sizes of fish within a population can be accumulated over many years to establish a norm for a specific water body. Any deviation from the norm would indicate some fluctuation within the population or some physical or chemical condition interacting with a segment of the population (Swingle and Shell 1971). Comparisons can also be made among populations to evaluate temporal and spatial differences or to evaluate influences of factors (such as parasites) that affect portions of populations (in effect, creating two populations: a population of affected individuals and a population of unaffected individuals; Box 10.6). Prentice (1987) used ANCOVA to test differences in species-specific weight–length relations among river systems and ecological regions within the state of Texas. He found differences among river systems and ecological regions for all species assessed. He also found differences between genders for many of the species he assessed. If a common currency is used to assess condition (such as W_r), comparisons can also be made among species. Condition indices can also indicate changes in environment and ecological processes (e.g., Gabelhouse 1991; Hubert et al. 1994; Liao et al. 1995). Finally, condition assessments are often important in manipulative studies to determine if treatments affect condition.

■ 10.7 CONCLUSION

Condition data have been and will continue to be an important component of ecological assessment in aquatic systems. When combined with other information

Box 10.6   Use of Fulton's Condition to Assess the Effects of Parasites

Parasites may negatively affect the condition of fish. Here we determine if condition of Arkansas River shiners (29–60 mm TL) is reduced when fish are parasitized by anchor worm, a cosmopolitan cyclopoid copepod. Arkansas River shiners were captured with a seine (see Hayes et al. [1996] for a discussion of this gear), measured (TL; mm), weighed (0.1 g), and inspected to determine the presence of the parasite (partial data set from Durham et al. 2002). Differences in condition among fish with and without the parasite were assessed using ANOVA to test differences in Fulton's condition (K), an appropriate assessment metric as the fish are from a single population over identical size ranges. Individual fish from this experiment were treated as the experimental unit because our research question asked if differences in condition existed between two populations of Arkansas River shiners (population PRESENT contained parasites and population ABSENT contained no parasites).

Table   Total length (TL; mm) and weight (WT; g) of Arkansas River shiners with and without anchor worm.

With parasite				Without parasite			
TL	WT	TL	WT	TL	WT	TL	WT
29	0.210	46	0.707	29	0.175	45	0.654
29	0.187	46	0.656	31	0.254	45	0.710
34	0.286	47	0.810	31	0.228	46	0.757
35	0.356	48	0.813	31	0.201	46	0.828
38	0.420	48	0.697	31	0.219	47	0.788
38	0.460	48	0.624	32	0.269	47	0.833
39	0.448	49	0.962	33	0.278	48	0.940
39	0.252	49	0.778	35	0.356	49	0.986
40	0.514	51	1.136	36	0.356	51	1.097
42	0.555	52	1.216	39	0.478	51	1.105
43	0.412	53	0.903	39	0.505	51	1.063
44	0.589	53	1.388	40	0.505	52	1.158
44	0.664	55	0.996	40	0.604	52	1.273
45	0.739	56	1.065	41	0.535	57	1.573
45	0.646	60	1.081	43	0.610	60	1.686

Program
The following SAS program provides output to compute length and weight summary statistics. Differences in condition were tested using ANOVA to test differences in Fulton's condition (K).

```
OPTIONS PS=54 LS=75;
PROC FORMAT;
VALUE PARACODE 0='ABSENT' 1='PRESENT';
DATA PARASITE;
INPUT TL WT PARASITE @@;
LOGTL=LOG10(TL);
LOGWT=LOG10(WT);
K=(WT/(TL*TL*TL))*100000;
FORMAT PARASITE PARACODE.;
CARDS;
```

(Box continues)

Box 10.6   *(continued)*

```
29   0.21    1   290.175 0
29   0.187   1   310.254 0
[Input complete data set];
PROC SORT; BY PARASITE;
PROC MEANS MEAN STDERR; BY PARASITE; VAR TL WT K;
PROC REG; BY PARASITE; MODEL LOGWT=LOGTL;
PROC ANOVA; CLASS PARASITE; MODEL TL=PARASITE;
PROC ANOVA; CLASS PARASITE; MODEL WT=PARASITE;
PROC ANOVA; CLASS PARASITE; MODEL K=PARASITE;
RUN;
```

Output

Table   Descriptive statistics.

Variable	Parasite absent		Parasite present	
	Mean	SE	Mean	SE
TL	42.6000000	1.5585139	44.8333333	1.3838837
WT	0.7008000	0.0747452	0.6857133	0.0566121
K	0.8020460	0.0102421	0.7195553	0.0220817

Table   Regression analysis of $\log_{10}$ transformed weight (LOGWT) on $\log_{10}$ transformed length (LOGTL) in the absence of parasite.

Analysis of Variance					
Source	*df*	SS	Mean square	*F*-value	*P* > *F*
Model	1	2.27177	2.27177	2782.11	<0.0001
Error	28	0.02286	0.00081656		
Corrected total	29	2.29463			
r^2	0.9900	Root MSE	0.02858		
Adjusted r^2	0.9897	Dependent mean	−0.23476		
CV	−12.17232				

Parameter Estimates				
Variable	*df*	Parameter estimate	SE	*t*-value	*P* > |*t*|
Intercept	1	−5.30889	0.09634	−55.11	<0.0001
LOGTL	1	3.13084	0.05936	52.75	<0.0001

Table Regression analysis of LOGWT on LOGTL in the presence of parasite.

Analysis of Variance					
Source	df	SS	Mean square	F-value	P > F
Model	1	1.29852	1.29852	215.29	<0.0001
Error	28	0.16888	0.00603		
Corrected total	29	1.46740			
r^2	0.8849	Root MSE	0.07766		
Adjusted r^2	0.8808	Dependent mean	−0.21406		
CV	−36.28050				

Parameter Estimates					
Variable	df	Parameter estimate	SE	t-value	P > |t|
Intercept	1	−4.69465	0.30570	−15.36	<0.0001
LOGTL	1	2.72350	0.18562	14.67	<0.0001

Table An ANOVA to test for differences in TL, WT, and K in the presence versus absence of the parasite ($n = 60$).

Class Level Information		
Class	Levels	Values
PARASITE	2	ABSENT PRESENT

ANOVA for Total Length					
Source	df	SS	Mean square	F-value	P > F
Model	1	74.816667	74.816667	1.15	0.2884
Error	58	3779.366667	65.161494		
Corrected total	59	3854.183333			
R^2	0.019412	Root MSE	8.072267		
CV	18.46496	TL mean	43.71667		

Source	df	SS	Mean square	F-value	P > F
Parasite	1	74.81666667	74.81666667	1.15	0.2884

(Box continues)

Box 10.6   *(continued)*

ANOVA for Weight

Source	df	SS	Mean square	*F*-value	*P* > *F*
Model	1	0.00341411	0.00341411	0.03	0.8727
Error	58	7.64884655	0.13187666		
Corrected total	59	7.65226067			
R^2	0.000446	Root MSE	0.363148		
CV	52.38295	WT mean	0.693257		

Source	df	SS	Mean square	*F*-value	*P* > *F*
Parasite	1	0.00341411	0.00341411	0.03	0.8727

ANOVA for *K*

Source	df	SS	Mean square	*F*-value	*P* > *F*
Model	1	0.10207080	0.10207080	11.48	0.0013
Error	58	0.51547644	0.00888752		
Corrected total	59	0.61754724			
R^2	0.165284	Root MSE	0.094274		
CV	12.39138	*K* mean	0.760801		

Source	df	SS	Mean square	*F*-value	*P* > *F*
Parasite	1	0.10207080	0.10207080	11.48	0.0013

Interpretation

Mean ± SE TL, WT, and *K* values for Arkansas River shiners (20–60 mm TL) not parasitized were 42.6 ± 1.6, 0.70 ± 0.07, and 0.80 ± 0.01, respectively. Mean ± SE total TL, WT, and *K* values for Arkansas River shiners (20–60 mm TL) parasitized by anchor worm were 44.8 ± 1.4, 0.69 ± 0.06, and 0.72 ± 0.02, respectively. When analyzed separately (ANOVA), no differences were found in length ($P = 0.29$) or weight ($P = 0.87$) of Arkansas River shiners with and without anchor worm ($P > 0.28$). However, differences ($P = 0.001$) were noted when *K* was assessed. Thus, it appears that parasitism by anchor worm causes condition to decrease in Arkansas River shiners. Note that visual examination of data (see figure below) suggests that about one-third of Arkansas River shiners parasitized by anchor worm have suppressed condition values, suggesting to us that about one-third of the Arkansas River shiners collected with anchor worm had been parasitized for a relatively long period (long enough to decrease condition), whereas the other two-thirds had been recently parasitized. This interpretation is not possible from the statistical assessment and illustrates the need to examine data visually.
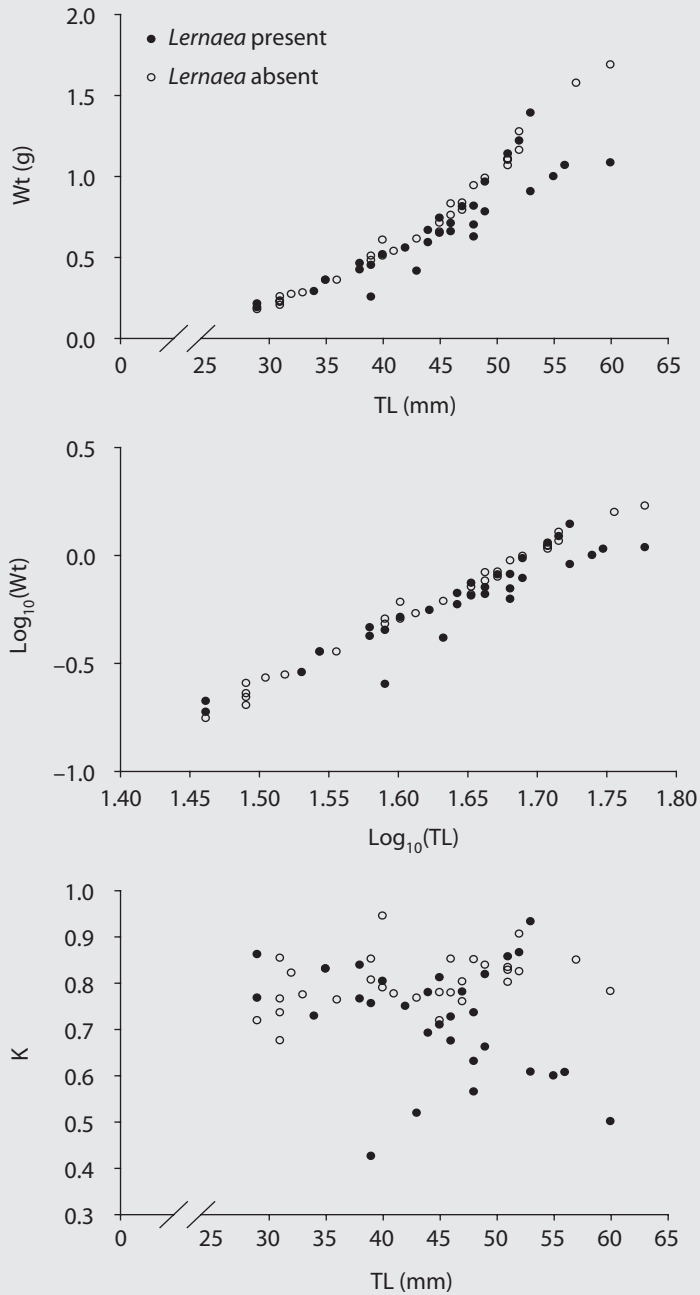
Figure   Graphical depiction of relationship between weight and length (top panel), $\log_{10}$ transformed weight and $\log_{10}$ transformed length (middle panel), and Fulton's condition (*K*) and length (bottom panel) for Arkansas River shiners with and without anchor worm *Lernaea cyprinacea.*

(e.g., density, prey availability, size structure, community composition, and exploitation), condition data provide fisheries scientists a more complete understanding of population dynamics (recruitment, growth, and mortality) and environmental influences. Several techniques have been used to assess fish condition, and it is clear that there is much debate regarding the most appropriate way to analyze and present condition data, mostly centered on statistical shortcomings of analysis techniques. Appropriately, analytical techniques continue to evolve, as demonstrated by the most recent critique of W_r provided by Brenden et al. (2003).

Because of the relative ease of computation and use, the popularity of condition indices will continue to increase. Condition indices offer fisheries scientists a tool to evaluate effects of various management strategies and, indirectly, ecological interactions in fish populations and communities (Murphy and Willis 1991). More research is necessary to determine both the statistical appropriateness and relativity (to proximate factors and other expressions of fitness) of the condition measure. However, it is apparent that condition indices are useful for assessing fish condition (Blackwell et al. 2000).

Given the limitations discussed herein, controversy about assessment of condition will likely continue as fisheries scientists attempt to separate effects of fish condition from effects of fish size. Detailed assessments of various measures of fish condition that are tested with multiple statistical analyses will provide a clearer picture of relationships among measures of condition and help clarify the usefulness and shortcomings of various techniques. In the meantime, morphometric assessments of condition can be assessed appropriately using graphical display of data in a bivariate plot and ANCOVA with length as a covariate. Further, ratios can be used for descriptive purposes.

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