fishR Vignette - Fish Condition and Relative Weights

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Condition is a measure of the physical health of a population of fish based on the fish's relative plumpness or fatness. Most often condition is computed by comparing the actual weight of a fish to some expectation of weight based on the length of the fish. In other words, measuring the condition of a particular fish is an exercise in determining if it weighs more or less than would be expected based on its length. An overall measure of condition for an entire population is obtained by averaging the condition of all fish in a sample.

The utility of measuring fish conditions was summarized by Blackwell *et al.* (2000) in the following manner:

> Fish condition can be extremely important to fisheries managers. Plump fish may be indicators of favorable environmental conditions (e.g., habitat conditions, ample prey availability), whereas thin fish may indicate less favorable environmental conditions. Thus, being able to monitor fish well-being can be extremely useful for fisheries biologists who must make management recommendations concerning fish populations.

There are at least eight metrics of condition (Bolger and Connolly 1989) of which three are commonly used by fisheries managers (Blackwell *et al.* 2000). These three measures are introduced in Section 1 and discussed within the context of four properties that should be evident in all condition metrics (Murphy *et al.* 1990). Those four properties are (1) consistency – similar statistical properties and meaning regardless of species or length; (2) tractability – analysis by standard statistical methods; (3) efficiency – relative precision from small samples; and (4) robustness – relative insensitivity to variations in the way the data was collected and analyzed. The relative weight metric will then be examined in more detail in Section 2.

This vignette requires functions in the `FSA` and `FSAdata` package maintained by the author. In addition, the `multcomp` package is needed for computing multiple comparisons in Section 3 and the `plotrix` package is needed for plotting confidence intervals in Section 3. These packages are loaded into R with

```
> library(FSA)
> library(FSAdata)
> library(multcomp)   # for glht() and mcp()
> library(plotrix)    # for plotCI()
```

1 Measures of Condition

1.1 Fulton's Condition Factor

Fulton's condition factor is calculated with

$$K = \frac{W}{L^3} * constant$$

where the constant is simply a scaling factor that is equal to 100000 if metric units are used (i.e., grams and millimeters) or 10000 if English units are used (i.e., pounds and inches)[1]. Fulton's condition factor *assumes isometric growth*[2]. If a fish stock does not exhibit isometric growth, which is often the case, then K tends to differ depending on the length of the fish, violating the consistency property. Furthermore, comparing K between species is problematic because both species would need to exhibit isometric growth for the comparison to be valid. Because of these limitations, Fulton's condition factor should be avoided.

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[1] These constants are used so that the values of K are not extremely small fractions.
[2] See the length-weight vignette for a brief discussion of isometric and allometric growth.

1.2 LeCren's Relative Condition Factor

The relative condition factor, introduced by Le Cren (1951), is calculated with

$$Kn = \frac{W}{W'}$$

where W' is the predicted length-specific mean weight for the population under study (Blackwell *et al.* 2000). The average Kn across all lengths and species is 1.0 (Anderson and Neumann 1996). Thus, Kn is consistent across lengths. Bolger and Connolly (1989), however, show that Kn comparisons are restricted to species or regions that have the same slope (b) in the length-weight relationship. Thus, W' is generally predicted from length-weight equations developed for a population (perhaps from several years of data) or for a region.

1.3 Relative Weight

The relative weight, introduced by Wege and Anderson (1978), is calculated with

$$Wr = \frac{W}{Ws} * 100 \tag{1}$$

where Ws is a "standard weight" for fish of the same length. In simplistic terms, a standard weight equation for a particular species is a length-weight relationship designed to predict the 75th percentile[3] mean weight for a given value of length[4]. Standard weight equations have been developed for a wide variety of species[5]. It should be noted that the standard weight equations have been developed for either metric or English unit measurements but that the log_{10} rather than the log_e transformation is used[6]. Blackwell *et al.* (2000) suggest that regional or population-specific Ws equations should NOT be developed. If regional or population-specific analysis is desired then Kn should be used.

Recent trends, following the work of Gerow *et al.* (2005), have resulted in standard weight equations that are quadratic rather than linear. Examples of the use of quadratic standard weight equations can be found in Ogle and Winfield (2009) and Cooney and Kwak (2010). While use of these types of standard weight equations is not illustrated in this vignette, their use is a simple and straightforward modification of what is demonstrated here.

The relative weight measure has become the most popular measure of condition (Blackwell *et al.* 2000). This popularity is partly due to the fact that relative weight summaries have been used as a surrogate measure of the general "health" of the fish (Brown and Murphy 1991; Neumann and Murphy 1992; Jonas *et al.* 1996; Brown and Murphy 2004; Kaufman *et al.* 2007; Rennie and Verdon 2008; but also see Copeland *et al.* 2008) as well as the environment (Liao *et al.* 1995; Blackwell *et al.* 2000; Rennie and Verdon 2008). Thus, relative weight summaries may be used as an indirect means for evaluating ecological relationships and the effects of management strategies (Murphy *et al.* 1991; Blackwell *et al.* 2000). In addition, Murphy *et al.* (1990) found the distributions of Wr values to typically be symmetric (but not normal). Because t-tests and analysis of variance tests are relatively robust to departures from normality, as long as the distribution is symmetric, typical parametric inferential statistics can be used with Wr values.

It should be noted, though, that Gerow (Gerow *et al.* (2004), Gerow *et al.* (2005), and Gerow (2010)) has been critical of the idea that traditionally developed standard weight equations produce relative weight values that are not dependent on the length of the fish.

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[3] However, see Ogle and Winfield (2009) for an equation that uses the 50th percentile in addition to the 75th percentile.

[4] Specific discussion of methods for computing the standard weight equations are discussed in detail in Murphy *et al.* (1990) and Blackwell *et al.* (2000)

[5] In R, examine the `data(WSlit)` data frame for all known equations

[6] This is in contrast to what is shown in the length-weight vignette.

2 Relative Weights in R

Throughout this vignette, the total length (in) and weight (g) data from Bluegill (*Lepomis macrochirus*) sampled in two years from a small catch-and-release lake in northern Wisconsin will be examined. These data (along with other data) can be found in the `InchLake2` data frame in the `FSAdata` package. The entire data frame is loaded into R and the structure and the first six rows of data are viewed with

```
> data(InchLake2)
> str(InchLake2)

'data.frame': 516 obs. of  6 variables:
 $ netID  : int  206 205 205 205 205 205 205 205 205 205 ...
 $ fishID : int  501 502 503 504 505 506 507 508 509 510 ...
 $ species: Factor w/ 9 levels "Black Crappie",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ length : num  1.5 1.7 2.2 2.1 1.5 1.9 1.9 1.4 1.2 1.4 ...
 $ weight : num  0.7 1.4 1.5 1.4 1 1.8 1.4 0.6 0.3 0.8 ...
 $ year   : int  2008 2008 2008 2008 2008 2008 2008 2008 2008 2008 ...

> head(InchLake2)

  netID fishID  species length weight year
1   206    501 Bluegill    1.5    0.7 2008
2   205    502 Bluegill    1.7    1.4 2008
3   205    503 Bluegill    2.2    1.5 2008
4   205    504 Bluegill    2.1    1.4 2008
5   205    505 Bluegill    1.5    1.0 2008
6   205    506 Bluegill    1.9    1.8 2008
```

As the types of units for the length (inches) and weight (grams) measurements do not match, either the lengths need to be converted to mm or the weights converted to pounds. Below, the length measurements are converted to the nearest whole mm and stored into a new variable

```
> InchLake2$lenmm <- round(InchLake2$length*25.4,0)
> head(InchLake2)

  netID fishID  species length weight year lenmm
1   206    501 Bluegill    1.5    0.7 2008    38
2   205    502 Bluegill    1.7    1.4 2008    43
3   205    503 Bluegill    2.2    1.5 2008    56
4   205    504 Bluegill    2.1    1.4 2008    53
5   205    505 Bluegill    1.5    1.0 2008    38
6   205    506 Bluegill    1.9    1.8 2008    48
```

The Bluegill data from 2007 are isolated with

```
> bg <- Subset(InchLake2,year==2007 & species=="Bluegill")
> str(bg)

'data.frame': 109 obs. of  7 variables:
 $ netID  : int  17 20 15 15 15 16 16 16 16 16 ...
 $ fishID : int  199 201 203 206 207 210 211 212 213 214 ...
 $ species: Factor w/ 1 level "Bluegill": 1 1 1 1 1 1 1 1 1 1 ...
 $ length : num  5.6 5.5 5.6 5.8 4.7 9 8.8 8.8 8.8 5.9 ...
 $ weight : num  59 54 40 30 20 280 260 260 240 60 ...
 $ year   : int  2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
 $ lenmm  : num  142 140 142 147 119 229 224 224 224 150 ...
```

Note, from the data frame structure, that the number of observations in `bg` is reduced from the original data frame and that *species* has only one level – the level of the species of interest.

2.1 "Manually" Computing Wr

Computing relative weights is a two-step process. First, the standard weight for each fish's observed length is computed by substituting each fish's observed length into the species-specific standard weight equation. Second, the relative weights are computed by dividing each fish's observed weight by it's calculated standard weight.

The coefficients for all known standard weight equations can be efficiently found with `wsVal()`. This function requires the desired species name, in quotes and spelled correctly[7], as the first argument and the desired units of measurement in `units=` (either `"metric"` for use with mm and grams or `"English"` for use with inches and pounds). Some standard weight equations have been developed for other than the 75th percentile (usually the 50th or, occasionally, also the 25th percentile). The default is to return values for the 75th percentile but this can be altered by including a value for another percentile in `ref=`. It should be noted that equations have not been developed for all species in both types of units and for other than 75th percentile reference points. If you ask for a species in a situation (units and reference combination) in which the standard weight equation does not exist, then an error will be produced by `wsVal()`.

The standard weight equation information for Bluegill is found and stored into an object called `bg.eqn` with[8]

```
> ( bg.eqn <- wsVal("Bluegill",units="metric") )
    species  units    type ref    int slope quad min.len max.len measure method
20 Bluegill metric linear  75 -5.374 3.316   NA      80      NA      TL  Other
   comment        source
20    none Hillman, 1982
```

Note that the results will indicate if the standard weight equation is of the linear or quadratic form (in *type*), what the minimum (and occasionally maximum) length (in *min.len* as mm) over which the equation should be applied, and which length measurement is applicable (in *measure* and nearly always total length (TL)).

As the standard weight equation is only valid for Bluegill of at least 80 mm, the `bg` data frame was reduced to only those fish larger than 80 mm with

```
> bg80 <- Subset(bg,lenmm>=bg.eqn$min.len)
```

A column of standard weights for each fish in the data frame is then constructed by predicting the $log_{10}(Ws)$ from the observed $log_{10}(L)$ with the provided equation coefficients and by "back-transforming" these to the observed scale by raising the result to the power of 10. This is accomplished with

```
> bg80$ws <- 10^(bg.eqn$int+bg.eqn$slope*log10(bg80$lenmm))
```

The relative weights are then calculated and appended to the data frame using (1) with

```
> bg80$wr <- (bg80$weight/bg80$ws)*100
```

The modified data frame now consists of the original data frame with new columns containing the standard and relative weights appended. The first six rows of this data frame are seen with

```
> head(bg80)
   netID fishID  species length weight year lenmm    ws    wr
48    17     199 Bluegill    5.6     59 2007   142 57.94 101.83
```

---

[7]Note that part of spelling correctly here means that only the first word in compound named species is capitalized.

[8]The "extra" parentheses around the second line simply forces R to print the results of the object at the time of assigning.

```
50    20    201 Bluegill    5.5     54 2007    140  55.28  97.69
52    15    203 Bluegill    5.6     40 2007    142  57.94  69.04
55    15    206 Bluegill    5.8     30 2007    147  64.99  46.16
56    15    207 Bluegill    4.7     20 2007    119  32.25  62.02
59    16    210 Bluegill    9.0    280 2007    229 282.63  99.07
```

2.2 Convenience Functions

The `wrAdd()` can be used to efficiently add the standard weight and relative weight columns to a data frame for a given species. This function requires a formula of the form `weight~length` as the first argument with a corresponding data frame in `data=` and the species being examined in `species=`, the appropriate measurement units in `units=`, and the chosen reference value in `ref=` as described for `wsVal()`. In addition, use `remove.submin=` to either completely remove (`=TRUE`) individuals below the minimum recommended length for application of the standard weight equation or simply have `NA` placed in the standard and relatve weight variables (`=FALSE`; default) for these individuals. For example, the standard and relative weights are added to the `bg` data frame with

```
> bg2 <- wrAdd(weight~lenmm,data=bg,species="Bluegill",units="metric",remove.submin=TRUE)
> head(bg2)
   netID fishID  species length weight year lenmm     ws     wr
48    17    199 Bluegill    5.6     59 2007    142  57.94 101.83
50    20    201 Bluegill    5.5     54 2007    140  55.28  97.69
52    15    203 Bluegill    5.6     40 2007    142  57.94  69.04
55    15    206 Bluegill    5.8     30 2007    147  64.99  46.16
56    15    207 Bluegill    4.7     20 2007    119  32.25  62.02
59    16    210 Bluegill    9.0    280 2007    229 282.63  99.07
```

Finally, a fisheries scientist is often faced with the task of computing the Wr values for a wide variety of species across a variety of groups (e.g., species, years, gear, lakes). This process is made more efficient by using `wrDataPrep()` to create the Ws and Wr variables at one time for all species in a data frame for which the standard weight equations have been defined. As might be expected, `wrDataPrep()` has some limitations. First, only equations for the 75th percentile will be allowed (as these are the vast majority of Ws equations). Second, the species names in the original data frame must be spelled exactly as they appear in the `WSlit` data frame[9]. For example, the species names in the original `InchLake2` data frame are not in the correct format (largely, the second names are capitalized)

```
> levels(InchLake2$species)

[1] "Black Crappie"     "Bluegill"          "Bluntnose Minnow" "Fathead Minnow"
[5] "Iowa Darter"       "Largemouth Bass"  "Pumpkinseed"       "Tadpole Madtom"
[9] "Yellow Perch"
```

The `recodeSpecies()` can be used to convert species names. This function is flexible but in its simplest form it will simply "re-capitalize" the names to match the required form. More complicated examples are illustrated in the `recodeSpecies()` help. A simple conversion for the `InchLake2` data frame is completed with (note that the new variable name is the same as the old variable name but with a "1" appended)

```
> InchLake2 <- recodeSpecies(~species,data=InchLake2)
> levels(InchLake2$species1)

[1] "Black Crappie"     "Bluegill"          "Bluntnose Minnow" "Fathead Minnow"
[5] "Iowa Darter"       "Largemouth Bass"  "Pumpkinseed"       "Tadpole Madtom"
[9] "Yellow Perch"
```

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[9]Primarily full common names with the first letter capitalized only on the first name for species with compound names

The `wrDataPrep()` requires three arguments – a formula of the form `weight~length+species` in the first argument, the data frame in `data=`, and the units of measurement in `units=`. Species for which no standard weight equation is known can be eliminated from the resulting data frame with `remove.other=TRUE`. Individuals that are below the minimum length for which the standard weight quation does not apply can be removed with `remove.submin=TRUE`. Removing the species without a known standard weight equation or those individual below the minimum length is not a requirement but it will speed-up the process and make the resulting tables less cluttered. The `InchLake2` data frame can be appended with the length categorization variable with

```
> InchLake2 <- wrDataPrep(weight~lenmm+species1,data=InchLake2,units="metric",
                          remove.other=TRUE,remove.submin=TRUE)
Warning:  The following species do not have known standard weight equations:
Bluntnose Minnow, Fathead Minnow, Iowa Darter, Tadpole Madtom
> head(InchLake2)
   netID fishID       species length weight year lenmm       species1    ws    wr
31   101    532 Black Crappie   12.6    508 2008   320 Black Crappie 577.7 87.93
33   101    534 Black Crappie   12.0    443 2008   305 Black Crappie 492.0 90.04
34   101    535 Black Crappie   12.1    440 2008   307 Black Crappie 502.9 87.49
36   101    537 Black Crappie   11.3    379 2008   287 Black Crappie 401.4 94.41
57    16    208 Black Crappie   11.6    380 2007   295 Black Crappie 440.1 86.34
58    16    209 Black Crappie   10.8    260 2007   274 Black Crappie 343.8 75.63
```

The data could then be subsetted and summarized as described more thoroughly in Section 3. For example, the following illustrates how to compute the mean Wr for each species and year combination

```
> Summarize(wr~year*species,data=InchLake2,digits=1)
Warning:  To continue, variable(s) on RHS of formula were converted to a factor.
    year          species  n   mean   sd   min    Q1 median    Q3   max percZero
1   2007    Black Crappie  6   87.2  6.7  75.6  86.6   87.4  89.8  96.0        0
2   2008    Black Crappie 19   91.2  5.6  82.5  86.9   91.7  94.5 105.0        0
3   2007         Bluegill 83   88.7 13.0  46.2  85.0   91.4  97.0 117.0        0
4   2008         Bluegill 77   83.5 12.5  42.8  80.8   86.5  90.4 101.0        0
5   2007 Largemouth Bass  1   80.9   NA  80.9  80.9   80.9  80.9  80.9        0
6   2008 Largemouth Bass 86   83.9  8.0  63.1  80.0   83.9  87.6 133.0        0
7   2007      Pumpkinseed 11   94.1 24.4  43.4  83.0  100.0 111.0 127.0        0
8   2008      Pumpkinseed  1  107.7   NA 108.0 108.0  108.0 108.0 108.0        0
9   2007     Yellow Perch 12   68.5  8.5  60.1  63.6   66.2  69.7  90.8        0
10  2008     Yellow Perch 14   72.9  4.6  65.4  70.2   72.2  76.5  81.9        0
```

3 Follow-up Analyses and Interpretation

3.1 Comparisons Among Length Categories

A measure of overall condition using Wr should not be computed without first determining if the Wr values differ across fish lengths (Blackwell *et al.* 2000). In particular, Murphy *et al.* (1991) suggested that Wr values should first be summarized within the usual five-cell length categories of Gabelhouse (1984) [10]. Use of the five-cell model can be problematic at times because of small sample sizes in the larger length categories. Thus, other authors have summarized by 25- or 50-mm length categories. The mean Wr values in the length categories are then tested with analysis of variance methods to determine if differences exist among the length categories. Adjacent length categories that are statistically equal can then be pooled together. If no statistical differences among categories exist, then all length categories can be pooled and an overall measure

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[10]The five-cell length categorization scheme of Gabelhouse (1984) was defined in the size structure vignette

of condition for the population can be computed. Relative weights should be reported as whole numbers (Blackwell *et al.* 2000).

A new variable containing the five-cell length categories is appended to the `InchLake2` data frame using `pssDataPrep()` which has largely the same arguments as `wsDataPrep()` with the exception that the formula is of the form `length~species` and the `units=` is set to `"mm"`, `"cm"`, or `"in"`, respectively. For example,

```
> InchLake2 <- pssDataPrep(lenmm~species1,data=InchLake2,units="mm")
> head(InchLake2)
   netID fishID       species length weight year lenmm     species1    ws    wr
31   101    532 Black Crappie   12.6    508 2008   320 Black Crappie 577.7 87.93
33   101    534 Black Crappie   12.0    443 2008   305 Black Crappie 492.0 90.04
34   101    535 Black Crappie   12.1    440 2008   307 Black Crappie 502.9 87.49
36   101    537 Black Crappie   11.3    379 2008   287 Black Crappie 401.4 94.41
57    16    208 Black Crappie   11.6    380 2007   295 Black Crappie 440.1 86.34
58    16    209 Black Crappie   10.8    260 2007   274 Black Crappie 343.8 75.63
     PSScat
31 memorable
33 memorable
34 memorable
36 preferred
57 preferred
58 preferred
```

As an illustration, the differences among length categories for Bluegill captured in 2007 were examined by first extracting this group of fish

```
> bg07 <- Subset(InchLake2, species=="Bluegill" & year==2007)
```

One-way analysis of variance is then used to determine if significant differences in mean Wr exist among the length categories. The one-way ANOVA is fit and the ANOVA table is extracted with

```
> lm1 <- lm(wr~PSScat,data=bg07)
> anova(lm1)
Analysis of Variance Table

Response: wr
          Df Sum Sq Mean Sq F value  Pr(>F)
PSScat     2   3088    1544    11.6 3.9e-05
Residuals 80  10681     134
```

These results show that there is a significant difference in mean Wr value among the length categories ($p < 0.005$). Tukey's multiple comparisons are constructed as shown below.

```
> mc1 <- glht(lm1,mcp(PSScat="Tukey"))
> summary(mc1)

 Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = wr ~ PSScat, data = bg07)
```

```
Linear Hypotheses:
                        Estimate Std. Error t value Pr(>|t|)
preferred - stock == 0     16.67       3.53    4.73   <0.001
quality - stock == 0       10.37       3.07    3.38   0.0032
quality - preferred == 0   -6.29       3.11   -2.02   0.1133
(Adjusted p values reported -- single-step method)
```

These results suggest that the mean Wr is significantly less for stock-size fish than quality- or preferred-size fish which have statistically equal means. A plot of the fitted means with significance letters (Figure 1) is constructed with

```
> nd <- expand.grid(PSScat=levels(bg07$PSScat))
> mm <- model.matrix(~PSScat,data=nd)
> nd <- within(nd,{
   lvlnum <- as.numeric(PSScat)
   Pred <- predict(lm1,nd)
   SE <- sqrt(diag(mm %*% vcov(lm1) %*% t(mm)))
   LCI <- Pred-1.96*SE
   UCI <- Pred+1.96*SE
   }
 )
> with(nd,plotCI(lvlnum,Pred,ui=UCI,li=LCI,pch=16,xaxt="n",ylim=c(75,103),
             xlab="Length Category",ylab="Mean Relative Weight"))
> with(nd,axis(1,at=lvlnum,labels=PSScat))
> with(nd,text(x=lvlnum,y=UCI,labels=c("a","b","b"),pos=3))
```
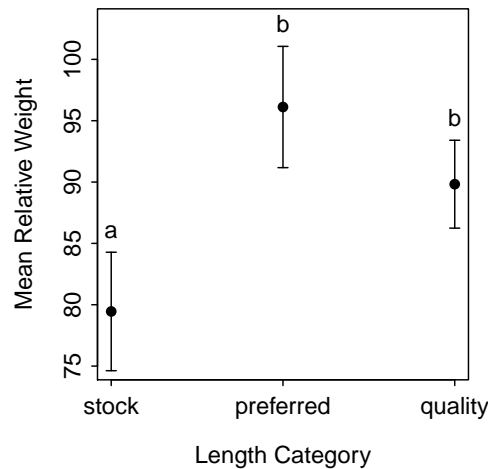

Figure 1. Mean relative weight of Inch Lake Bluegill captured in 2007 by length category.

The relatively small values of Wr (i.e., much less than 100) for stock-sized fish suggests that Bluegill between 3 and 6 inches in Inch Lake in 2007 were relatively skinny fish. Bluegills larger than 6 inches were very near the standard size.

3.2   Comparisons Among Years

The relative weight of Bluegill in Inch Lake was compared between years (2007 and 2008) to determine if the condition of Bluegill had changed between those two years. Analysis for 2007 (see above) suggested that

relative weight differed significantly among lenght categories. Thus, these data are best analyzed with a two-way ANOVA.

The Bluegills were isolated and a factored year variable created with

```
> bg <- Subset(InchLake2,species=="Bluegill")
> bg$fyear <- factor(bg$year)
> str(bg)
'data.frame': 160 obs. of  12 variables:
 $ netID   : int  101 101 101 101 101 101 101 101 101 101 ...
 $ fishID  : int  533 538 539 540 541 542 543 544 545 546 ...
 $ species : Factor w/ 1 level "Bluegill": 1 1 1 1 1 1 1 1 1 1 ...
 $ length  : num  8.4 8.5 8.5 9.1 7.6 8.9 6.4 8.8 7 7.1 ...
 $ weight  : num  190 198 210 258 138 236 75 229 101 110 ...
 $ year    : int  2008 2008 2008 2008 2008 2008 2008 2008 2008 2008 ...
 $ lenmm   : num  213 216 216 231 193 226 163 224 178 180 ...
 $ species1: Factor w/ 1 level "Bluegill": 1 1 1 1 1 1 1 1 1 1 ...
 $ ws      : num  222 233 233 291 160 ...
 $ wr      : num  85.5 85 90.2 88.7 86.1 ...
 $ PSScat  : Factor w/ 3 levels "stock","preferred",..: 2 2 2 2 3 2 3 2 3 3 ...
 $ fyear   : Factor w/ 2 levels "2007","2008": 2 2 2 2 2 2 2 2 2 2 ...
```

A two-way ANOVA to compare the mean relative weight between the two years and among the length categories is conducted with

```
> lm2 <- lm(wr~fyear*PSScat,data=bg)
> anova(lm2)
Analysis of Variance Table

Response: wr
             Df Sum Sq Mean Sq F value  Pr(>F)
fyear         1   1076    1076    8.88  0.0034
PSScat        2   6999    3500   28.86 2.3e-11
fyear:PSScat  2     66      33    0.27  0.7626
Residuals   154  18673     121
```

These results suggest that there is not a significant interaction between capture year and length category. Thus, a model without the interaction is fit and multiple comparisons are constructed for each factor.

```
> lm2a <- lm(wr~fyear+PSScat,data=bg)
> mc2y <- glht(lm2a,mcp(fyear="Tukey"))
> summary(mc2y)


 Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = wr ~ fyear + PSScat, data = bg)

Linear Hypotheses:
                Estimate Std. Error t value Pr(>|t|)
2008 - 2007 == 0    -5.33       1.74   -3.06   0.0026
(Adjusted p values reported -- single-step method)
```

```
> mc2l <- glht(lm2a,mcp(PSScat="Tukey"))
> summary(mc2l)


 Simultaneous Tests for General Linear Hypotheses


Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = wr ~ fyear + PSScat, data = bg)

Linear Hypotheses:
                      Estimate Std. Error t value Pr(>|t|)
preferred - stock == 0    17.19       2.31    7.43   <1e-04
quality - stock == 0      11.79       2.11    5.58   <1e-04
quality - preferred == 0  -5.40       2.09   -2.59    0.028
(Adjusted p values reported -- single-step method)
```

These results suggest that the mean Wr is signficantly lower in 2008 for all length categories and that the mean Wr increases progressively from stock- to quality- to preferred-size Bluegill within each year.

```
> nd <- expand.grid(fyear=levels(bg$fyear),PSScat=levels(bg$PSScat))
> mm <- model.matrix(~PSScat*fyear,data=nd)
> nd <- within(nd,{
    lvlnum <- as.numeric(PSScat)
    Pred <- predict(lm2,nd)
    SE <- sqrt(diag(mm %*% vcov(lm2) %*% t(mm)))
    LCI <- Pred-1.96*SE
    UCI <- Pred+1.96*SE
    }
 )
> with(Subset(nd,fyear==2007),plotCI(lvlnum-0.05,Pred,ui=UCI,li=LCI,pch=16,xaxt="n",
               xlim=c(0.9,3.1),ylim=c(67,102),
               xlab="Length Category",ylab="Mean Relative Weight"))
> with(Subset(nd,fyear==2008),plotCI(lvlnum+0.05,Pred,ui=UCI,li=LCI,pch=16,col="blue",add=TRUE))
> with(nd,axis(1,at=lvlnum,labels=PSScat))
> legend("topleft",levels(nd$fyear),pch=16,col=c("black","blue"),bty="n")
```
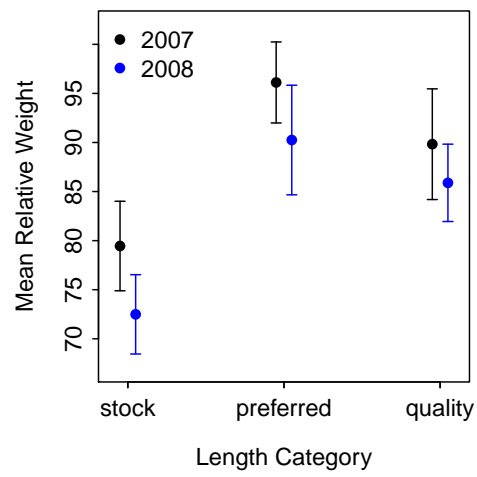
Figure 2. Mean relative weight of Inch Lake Bluegill by length category and capture year.

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Reproducibility Information

Version Information

- **Compiled Date:** Mon Dec 16 2013
- **Compiled Time:** 9:15:01 PM
- **Code Execution Time:** 3.24 s

R Information

- **R Version:** R version 3.0.2 (2013-09-25)
- **System:** Windows, i386-w64-mingw32/i386 (32-bit)
- **Base Packages:** base, datasets, graphics, grDevices, methods, splines, stats, utils
- **Other Packages:** FSA_0.4.3, FSAdata_0.1.4, gdata_2.13.2, knitr_1.5.15, multcomp_1.3-1, mvtnorm_0.9-9996, plotrix_3.5-2, survival_2.37-4, TH.data_1.0-2
- **Loaded-Only Packages:** bitops_1.0-6, car_2.0-19, caTools_1.16, cluster_1.14.4, evaluate_0.5.1, formatR_0.10, Formula_1.1-1, gplots_2.12.1, grid_3.0.2, gtools_3.1.1, highr_0.3, Hmisc_3.13-0, KernSmooth_2.23-10, lattice_0.20-24, MASS_7.3-29, nlme_3.1-113, nnet_7.3-7, quantreg_5.05, sandwich_2.3-0, sciplot_1.1-0, SparseM_1.03, stringr_0.6.2, tools_3.0.2, zoo_1.7-10
- **Required Packages:** FSA, FSAdata, multcomp, plotrix and their dependencies (car, gdata, gplots, graphics, Hmisc, knitr, mvtnorm, nlme, quantreg, sandwich, sciplot, stats, survival, TH.data)