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STREAM FISH SAMPLING: ABUNDANCE VERSUS BIOMASS MEASUREMENTS AND DETERMINING A MINIMUM NUMBER OF YEARS TO SAMPLE

by

SARAH B. VIED

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STREAM FISH SAMPLING: ABUNDANCE VERSUS BIOMASS MEASUREMENTS AND DETERMINING A MINIMUM NUMBER OF YEARS TO SAMPLE

by

SARAH B. VIED

Under the Direction of Doug McElroy

ABSTRACT

Abundance and biomass are commonly used for estimating stream fish assemblage and community structure, yet questions arise whether one measurement contains more information about an assemblage and how long sampling should be. Principal component loadings derived from fish biomass measurements taken from Buck Creek in Allen County Kentucky were statistically compared to corresponding measures of abundance to test for significant differences in the two data sets. A sliding window analysis based on abundance was used to determine the minimum number of years a stream should be sampled. Abundance and biomass were not found to be significantly different; correlations of the first three component loadings among data sets were highly significant. A six-year minimum for consecutive sampling years to estimate the total result of the eight-year study was found through subsampling of the abundance data, however, this number should not be thought of as a standard to use in all studies.

INDEX WORDS: Abundance, Biomass, Stream fish sampling, Long-term sampling, Sliding window, PCA

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May 2009

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TABLE OF CONTENTS

ACKNOWLEDGEMENTS v

LIST OF FIGURES vii

CHAPTER

1 INTRODUCTION 1

2 METHODS AND MATERIALS 4

Principal Component Analysis (PCA) 4

Sliding Window Analysis 4

3 RESULTS 6

Principal Component Analysis 6

Sliding Window Analysis 7

4 DISCUSSION 10

Abundance vs. Biomass 10

Sliding Window 11

LITERATURE CITED 14

LIST OF FIGURES

Figure 1: Results of PCA for 31 Fish Species in Buck Creek 6

Figure 2: Sliding Window Analysis: Loadings Based on PC I, PC II, and PC III 9

INTRODUCTION

Awareness of fish community structure is not only important for constructing an accurate representation of what is occurring in any given stream within a period of time—allowing detection of any possible perturbations—but also for giving insight as to how to act in restoring a stream. Stream fish sampling is a classic tool for examining and implementing strategies concerning conservation of biodiversity (Wichert and Rapport 1998, Fausch et al. 2002). Sampling can also yield information about how environmental factors (Ross et al. 1985, Taylor et al. 1993), agriculturally impacted streams (Hoyt et al. 2001), or streams experiencing disturbances such as acidification (Baker et al. 1996) can influence fish assemblages. At the same time, the need for information about community structure in streams requires that sampling methods be accurate and conservative of time and money—limiting factors for many research projects.

A considerable amount has been written concerning fish sampling sufficiency and fish assemblage structure. Cao et al. (2001) developed a model to determine species richness sampling sufficiency in the field. Other studies (Hayes et al. 1996, Meador et al. 2003, Meador and McIntyre 2003, Thompson 2003) have sought to examine the strengths and weaknesses of in-stream sampling strategies such as single or multiple-pass electrofishing passes, seining, and snorkeling. More generally, some have questioned whether or not stream fish assemblages are sufficiently stable to be predictable for fisheries managers to accurately determine assemblage changes that may be due to environmental disturbances. Fish assemblages have been shown to be stable, especially in environmentally steady streams (Matthews et al. 1988), but indications that fish assemblages in a small stream are

unpredictable and change over the course of a year have also been shown (Matthews and Marsh-Matthews 2006).

Several determinants influence stream biota and are important variables in designing sampling protocols. Pringle et al. (1988) found that spatial and temporal scales for ecological research depended on the type of organism being studied and a sufficient time interval that would allow environmental oscillations to produce detectable changes to that organism; these factors should be considered carefully when planning a sampling procedure. Multiple authors have acknowledged that a proper time scale accounting for spatial and temporal patterns of fish assemblages is critical to designing optimal sampling methods (Meador and Matthews 1992, Taylor et al. 1993, Meador and McIntyre 2003, Thompson 2003, Adams et al. 2004). Meador and Matthews (1992) noted that sampling methods depended on knowing whether fish assemblages vary more in space or in time in any given stream. In an analysis of streams in the upper coastal plain of Mississippi, Adams et al. (2004) found high temporal variability, which may be attributed to sampling over a period of several years and multiple habitat types. Dunham et al. (2002) also focused on using spatial and temporal data and applying regression quantiles to estimate the relationship between *Oncorhynchus clarki henshawi* standing crop and habitat. Results indicated that increasing spatial sampling of this particular species would be more advantageous than temporal sampling.

In compliance with establishing optimal stream fish sampling strategies, researchers have also questioned how long sampling should extend. Taylor et al. (1993) recognized that short-term sampling over many sites tends to hide temporal variation; even though patterns of fish abundance could be attributed to the environment, relationships between the exact nature of the environmental variation and the effect on the fish assemblage would require

additional sampling. While the need for long-term data that varies spatially and temporally has been recognized, several papers pointed out that few studies are conducted over a long-term period (Matthews et al. 1988, Meador and Matthews 1992).

Here we use a long-term data set consisting of fish abundance and biomass from Buck Creek (Allen County, Kentucky) that varied both temporally and spatially to test two aspects of sampling design. Utilizing multivariate analyses, we first ask if abundance and biomass data yield different spatial or temporal patterns of community structure. We then use a sliding window analysis to consider the minimum number of consecutive sampling years required to achieve the same information about the fish assemblage as the full eight-year study. We discuss our findings with respect to stream fish monitoring effort and sampling sufficiency in the future.

MATERIALS AND METHODS

Fish samples were collected from Buck Creek, a 3rd order tributary that flows into Trammel Fork of Drake's Creek, located in Allen County Kentucky. Samples were obtained from two stations approximately 1 km apart, using portable electrofishing equipment and block nets above and below each station. Collections were taken in fall and spring, beginning September-October 1992 and concluding in May-June 2000. Both abundance and total biomass in pounds per acre of each species were recorded. 17,734 individual samples comprised the data set. Complete site and sampling details are given in Hoyt et al. (2001).

Principal Component Analysis (PCA)

All analyses were done using SYSTAT 11.0 (SPSS, Inc. 2004). Principal component analysis (PCA) of the correlation matrix from the biomass data was employed to determine variation in species composition among samples from Buck Creek. The sample from Station I in fall 1999 was excluded, as only a single fish was recovered during that sample (a result of extreme drought conditions). Biomass data were converted to z-scores before analysis to minimize potential non-linearities in relationships among taxa.

The percent of total variance explained and patterns of component loadings were used to compare the results of the biomass analysis and a similar analysis of abundance data from Hoyt et al. (2001). Pearson correlation coefficients of the first three vector loadings were computed for corresponding pairs of axes from the biomass and abundance analyses. Significance was determined using Bonferroni-adjusted criteria.

Sliding Window Analysis

A sliding window analysis of abundance data from Hoyt et al. (2001) was used to determine the minimum number of years a stream might need to be sampled to extract approximately the same information about community structure evident in a longer-term data

set. Window sizes ranged from one to seven years over the eight-year study period (1992-2000) with eight subsamples of consecutive years for each window size (i.e., for a three-year window, subsamples consisted of years 1+2+3, 2+3+4, . . . , 8+1+2).

Each of the 56 subsamples generated was subjected to a PCA of the correlation matrix. Only species that were present and showed variation in subsample data set were included in the analyses. Vectors of loadings for the first three resultant principal components (PC) were saved. Replicate sets of loadings were each correlated with the corresponding loadings vector from the total eight-year data set. 95% confidence intervals around the mean correlation were computed for each window size to determine the size of the window needed to generate results not significantly different from the total data set.

RESULTS

Principal Components Analysis

Over the study period, a total of 17,734 fish, 29 species, and two hybrids were taken from Buck Creek (Hoyt et al. 2001). The first three principal components of the biomass data accounted for 40.99% of the data's total variation. Principal component one (PC I – 18.93% of the total variance) separated upstream from downstream samples (Fig. 1); principal component two (PC II – 12.03%) provided some separation of fall and spring samples, particularly from the downstream site (Fig. 1). Principal component three (PC III – 10.03%) was not included in the PCA since it did not show any separation in the samples, however it was still included in the analyses because it explained a fair amount of the total variation. Station 2 samples showed more temporal variation than Station 1 samples (Fig. 1). 12 of the 31 total latent roots from the principal component analysis consisted of significant information (eigenvalues > 1.0).

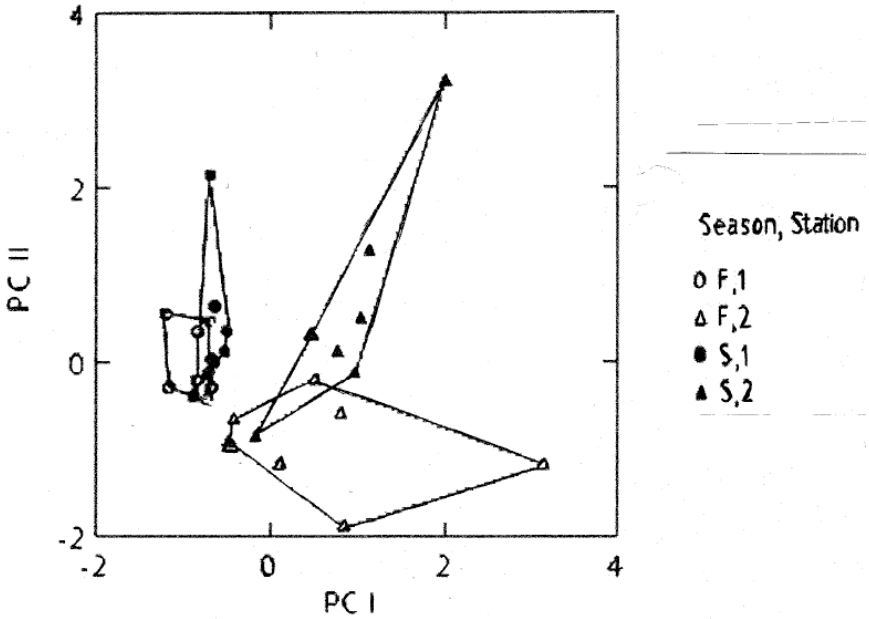

Figure 1. Results of PCA for 31 Fish Species in Buck Creek. Axes depict the first two principal components. Solid symbols represent samples taken in the spring, while unfilled symbols represent samples taken in the fall. Circles represent Station 1 (upstream site) and triangles represent Station 2 (downstream site).

Of the 12 significant component loadings found from the biomass analysis, the first three components were examined more closely to see which species had the most influence within each loading. On PC I, *Etheostoma blennoides, Pimephales notatus*, *Semotilus atromaculatus*, *Lythrurus fasciolaris*, and *Etheostoma bellum* loaded heavily based on biomass variation. Species *Etheostoma barrenense*, *Etheostoma caeruleum*, and *Etheostoma kantuckeense* loaded heavily on PC II. *Catostomus commersoni*, *Ambloplites rupestris*, and *Etheostoma bellum* were the most influential species with respect to PC III.

Ordination plots in principal component space of Buck Creek samples varying in station and season exhibited similar patterns among samples in both the abundance and biomass data sets. The percentage of the principal components' total variation was comparable to the value found in the abundance study by Hoyt et al. (2001). Moreover, the distribution of loadings and positions of samples in multivariate space were qualitatively and quantitatively similar. Vectors of loadings from corresponding principal components of both the abundance and the biomass were highly correlated ($r = 0.805$, 0.796, and 0.580 for PC I, PC II, and PC III, respectively). These correlations were each statistically significant based on Bonferroni-adjusted criteria comparisons of abundance and biomass loadings ($p < 0.0005$ for PC I and PC II, $p < 0.001$ for PC III).

Sliding Window Analysis

The correlation of loadings based on PC I showed that six consecutive years of sampling was needed to approximate the information gained in eight years; the 95% confidence interval at this point overlapped 1.0 (Fig. 2a). The error bars also tended to decrease in size with an increase in the number of consecutive years sampled; however, substantial variation among subsamples was still present even at large window sizes (Fig.

2a). A single year of sampling generated an average correlation of 0.5 relative to the entire eight-year data set. The approach to a correlation of 1.0 increased as the number of consecutive sample years also increased (Fig. 2a).

Results from PC II also revealed that sampling for six consecutive years was necessary to approximate the information contained in the eight-year data set (Fig. 2b). Likewise, the correlation with the total result still increased over the sampling years. However, the dynamics of this graph differed in several respects from what was seen for PC I. One year of sampling showed only a 0.39 correlation of the total eight-year data set (Fig. 2b). Once again, the factor loadings demonstrated a higher correlation with the overall eight-year study data the more consecutive years that samples were taken (Fig. 2b). However, in contrast to PC I, the trend with larger window sizes was fairly linear.

The results from PC III showed that a minimum of five to six consecutive sampling years was required to achieve the information found in the full eight-year study (Fig. 2c). While the overall trend of a rising correlation in the number of consecutive years sampled increased still remained (Fig. 2c), it showed considerably more variation than loadings from PC I and PC II (Fig. 2a and Fig. 2b). In addition, multiple years of consecutive sampling were needed before any real increase in correlation was apparent. The error bars were also much larger and more varied for this loading (Fig. 2c).

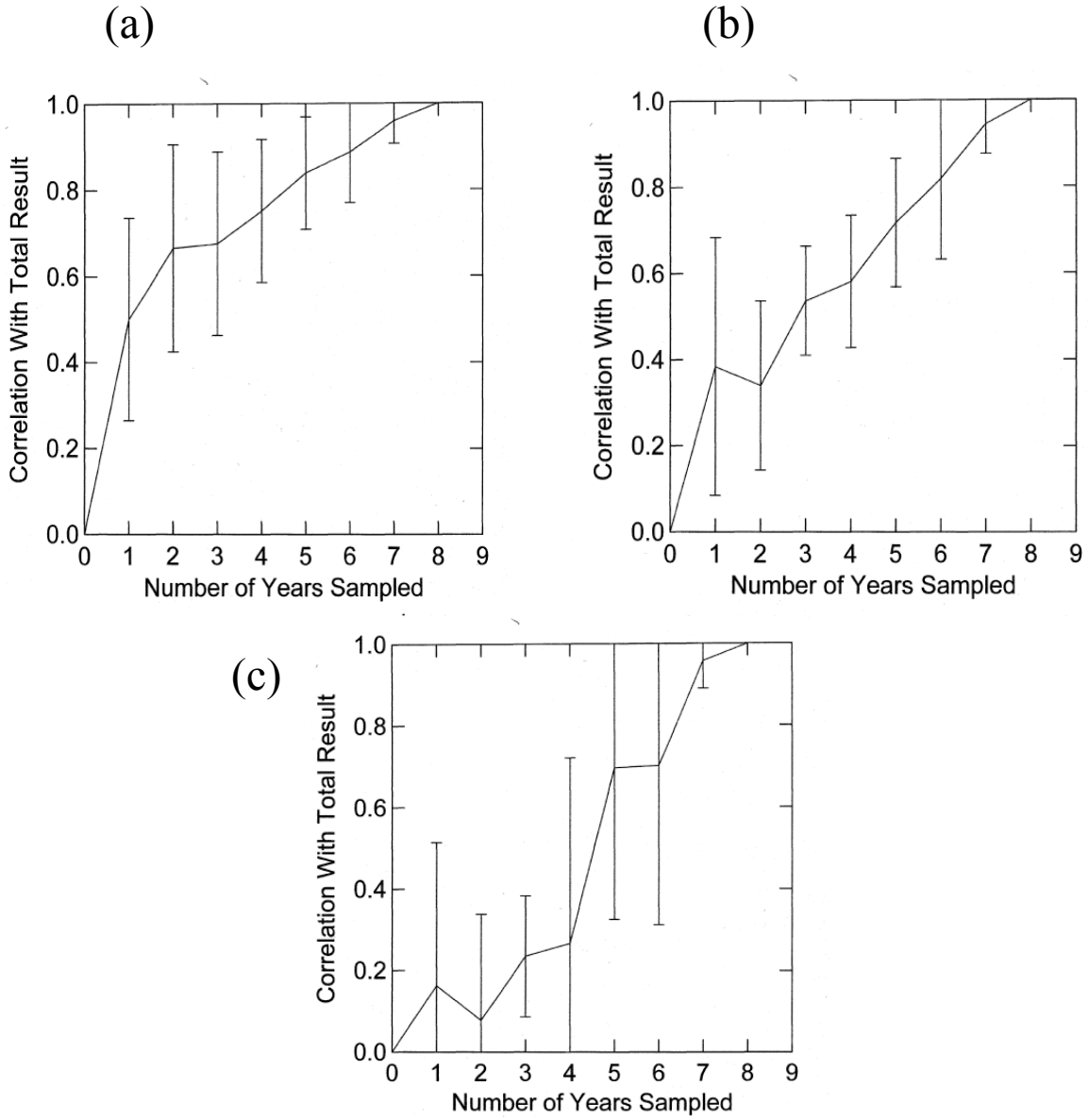

Figure 2. Sliding Window Analysis: Loadings Based on (*a*) PC I, (*b*) PC II, (*c*) PC III. Factor one (*a*), factor two (*b*), and factor three (*c*) loadings were correlated with the corresponding loadings vector from the total abundance data set. All three of the loadings show a similar trend with the more consecutive years sampled. Error bars are shown at the 95% confidence interval and overlap at 1.0 with six years of consecutive sampling in (*a*) and (*b*), but with five years in (*c*). Realistically, seven years of sampling may be needed.

DISCUSSION

Obtaining accurate and sufficient measurements of fish from in-stream sampling is necessary for properly assessing water quality, conserving biodiversity, and determining how a habitat might be influenced by environmental factors and thereby restored. Our stream fish abundance and biomass data varying both temporally and spatially enables abundance measurements and biomass measurements to be compared, and the long-term data allows an examination of the consecutive sampling years to determine a minimum number of sampling years with a correlation similar to the full data set.

Abundance vs. Biomass

Biomass measurements should yield more information about a fish assemblage than abundance measurements since not only a count of each species is found, but also the mass of each species is determined. However, our results indicate that biomass results from PC analysis of the data were not significantly different from those based on abundance data, reported in Hoyt et al. (2001). Furthermore, the PCA plot of the first two principal components from this biomass analysis even show a similar separation of samples as the PCA plot of first two principal components from the corresponding abundance analysis provided in Hoyt et al. (2001). The percentage of the total variation explained by the first three principal components from the abundance and from the biomass analyses were very similar and patterns of loadings were significantly positively correlated. In general, our study indicates that abundance measurements of fish assemblages appear to be a valid a proxy for biomass measurements.

Abundance estimates of fish species, usually accomplished through electrofishing, is one of the accepted methods of describing fish community structure (Meador et al. 2003).

Less effort is usually involved in finding abundance measurements of stream species, whether the study organisms are fish or invertebrates. Few, if any, studies compare stream fish abundance measurements with biomass measurements; however studies using other organisms have been conducted. Our conclusions agree with the findings of a study using stream invertebrates. Wallace et al. (1995) compared stream invertebrate abundance and biomass measurements in a North Carolina stream using the North Carolina Biotic Index (NCBI); they argued that, while biomass measurements account for larger proportional changes than abundance measurements, biomass NCBI measures may not be as beneficial because of the greater expense and effort associated with weighing and measuring samples. In our case, the additional amount of total variation explained by the biomass data was small (3.22%); this suggests that biomass may not yield sufficiently new information to make it cost-effective.

Sliding Window

Given the inherent variability in sampling fish in stream communities because of the numerous factors that influence assemblages (Gorman and Karr 1978, Horwitz 1978, Meador and Matthews 1992, Taylor et al. 1993), one would expect more extensive sampling to reveal much more valuable knowledge about the fish community as a whole. The sliding window analysis shows that at least six consecutive sampling years are needed to approximate the data from the full eight-year long study.

The six-year minimum found in this study should not be generally applied to all streams but instead may hold true for streams that are similar to the study stream. In streams with lots of variation, sampling for a longer period and more times may be required. For example, intermittent streams may show more variation (Meador and Matthews 1992) and

require a different sampling method spatially or temporally than permanent streams. Streams that experience more stress (based on yearly water and temperature fluctuations) than permanent streams can have less assemblage stability, as in the case of Brier Creek in southern Oklahoma compared to Piney Creek in Arkansas (Ross et al. 1985). Furthermore, individual streams may have characteristic fish assemblages and may also vary more temporally or spatially. Adams et al. (2004) noted that the fish assemblages in each of three streams in northwestern Mississippi retain assemblage characteristics relative to their particular streams, but have high temporal variability. However, Matthews (1990) suggested that sampling fish assemblages throughout all seasons or over several years has the potential of increasing temporal variation relative to spatial variation. Each stream varies to some extent, and unique characteristics of a stream under study will dictate how to approach stream fish sampling.

The wide error bars seen in our study further demonstrate that six consecutive sampling years should not be broadly applied across all streams. It would be inaccurate to assume that there is a "magic number" of sampling years and that in the future, that number would not change. Each year of sampling is a snapshot of the fish assemblage at that particular time, and there is a possibility of either getting the same minimum number of consecutive years to sample a stream found in our study or getting a different minimum number of years. Since a standard number of years cannot be established, this study further serves to point out the inherent problem in time-point sampling. Any particular abundance or biomass sample represents the fish assemblage at that particular time as a result of stream habitat conditions, environmental factors, anthropogenic influences, fish life history characteristics, the season the sample is taken, where the sample is taken spatially, etc.

Multiple measurements of abundance or biomass taken at different times in the future could either be close to one another or different from one another, depending on the aforementioned factors that influence fish assemblages. Interpretations of fish assemblages from only a few snapshots could hide the complete range of the fish community structure that occurs between those snapshots, and conclusions made about the assemblage would then be based on an incomplete picture.

Our results have implications for the future development of stream fish sampling methods. If the observation that biomass measurements are not effectively different from abundance measurements continues to hold true, then fisheries managers could benefit from only having to take fish abundance measurements—a much simpler approach than sampling fish for biomass. Additionally, our data collected over multiple consecutive years and seasons supports previous assertions that long-term sampling is necessary to predict changes in fish assemblages and to implement successful planning of stream fish monitoring.

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