Analysis of Hudson River Fish Populations

from the Utilities Monitoring Program

Final Report to the Hudson River Foundation

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Table of Contents

Chapter 1

Overview of Project

This report summarizes results from Hudson River Foundation grant 004/87R/-009, "Hudson River Fish Populations: Analysis of Distribution and Abundance from Existing Data". This report is organized into chapters which represent the major areas of effort funded under this grant.

Chapter 2, "Sampling Larval Fish Populations: Choice of Sample Number and Size" authored by Hélène Cyr, John Downing, Sophie Lalonde, Stephen Baines, and Michael Pace was published in Transactions of the American Fisheries Society 121: 356-368. In this chapter a general equation is developed to predict sampling variance from a review of the literature. This equation is tested with data from the Hudson River fish monitoring program and then general recommendations about sample number and size are presented.

Chapter 3, "Evaluation of Utilities Monitoring Surveys for Evidence of Faunal Decline in the Upper Hudson River" authored by Michael Pace, Hélène Cyr, and Stephen Baines is an unpublished report. Declines of some populations, particularly small bait fishes, have been reported by commercial fishermen in the upper Hudson estuary. Trends in the abundance of 12 species are presented and evaluated in this chapter.

Chapter 4, "Relationships Among Early Life History Stages of *Morone americana* and *Morone saxatilis* from Long Term Monitoring of the Hudson River Estuary" authored by Michael Pace, Stephen Baines, Hélène Cyr, and John Downing will be submitted to Canadian Journal of Fisheries and Aquatic Sciences. This paper describes interannual variation in eggs, yolk-sac larvae, post yolk-sac larvae, and young-of-the-year for white perch (*Morone americana*) and striped bass (*Morone saxatilis*) for the years 1974-1990. Relationships between enviromental conditions and early life history stages are evaluated. In addition, relationships among early life history stages are considered to determine if and at what stage year class success is evident for these populations.

Chapter 2

Sampling Larval Fish Populations:

Choice of Sample Number and Size.

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Abstract. *The number and size of larval fish samples are usually determined arbitrarily, despite the influence of these decisions on the precision of abundance estimates and the ability to detect differences among population estimates. Review of the literature suggests that most surveys of larval fish are based on few (median, 4), large (median, 300m^3) samples. To evaluate current sampling designs, we developed a model, based on published data, to predict the variance in larval fish abundance among replicate samples. Inter-replicate variance (s^2) is strongly related to mean abundance ($\bar{x}$) as: $\log_{10}s^2 = 0.19 + 1.74 \bullet \log_{10}\bar{x}$ ($r^2=0.93$, $P<0.0001$). This relationship was tested with an extensive data set collected in the Hudson River (weekly samples over 14 years in 12 regions of the 250-km-long river) and was found to be general across environments, life history stages and species. The model was not affected by sample volume. Our analysis shows that half of published studies estimated larval abundance with a coefficient of variation on the mean ($SE/\bar{x}$) of 0.5 or more and could only detect order-of-magnitude differences among sites or time periods. The $s^2/\bar{x}$ equation provides guidelines to select the number and size of samples that should be taken to achieve a required level of precision and to detect a given difference among population means.*

Introduction

Estimates of the abundance of larval and juvenile fish populations are essential to both the theoretical study and the practical management of fish stocks. It is important that these estimates be both accurate (unbiased) and precise (low variance). Recent interest in larval fish sampling has concentrated on the accuracy of larval fish sampling methods and equipment (e.g., Kriete and Loesch 1980; Gallagher and Conner 1983; Thayer et al. 1983; Burczynski and Johnson 1986; Gregory and Powles 1988; Johnson et al. 1988; DeAlteris et al. 1989; Mesa and Schreck 1989). Although accurate sampling is important, the well known heterogeneous spatial distribution of fish larvae (Silliman 1946), and the resulting high variance among replicate samples (Hildén and Urho 1988), may render useless the population estimates obtained with even the least biased sampling method.

The precision with which larval density is measured can be estimated as the coefficient of variation of the mean ($CV_{\bar{x}}=SE/\bar{x}$; not to be confused with the coefficient of variation of samples, $SD/\bar{x}$). The coefficient of variation of the mean is a function of the average number of larvae found per sample ($\bar{x}$), inter-replicate variance (s^2), and the number of replicate samples collected (n)

$$CV_{\bar{x}} = s \bullet \bar{x}^{-1} n^{-0.5}. \quad (1)$$

Therefore $CV_{\bar{x}}$ can be adjusted by changing sample volume (changing $\bar{x}$) and/or the number of samples collected. Measures of both s^2 and $\bar{x}$ are necessary to design a sampling program. Sampling recommendations have been made for specific populations in specific systems (Silliman 1946; Taylor 1953; Zweifer and Smith 1981; Santander et al. 1982), but it is unknown how these recommendations apply to other populations.

Recent studies of spatial heterogeneity and sampling design for other fauna have shown that s^2 is a constant and predictable function of $\bar{x}$. Estimates of $\bar{x}$ alone can then be used to calculate a priori the requisite sample number ($\hat{n}$) to obtain acceptable levels

of precision on population estimates. Acceptable levels of precision will be specific to the question being asked. Many authors (Standen and Latter 1977; McElhone 1978; Downing 1979; Gilyarov et al. 1979; Jones and Francis 1982; Way and Wissing 1982; Drake 1983; Downing and Cyr 1985; Morin 1985; Pont 1986; Downing et al. 1987; France 1987; Morin 1987; Stocker and Bergquist 1987; Vézina 1988; Pace et al. 1991) have demonstrated that the sampling variance for sets of replicate samples of benthos, phytoplankton and zooplankton from streams, lakes and marine environments varies consistently as

$$s^2 = a \cdot \bar{x}^{\,b}; \tag{2}$$

where a and b are constants fitted by regression analysis. Combination of variance functions (e.g., equation 2) with equation 1 has shown that the density of other fauna is often estimated with low precision (high $CV_{\bar{x}}$) because ecologists take too few samples, and that, for a given level of precision, sampling cost can be reduced as much as 30 fold by choosing to take large numbers of smaller samples (Downing and Anderson 1985; Downing 1979, 1989).

In spite of the great economic and ecological importance of larval fishes, we now possess no general model which predicts the number of samples necessary to obtain acceptable levels of precision. Because sampling surveys for larval fishes are often intended to assess impacts on this sensitive life stage (e.g., Holland 1986; Murphy et al. 1986; Moore and Gregory 1988; Uphoff 1989), levels of precision and numbers of samples should be dictated by the magnitude of impact that one wishes to detect, the power of the test to be used, and a stated α level. Handbooks on sampling fish populations lend little guidance about the number of samples needed or the size of samples to be taken; thus choices of sampling design are made arbitrarily.

The objective of this study was to assemble information on the inter-replicate variance found among samples of fish larvae in freshwater and marine environments, and to develop an equation to characterize this variability. Because spatial variation in

populations of fish larvae may differ among sites, species, dates, sampling gear and environments (Silliman 1946; Hildén and Urho 1988), a second objective was to compare such a general model to a highly specific data set drawn from a long series of samples collected from the Hudson River estuary, where fish larvae were sampled routinely in one ecosystem with constant sampling methods throughout many years. These analyses are then used to make recommendations about sample number and size for efficient larval fish population estimation and the detection of anticipated impacts on larval fish populations.

Methods

Literature data.--Sampling data on young fish including eggs, larvae, young-of-the-year, and yearlings were collected from the literature. In this paper we use the term larval fish to refer collectively to these early life history stages. We systematically reviewed all papers published in six journals: Canadian Journal of Fisheries and Aquatic Sciences (1975-1990); Estuaries (1979-1990); Journal du conseil - Conseil international pour l'exploration de la mer (1980-1989); Journal of Fish Biology (1980-1990); Marine Ecology Progress Series (1985-1990); and Transactions of the American Fisheries Society (1970-1989). Data were drawn from papers reporting mean abundance, inter-replicate variance, number of replicate samples (taken at the same station on the same date with the same gear), sampling technique, sampling gear and type of environment sampled (i.e., lake, river, estuary, ocean). In many papers, methods were either incompletely described or unclear, so that many data appearing in the literature were difficult to interpret in any statistical context and could not be used in our analyses. Where possible, we also recorded the volumes of replicate samples.

Hudson River data.--We used estimates of the abundance of eggs, yolk-sac larvae and post yolk-sac larvae of white perch, Morone americana, and striped bass, M. saxatilis, in the Hudson River from 1974 to 1987. A random stratified sampling design was used; sampling protocol was consistent throughout the study (Barnthouse et al. 1988; Lawler et al. 1989).

The river was divided into 12 regions, and two or three stations (channel, bottom, shoals) were sampled within each region. Fish eggs and larvae were sampled weekly from April-May to July-August, for a total of 9-21 sampling series per year. Two to 40 replicate samples (median, 5) were collected at random locations at each station within each region. Ichthyoplankton were sampled with a 505-μm mesh net mounted on a Tucker trawl to sample the channel or on an epibenthic sled to sample the bottom. Both frames were used to sample the shoal. Larval samples were preserved in formalin (about 5%). Eggs, yolk-sac larvae and post yolk-sac larvae were identified and counted in each sample. Mean abundance per average sample volume ($\bar{x}$) and the variance (s^2) among replicate samples were calculated by species, station (channel, bottom, shoals), region, sampling series, and year.

Statistical and mathematical analyses.--The relationship between mean abundance ($\bar{x}$) and variance (s^2) of fish larvae in replicate samples (equation 2) was determined by least-squares linear regression analysis of $\log_{10}s^2$ on $\log_{10}\bar{x}$. Differences among classes of data were sought by analysis of covariance (ANCOVA; Draper and Smith 1981). The expected precision ($CV_{\bar{x}} = SE/\bar{x}$) of a projected sampling program was calculated by substituting equation 2 into equation 1:

$$CV_{\bar{x}} = a^{0.5}\,\bar{x}^{(b/2)-1}\,n^{-0.5}. \qquad (3)$$

The number of replicate samples ($\hat{n}$) needed to obtain a given level of precision was calculated by rearranging equation 3:

$$\hat{n} = a \bullet \bar{x}^{b-2}\,CV_{\bar{x}}^{-2}. \qquad (4)$$

Both precision and sample numbers predicted for $\bar{x} < 1$ were checked against the theoretical range of variances that can be calculated using discrete object counts (Downing 1989).

In most cases, the required precision of a sampling program will not be determined simply by the variation around each population mean, but by specific questions. For example, it may be important to test for differences in mean larval densities among sites or time periods, or to detect trends over a series of observations (e.g., Gerrodette 1987). A given $CV_{\bar{x}}$, 20% for example, may or may not be adequate, depending upon the size of difference that must be resolved or discerned. A power analysis can help optimize the sampling design used to test a specific hypothesis (Cohen 1988; Peterman 1990). We present the analysis used to calculate, a priori, the number of samples required to detect a given difference between two mean population densities using a *t*-test. The analysis includes two steps. First, we calculated the difference among means that is significant at a predetermined α level, given the variance associated with each mean. This critical difference is then compared with the probability distribution of the alternative hypothesis that the two means are different. The power of the test is the probability of accepting the alternative hypothesis when it is true.

The number of samples ($n=n_1=n_2$) necessary to reach a given level of α and ß (1-power) was determined iteratively for pairs of μ_1 and μ_2, where μ_1 and μ_2 varied between 1 and 1000 organisms per sample. Equation 2 predicts the variance (s^2) associated with a given mean (μ), which we assume is equal to σ^2. Because equation 2 has a high fit ($r^2=0.93$), the error around predicted s^2 are small, and the assumption that $\sigma^2=s^2$ has very little effect on our results. Since the variances associated with different means are expected to be unequal (equation 2), the variance of the difference in means ($s^2_{\bar{x}_1-\bar{x}_2}$) ($s^2_{\bar{x}_1-\bar{x}_2}$) is calculated according to Steel and Torrie (1980, p.106).

$$s^2_{\bar{x}_1-\bar{x}_2} = \frac{s^2_1 + s^2_2}{n}; \qquad (5)$$

and the degrees of freedom (df) are approximated as

$$df = \frac{((s^2_1 + s^2_2)/n)^2}{((s^2_1/n)^2 + (s^2_2/n)^2) / (n-1)}; \quad (6)$$

where s^2_1 and s^2_2 are estimated from equation 2, and n is the number of samples used in the estimation of $\bar{x}_1$ and $\bar{x}_2$. For each combination of μ_1 and μ_2, we calculated the difference in means ($d_{\alpha/2}$) above which the means would be significantly different

$$d_{\alpha/2} = t_{\alpha/2\ \bar{x}1 - \bar{x}2}\ ; \quad (7)$$

where $t_{\alpha/2}$ is taken from a standard t table and $s_{\bar{x}-\bar{x}}$ is the standard deviation of the difference in means (equation 5). The critical difference, $d_{\alpha/2}$, is then compared to the difference between the selected means ($\Delta = \mu_1 - \mu_2$) using

$$t' = \frac{d_{\alpha/2} - \Delta}{s_{\bar{x}1 - \bar{x}2}}. \quad (8)$$

The power of the test is calculated as

$$1-\beta = P(t' < -t'_{\alpha/2,\delta}) + P(t' > t'_{\alpha/2,\delta}); \quad (9)$$

where $t'_{\alpha/2,\delta}$ is from a noncentral t-distribution, with noncentrality parameter $\delta = (\mu_1 - \mu_2)/\sigma_{\mu 1 - \mu 2}$ (Steel and Torrie 1980; Vaughan and Van Winkle 1982). The probabilities were calculated with the PROBT procedure in SAS. This analysis was repeated for many combinations of $\bar{x}_1$ and $\bar{x}_2$ and at three levels of α and β (0.01, 0.05, 0.10). The β- and α-levels were set equal, assuming that in impact studies it is equally important to minimize the probability of not finding a difference when it actually exists (type II error) and the probability of finding a difference when it actually does not exist (type I error).

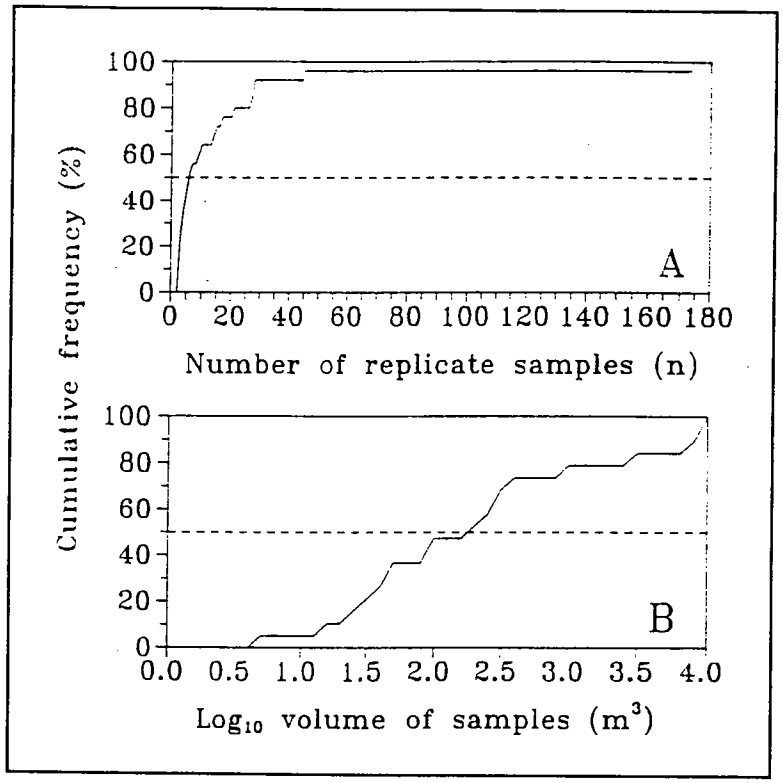

Figure 1. a) Cumulative frequency distribution of the average number of replicate samples taken in each of the references summarized in Table 1 in which n was listed. The broken line indicates the median average number of samples taken (4). b) Cumulative frequency distribution of the logarithm of the average sample volume employed in the studies summarized in Table 1. The broken line indicates the median average sample volume employed (335 m^3).

This is only one possible assumption. When costs of type I and type II errors are different, α and β should be adjusted accordingly (Parkhurst 1990).

Results and Discussion

Number and Volume of Samples Used in Larval Fish Studies

We obtained 703 estimates of $\bar{x}$ and s^2 from the published literature (Table 1). Average numbers of larvae in these samples ranged from 0.2 to 330,000. Sample volumes ranged from 0.1 to 38,000 m^3, and numbers of replicate samples ranged from 3 to 174. Samples were taken with a wide variety of sampling gear. Data represented four stages of development (8% eggs, 51% larvae, 32% young-of-the-year, 9% yearlings) and

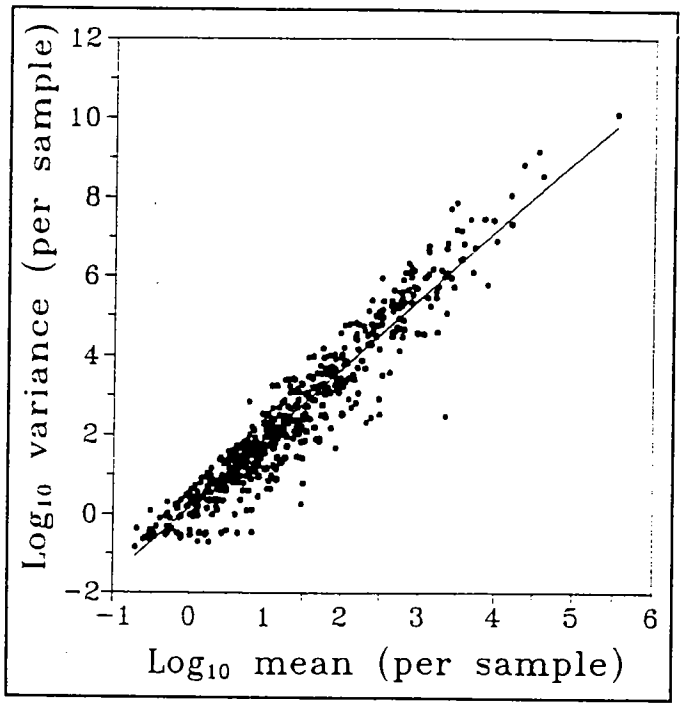

Figure 2. The relationship between the mean ($\bar{x}$) and variance ($\underline{s}^2$) of 703 published (Table 1) estimates of fish egg, larva, young-of-the-year and yearling abundance. The solid line represents equation 10 ($\log_{10}\underline{s}^2 = 0.19 + 1.74 \log_{10}\bar{x}$).

were collected in four types of habitats (3% estuaries, 24% lakes, 25% rivers and streams, 48% marine). Data on yearlings were included only if they were pelagic and collected in the same samples as larvae and/or eggs. Analysis of the current literature suggests that most surveys of larval fish are based on small numbers (median, 4; Figure 1a) of very large (median, 300 m^3; Figure 1b) samples.

Predictability of Sampling Variance

Sampling variance was strongly correlated with the mean number of larvae per sample. Across habitats and fish species, inter-replicate variance can be predicted with

$$\log_{10}s^2 = 0.19 + 1.74 \log_{10}\bar{x} \qquad (10)$$

($r^2 = 0.93$, $N = 703$, *Residual Mean Square* $= 0.32$, $P << 0.0001$). As in other studies (Vézina 1988), sample volume did not affect the $s^2/\bar{x}$ relationship, although it ranged more than

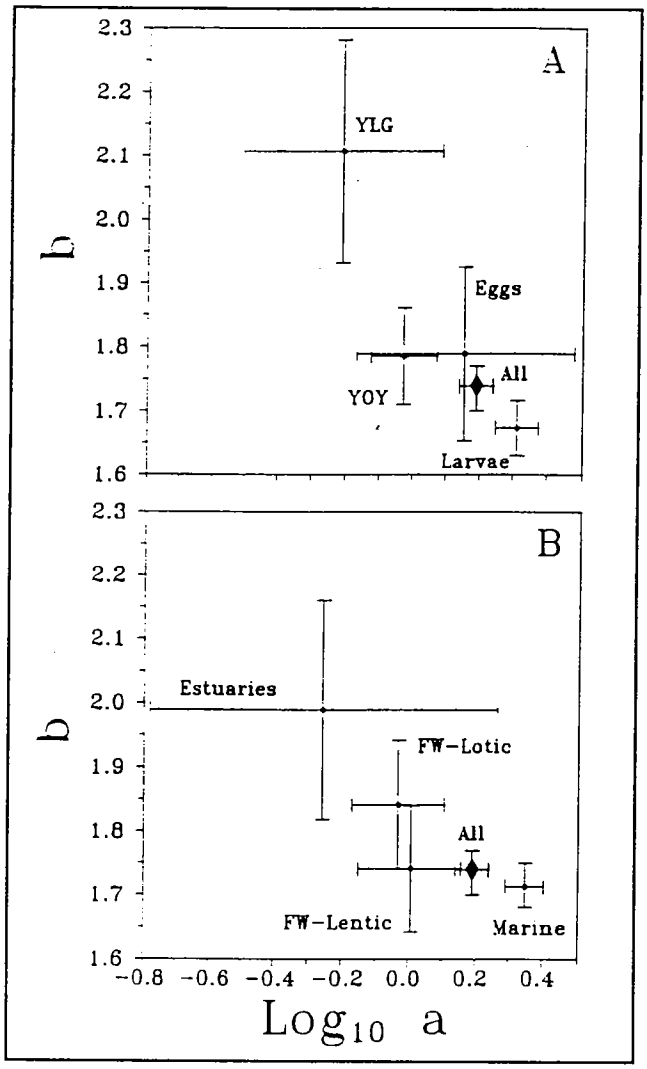

Figure 3. Confidence intervals (95%) for estimates of log a and b (equation 2) for different categories of fish sample data taken from the published literature (Table 1): A) comparison of life stages; B) comparison of habitats. YOY=young-of-the-year (age 0); YLG=yearlings (age 1); FW=freshwater.

five orders of magnitude in different studies. Although this general function fits the data well (Figure 2), ANCOVA suggests differences among life stages and habitats. Yearlings were slightly more aggregated (higher s^2:$\bar{x}$ ratio) than other stages; estuarine and marine larvae were more highly aggregated than freshwater lentic or lotic populations. These differences, however, are minor. There was considerable overlap of the coefficients of equation 2 (a, b) when estimated for individual life stages (Figure 3a) or habitats

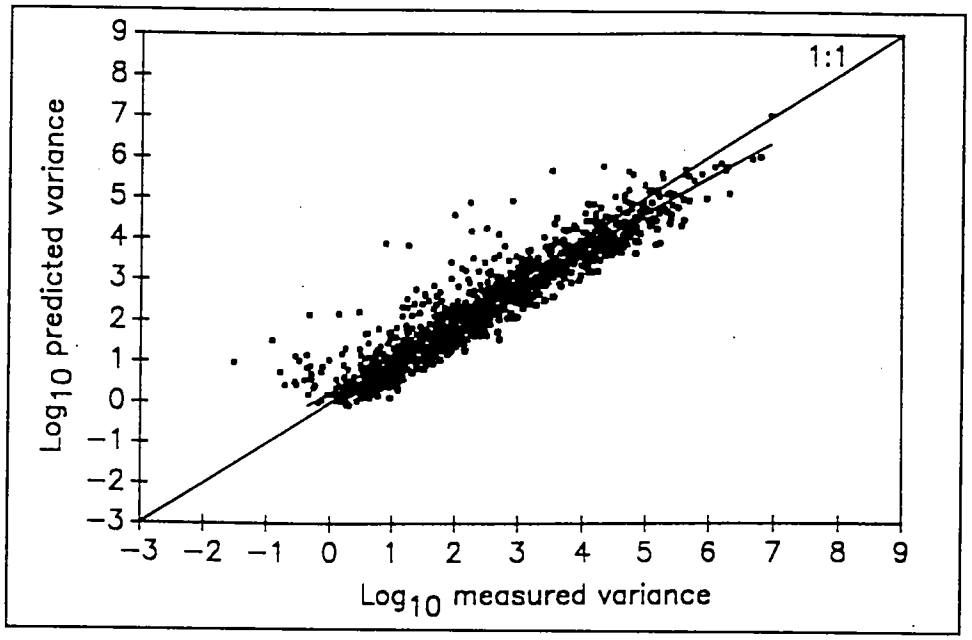

Figure 4. Comparison of the among-replicate variance measured in the Hudson River and predicted from equation 10 ($\underline{s}^2 = 3.61 \bar{x}^{1.74}$). Egg and larval densities were calculated as numbers per mean-sample volume (312.72 m^3). The 1:1 line represents perfect agreement. 1000 points, randomly selected from 10,149 values, are shown.

(Figure 3 b). The highest values of b in Figure 3 were for yearlings and estuaries, two categories for which we found few data. These high values of b were therefore probably overestimated (Downing 1986). We conclude that a common variance relationship (equation 10) provides good general predictions of s^2 for all life stages included in the analysis.

The literature model adequately predicts the variance among replicate samples of fish larval abundance in the Hudson River (Figure 4). Equation 10 was tested with 10,149 replicated measurements of abundance for striped bass and white perch made in different regions of the Hudson River between 1974 and 1987. Mean abundance ranged from 0.7 to 12,259 eggs or larvae per standard sample (volume adjusted to 313 m^3); variance ranged over 13 orders of magnitude. Despite a small bias, s^2 predicted from equation 10 agrees very closely to the measured s^2. This analysis corroborates the generality of the literature model.

The extensive data on larval fish abundance from the Hudson River also provide a comparison of $s^2/\bar{x}$ patterns for particular species within a system. As with the literature data, there were strong relationships between s^2 and $\bar{x}$ for both striped bass and white perch. Relationships for these species were highly significant (striped bass: $r^2=0.85$, $N=4{,}107$, $P<<0.0001$; white perch: $r^2=0.87$, $N=6{,}042$, $P<<0.0001$) but were not significantly different from each other ($P=0.11$). We therefore combined data for these two species, and found that inter-replicate variance varied as

$$\log_{10}s^2 = 0.19 + 1.78 \log_{10}\bar{x} \qquad (11)$$

($r^2=0.85$, $N=10{,}149$, *Residual Mean Square*$=0.33$, $P<<0.0001$). This equation is nearly identical to that derived from the literature data and predicts sampling variation that is only slightly greater than equation 10.

An ANCOVA was used to test for effects of year and sampling region in the Hudson River. In this analysis, mean abundance ($\bar{x}$) is overwhelmingly important (Table 2). Region and year were also significant, and there was a significant interaction between $\bar{x}$ and YEAR (Table 2). These additional factors, however, only increased the overall R^2 by 0.005 and thus contribute little to improving predictions of equation 11. Our ability to detect highly significant effects for minor factors is due to the large number of samples used in the analysis (10,149 sets of replicate samples).

Analysis of covariance of s^2, with $\bar{x}$ as a covariable, shows that larval fish populations have higher s^2:$\bar{x}$ ratios ($P<0.001$) than the marine and freshwater zooplankton samples analyzed by Downing et al. (1987). This finding suggests that planktonic fish larvae are more aggregated than zooplankton. An alternate explanation of the higher s^2:$\bar{x}$ ratios could be that larger sampling scales were used in ichthyoplankton surveys than for zooplankton. Pinel-Alloul et al. (1988) found that replicate samples of zooplankton taken over a 10,000-m^2 area gave significantly higher s^2 than replicates collected over a 100-m^2 scale. Because ichthyoplankton are typically less abundant than zooplankton (median density in Table 1 is 0.02 larvae/m^3; Downing et al. 1987), samples are typically

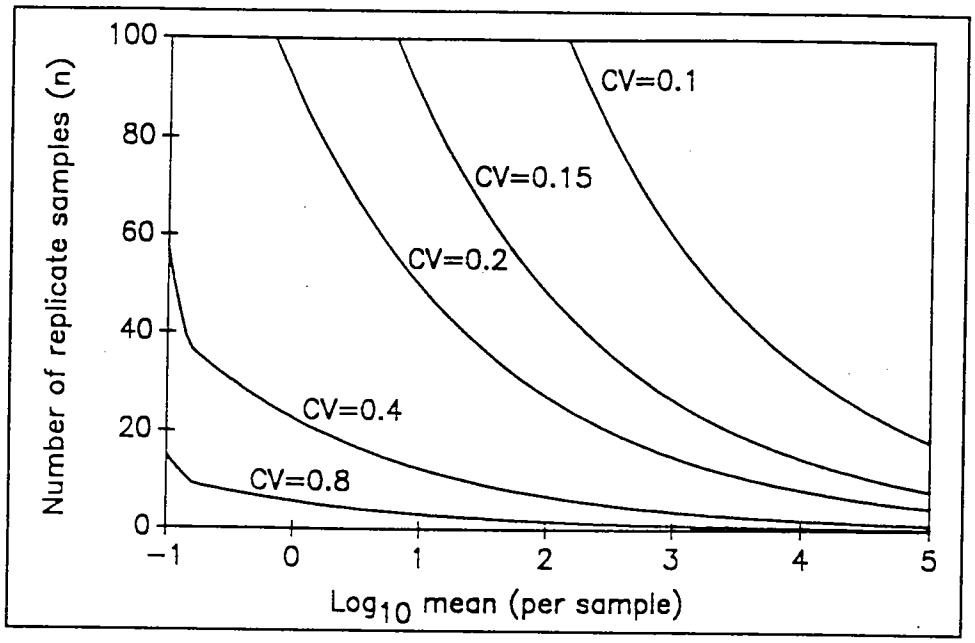

Figure 5. Predictions of the minimum number of samples ($\underline{n}$) needed to obtain a given coefficient of variation ($CV_{\bar{x}}$). The predictions are based on published data of inter-replicate variation found in larval fish sampling surveys of freshwater, marine and estuarine populations of eggs, larvae and yearlings. Predictions were made by substitution of the coefficients of equation 12 into equation 4 ($\underline{n} = 3.61\ \bar{x}^{-0.26}\ CV_{\bar{x}}^{-2}$). For mean abundances smaller than 1, predicted $\underline{n}$ were compared with the necessary $\underline{n}$ to achieve minimum $CV_{\bar{x}}$ (equation 3 in Downing 1989) and the largest value is presented.

much larger and replicate samples must, therefore, be more widely spaced. The large sampling scale used in ichthyoplankton research may lead to higher perceived spatial aggregation in fish larvae populations even if zooplankton and ichthyoplankton were aggregated to the same degree.

Predicting Precision and Requisite Sample Number

Predictions of inter-replicate variance are useful in evaluating different sampling protocols. Predicted s^2 can be used to calculate the precision of mean abundance estimates or the number of samples that would be required to achieve a given precision.

For this analysis, inter-replicate variance predicted from equation 10 must be corrected for detransformation from the logarithmic to the arithmetic scale (Sprugel 1983), leading to the equation

$$s^2 = 3.61\ \bar{x}^{1.74}. \qquad (12)$$

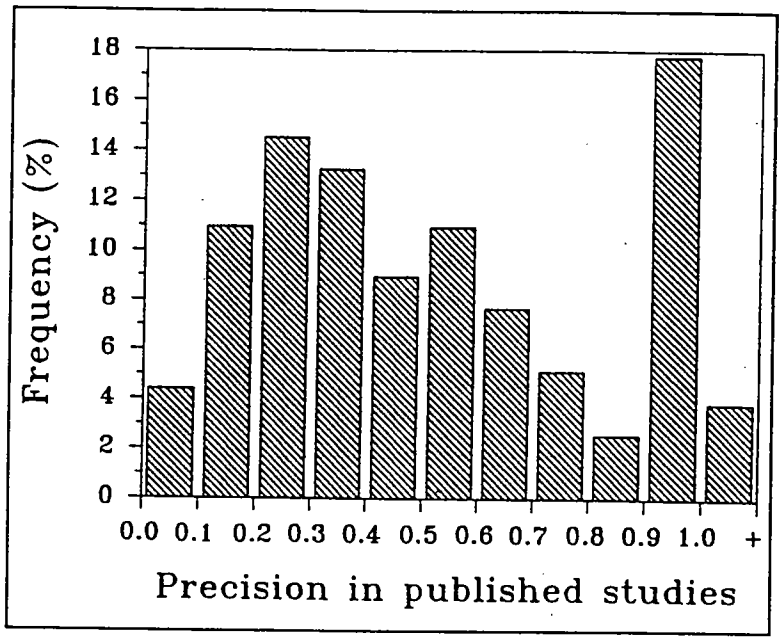

Figure 6. Frequency distribution of precision ($CV_{\bar{x}}$) measured in published studies (Table 1; $\underline{N}$=703).

Predicted s^2 can then be used in equation 3 to calculate the sampling precision associated with various sampling strategies. In general, the precision of an estimated population density improves ($CV_{\bar{x}}=SE/\bar{x}$ decreases) with increased sample number and mean density per sample (Figure 5). Sampling precision of 20% is obtained by taking a large number of samples (sometimes > 50) if, on average, less than one larva is collected in each sample. In published studies, few samples are taken (median n=4) and mean larval abundance in these samples is low (median $\bar{x}$=7). Fifty percent of published estimates of larval abundance have levels of precision of 0.5 or more (Figure 6).

The number of samples needed to obtain various levels of precision can be calculated by substituting the coefficients of equation 12 into equation 4. The resulting equation shows that the number of samples needed ($\hat{n}$) rises rapidly with decreased $\bar{x}$ and increased precision (Figure 5). Although small numbers of samples are adequate when larval densities are high, one is required to take large numbers of samples in sparse populations.

Two options are available for increasing sample precision of fish larvae. Since the volume of water sampled has no discernible independent effect on precision, sampling larger volumes can increase precision by increasing the mean number of individuals per sample (Figure 5). Reductions in the filtration efficiency of sampling nets as more water is processed, however, may constrain sample volume, particularly in environments with large amounts of suspended matter. Processing costs may also be higher for large samples. The alternative strategy would be to take large numbers of small samples (Figure 5). This approach has the advantage of reducing per sample processing costs, but increases the amount of sampling effort. For a required precision level, the investigator must balance the conflicting concerns of equipment performance, sampling costs and sample processing costs in order to determine the appropriate sampling strategy.

The majority of larval fish density estimates that have been published to date have low precision. Taking four replicate samples, the median number of samples taken in population studies of larval fish, one would have to count more than 30,000,000 larvae per sample on average to yield $CV_{\bar{x}}=0.1$. A $CV_{\bar{x}}$ -value of 0.2 could only be obtained with $n=4$ if one counted around 160,000 larvae per sample, on average. Even at very imprecise levels like $CV_{\bar{x}}=0.4$ one must have an $\bar{x}$ greater than 775 if $n=4$. Yet, the median number of larval fish per sample found in published studies is around seven.

Detecting Differences Between Population Means

Surveys of larval fish abundance are often motivated by a concern that human activities may have a negative impact on this fragile and sensitive life-stage. Of paramount importance then is not as much the precision associated with each population estimate, but our ability to detect changes in population levels before and after a given change in the environment. This was the impetus behind the Hudson River sampling program that we analyzed here, and which may be the most extensive estimation of a fish larvae population ever attempted. The variance functions that we derived permit us to

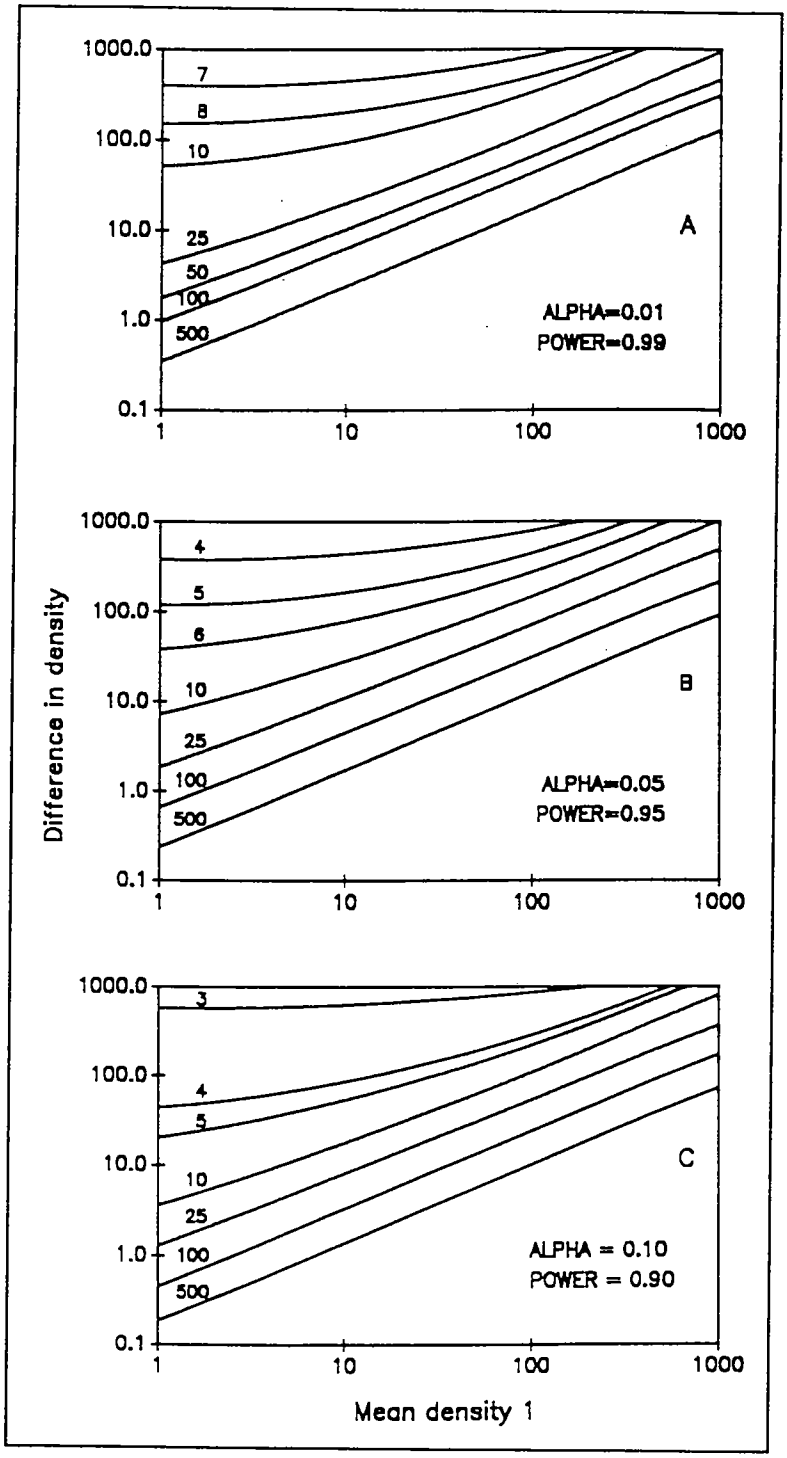

Figure 7. Minimum number of samples from which each mean must be estimated in order to find a significant difference between two larval fish densities. The analysis is based on equation 12 ($\underline{s}^2 = 3.61\ \bar{x}^{1.74}$) and is presented for $\underline{\alpha}=\underline{\beta}$ of A) 0.01, B) 0.05 and C) 0.10.

determine the probable number of samples that would be needed to differentiate between mean densities at two sites or at two time periods.

The number of replicate samples needed to detect significant differences decreases as the differences among means increase (Figure 7). Figure 7 indicates that sampling surveys based on the median number of replicate samples taken in current studies ($n=4$) could detect an 8 fold difference at large densities (100 larvae/sample) but only a 350-fold difference at low densities (1 larva/sample) with a significance level of $\alpha=0.05$. Detection of a 50% change in population density would take 64 samples to derive each mean at $\bar{x}=1$, 33 samples at $\bar{x}=10$, 19 samples at $\bar{x}=100$, and 11 samples at $\bar{x}=1{,}000$. Use of one-tail *t*-tests would reduce the number of samples needed. Because the coefficients of equation 11 are greater than those of equation 10, slightly more samples are needed in the Hudson River than is generally recommended, although the patterns of variation are largely the same.

In this study, we provide guidelines to obtain estimates of larval fish abundance at one site with a desired level of precision. For studies of large systems where many stations need to be sampled as well as studies of changes in abundance through time, consideration must also be given to patterns of spatial and temporal variation. To arrive at an efficient allocation of sampling effort each scale of variation must be considered.

Our calculations show that past sampling designs had been inadequate for the comparison of larval fish abundance among sites or time periods. Fortunately, fisheries ecologists can improve sampling designs by predicting the number and size of samples necessary to achieve desired precision. Determining how precise samples need to be involves nonstatistical judgments concerning acceptable levels of α and β, and what differences in abundance are important to detect. Careful consideration of precision in the context of study objectives will improve the quantitative evaluation of fish populations.

Acknowledgments

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