

Assessing the Efficacy of Single-Pass Backpack Electrofishing to Characterize Fish Community Structure

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Abstract.—Two-pass backpack electrofishing data collected as part of the U.S. Geological Survey's National Water-Quality Assessment Program were analyzed to assess the efficacy of single-pass backpack electrofishing. A two-capture removal model was used to estimate, within 10 river basins across the United States, proportional fish species richness from one-pass electrofishing and probabilities of detection for individual fish species. Mean estimated species richness from first-pass sampling (\hat{p}_{s1}) ranged from 80.7% to 100% of estimated total species richness for each river basin, based on at least seven samples per basin. However, \hat{p}_{s1} values for individual sites ranged from 40% to 100% of estimated total species richness. Additional species unique to the second pass were collected in 50.3% of the samples. Of these, cyprinids and centrarchids were collected most frequently. Proportional fish species richness estimated for the first pass increased significantly with decreasing stream width for 1 of the 10 river basins. When used to calculate probabilities of detection of individual fish species, the removal model failed 48% of the time because the number of individuals of a species was greater in the second pass than in the first pass. Single-pass backpack electrofishing data alone may make it difficult to determine whether characterized fish community structure data are real or spurious. The two-pass removal model can be used to assess the effectiveness of sampling species richness with a single electrofishing pass. However, the two-pass removal model may have limited utility to determine probabilities of detection of individual species and, thus, limit the ability to assess the effectiveness of single-pass sampling to characterize species relative abundances. Multiple-pass (at least three passes) backpack electrofishing at a large number of sites may not be cost-effective as part of a standardized sampling protocol for large-geographic-scale studies. However, multiple-pass electrofishing at some sites may be necessary to better evaluate the adequacy of single-pass electrofishing and to help make meaningful interpretations of fish community structure.

Accurate quantitative data on fish communities are needed by fishery biologists and water quality managers to formulate management strategies. However, quantitative data can be difficult to collect, and the efficacy of quantitative sampling to provide fish community data is rarely evaluated (Peterson and Rabeni 1995; Pusey et al. 1998) even though such evaluations are essential to developing scientifically sound environmental monitoring programs (Maher et al. 1994; Peterson and Rabeni 1995).

Characterizing fish community structure consists of quantitative estimates of species richness and abundance of individual taxa. Absolute abundance of an individual taxon can be estimated by

well-documented mark-recapture and removal methods (Zippin 1956; Carle and Strub 1978; Pollock 1991). However, these approaches are most often used for populations rather than communities and designed for analysis of intensive small-scale investigations. Whereas capture-recapture and removal methods have been used to estimate mammal and avian species richness (Burnham and Overton 1979; Nichols and Conroy 1996; Boulinier et al. 1998), little attention has been devoted to estimating fish species richness and proportional or relative abundances. Additionally, the level of effort required to accurately estimate these attributes has not been established.

Angermeier and Smogor (1995) noted that determination of the appropriate level of sampling effort to characterize fish species richness at a site is difficult. Too little sampling may negatively influence the reliability of conclusions, whereas too

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Received November 13, 2000; accepted June 19, 2002

TABLE 1.—List of the 10 National Water-Quality Assessment Program study units that were included in the present study.

Study unit name	States in study unit	Study unit abbreviation
Central Columbia Plateau	Idaho, Washington	CCPT
Connecticut, Housatonic, and Thames River Basins	Connecticut, Maine, New Hampshire, New York, Rhode Island, Vermont	CONN
Hudson River Basin	Connecticut, Maine, New Jersey, New York, Vermont	HDSN
Lower Susquehanna River Basin	Maryland, Pennsylvania	LSUS
Potomac River Basin	Washington, D.C., Maryland, Pennsylvania, Virginia, West Virginia	POTO
Red River of the North	Minnesota, North Dakota, South Dakota	REDN
Rio Grande Valley	Colorado, New Mexico, Texas	RIOG
Trinity River Basin	Texas	TRIN
Upper Snake River Basin	Idaho, Montana, Nevada, Utah, Wyoming	USNK
Western Lake Michigan Drainage	Michigan, Wisconsin	WMIC

much sampling may be unnecessarily expensive. A thorough sampling effort occurs when the measurement of a desired attribute (such as species richness) approaches an asymptotic level and additional sampling yields comparatively little new information (Lyons 1992; Paller 1995).

Characterizing stream fish community structure (species richness and relative abundance of individual species) is one component of the U.S. Geological Survey's (USGS) National Water-Quality Assessment (NAWQA) Program. Although the NAWQA sampling strategy consists of using multiple gear types, two-pass electrofishing is the primary collection method (Meador et al. 1993). However, questions have arisen regarding the efficacy of one-pass electrofishing in an attempt to reduce sampling effort at a single site, thereby increasing the number of sites that could be sampled (Mitro and Zale 2000).

We analyzed NAWQA data to address the following question: How effective is single-pass backpack electrofishing at describing species richness and relative abundance of individual species? Specific objectives included (1) assessing relative proportions of species richness collected in first-pass sampling, and (2) assessing probabilities of detection based on abundance of selected taxa collected in first-pass sampling. Based on the NAWQA data analyses, we suggest ways to optimize sampling effort for backpack electrofishing studies that are part of large-scale environmental monitoring programs.

Study Area

The NAWQA Program focuses on 59 major river basins across the United States. To make the program cost-effective and manageable, sampling ac-

tivities within the 59 river basins (known as study units) are conducted on a rotational basis, one-third of the study units being investigated for 3–5 years. In 1991, NAWQA began the transition from a pilot program to a full-scale program by implementing sampling in 20 of the 59 study units. In 10 (all relatively small, Wadeable streams) of the 20 study units, two-pass backpack electrofishing had been used consistently (Table 1), which enabled assessment of the efficacy of a single-pass sample to characterize fish community structure in these streams.

Methods

Fish collected in the 10 study units were sampled during summer low-flow periods during 1993–1995 following standard sampling protocols as described by Meador et al. (1993). Sampling sites typically were located near USGS gaging stations, and a sampling reach was identified at each site. Reach lengths were based on habitat types (pools, riffles, and runs) and meander wavelength. Attempts were made to include at least two examples each of two different habitat types. Where this was not possible, reach length was a distance of 20 times the mean channel width, or roughly one meander wavelength (Fitzpatrick et al. 1998).

A total of 80 sites in the 10 study units combined were sampled using two-pass backpack electrofishing. At 23 of the sites, three reaches were sampled within a given year (69 samples total). In these cases, the three reaches were approximately 150 m apart. At 37 sites, sampling was conducted at a single reach, each being sampled once during the 3-year period (37 samples). At the remaining 20 sites, sampling was conducted more often: twice per year, annually for 2 years, and annually

for 3 years (77 samples combined). Thus, a total of 183 samples were analyzed from the 80 sites.

Backpack electrofishing was conducted using pulsed direct current. Recommended pulse frequencies ranged from 30 to 60 pulses/s (Meador et al. 1993). Operators of electrofishing equipment received training in the sampling protocol (Meador et al. 1993) and in electrofishing principles, such as power transfer theory, to help standardize effort and increase the efficiency of electrofishing operations (Reynolds 1996). A single backpack electrofishing unit was used to conduct a sample.

All backpack electrofishing was conducted in an upstream direction. Upon completion of the first pass, fish that could be identified in the field were counted and transported downstream of the sampling reach. A second pass was then conducted. Fish that could not be identified in the field were retained for identification and enumeration in the laboratory (Walsh and Meador 1998).

Data analysis.—Species richness was estimated using the removal model (Zippin 1956; Seber 1982; Nichols and Conroy 1996). The removal model estimates two population parameters: total number (such as total population abundance; \hat{N}) and the probability of detection (\hat{p}). Formulas for the simplest removal model followed Seber and Le Cren (1967):

$$\hat{N} = (n_1)^2 / (n_1 - n_2) \quad \text{and} \quad \hat{p} = (n_1 - n_2) / n_1,$$

where n_1 represents the number of individuals (or species) from the first capture event and n_2 represents the number of individuals (or species) from the second capture event. The assumptions of the simplest removal model are (1) the population is closed, (2) probability of detection is constant among all individuals in the population, and (3) probability of detection is constant between samples. Whereas the simplest removal model can be used with two capture events, it does not allow for heterogeneity of probabilities of detection. However, the removal method can be generalized to allow for heterogeneous probabilities of detection with three or more capture events.

For each sample, species richness from the first pass was determined and the second pass was evaluated to determine if additional species were collected. Total species richness was estimated using the removal model formula:

$$\hat{S} = (s_1)^2 / (s_1 - s_2),$$

where s_1 is species richness collected in the first pass, s_2 is the number of additional species col-

lected in the second pass, and \hat{S} is the total estimated species richness (Nichols and Conroy 1996). Percent species richness of the first pass (percent of estimated total species richness) was determined using the formula $\hat{p}_{s_1} = (s_1 / \hat{S}) 100$. Note that this value is the same value as the probability of detection of a species based on presence-absence data. However, in using the above formula, \hat{p}_{s_1} is expressed as proportional species richness and not the probability of detection. In two of the 183 samples (1%), the number of unique fish species collected in the second pass was equal to or greater than that in the first pass; thus, species richness could not be estimated using the removal model for those samples. Proportional species richness values were examined for normality using normal probability plots and were arcsine-square-root-transformed to improve normality. Analysis of variance (ANOVA) was conducted to assess variation in \hat{p}_{s_1} among study units (SAS Institute 1989). Spearman's rank correlation was used to examine relations between \hat{p}_{s_1} and mean channel width for each study unit. Statistical significance was declared at $\alpha = 0.05$ for all statistical analyses.

The removal model described above estimates species richness by using information based on species presence only and does not include information about the abundance of each species. The removal model also was used to estimate probability of detection (\hat{p}_j) for each species using the formula

$$\hat{p}_j = (n_{1j} - n_{2j}) / n_{1j},$$

where n_{1j} is the number of species j individuals collected in the first pass, and n_{2j} is the number of species j individuals collected in the second pass. Values of \hat{p}_j were determined for each species j . Population abundance was estimated for each of 1,843 species entries. Of these, n_{2j} was greater than or equal to n_{1j} for 881 entries (48%). Thus, the two-pass removal model failed to calculate probabilities of detection for these entries. Given the relatively high failure rate of the removal model to estimate probabilities of detection, additional analyses related to abundance data were not conducted.

Results

Mean basin areas for each study unit ranged from 1,301 to 3,980 km² (Table 2). Mean channel widths ranged from 7.0 to 15.3 m. Mean sampling reach lengths ranged from 159.8 to 253.3 m. Mean \hat{S} values for study units ranged from 3.5 to 17.8.

TABLE 2.—Mean values of basin area, channel width, and sampling reach length for each study unit as described with abbreviations in Table 1.

Study unit	Basin area (km ²)	Channel width (m)	Reach length (m)	Number of sites
USNK	2,205	13.8	159.8	7
TRIN	2,362	9.4	251.3	8
CONN	3,642	14.8	246.1	8
REDN	3,980	10.1	160.4	10
POTO	3,421	15.3	223.6	8
WMIC	2,311	12.5	184.9	9
RIOG	1,301	7.0	185.9	4
HDSN	1,771	10.2	173.6	15
LSUS	2,140	11.9	179.8	7
CCPT	2,913	11.5	253.3	4
Combined	2,605	11.4	201.9	80

Mean \hat{p}_{s1} values for each study unit ranged from 80.7% to 100%, whereas \hat{p}_{s1} values for each site ranged from 40% to 100% (Table 3). The mean \hat{p}_{s1} value for all 10 study units combined was 89.9%. The ANOVA indicated significant differences in \hat{p}_{s1} among study units ($P = 0.003$).

The second pass produced additional species in 50.3% of the samples collected. Seven common taxonomic families—Catostomidae, Centrarchidae, Cottidae, Cyprinidae, Ictaluridae, Percidae, and Salmonidae—were selected for comparison (Table 4). Combined, these seven families contributed 115 of the 138 (83%) total taxa collected. Other families included Anguillidae, Aphredoderidae, Atherinidae, Clupeidae, Cyprinodontidae, Esocidae, Gadidae, Gasterosteidae, Lepisosteidae, Percopsidae, Petromyzontidae, Poeciliidae, Sciaenidae, and Umbridae.

Across all samples collected, cyprinids and centrarchids were the families most likely to be captured in the second pass if absent in the first pass. Cyprinids, in that way unique to the second pass, were collected in 21.9% of second-pass samples, whereas centrarchids unique to the second pass were collected in 17.5% of samples (Table 4). Collection of these two families was unique to the second pass in at least 8 of the 10 study units sampled. Of the centrarchids, largemouth bass *Micropterus salmoides* and bluegills *Lepomis macrochirus* combined contributed 9.8% of the species collected unique to the second pass. The five other families were unique to the second pass in less than 8% of all samples.

Estimates of the percent species richness of the first pass increased significantly with decreasing channel width in the Hudson River basin ($\rho = -0.55$, $P = 0.034$). Channel width was not sig-

TABLE 3.—Statistical results of estimates of total (\hat{S}) and proportional fish species richness (\hat{p}_{s1}) from 183 first-pass samples in 10 study units, as defined with abbreviations in Table 1 (estimates could not be derived for two samples using the removal method).

Study unit	Mean \hat{p}_{s1}	Range	SD	Mean \hat{S}	Number of samples
USNK	80.7	40.0–100	26.2	6.3	7
TRIN	83.0	50.0–100	16.4	10.6	27
CONN	84.0	55.6–100	16.1	9.7	23
REDN	88.1	50.0–100	14.7	10.9	30
POTO	92.1	76.9–100	7.8	17.8	16
WMIC	92.6	75.0–100	11.1	10.9	9
RIOG	93.1	66.7–100	13.7	3.5	9
HDSN	94.1	80.0–100	6.5	10.1	32
LSUS	96.3	85.7–100	5.0	11.4	19
CCPT	100	100–100	0	6.4	9
Combined	89.9	40.0–100	13.7	10.4	181

nificantly correlated with \hat{p}_{s1} for any other study unit (all $P > 0.05$). Examination of the relation between channel width and \hat{p}_{s1} suggests that \hat{p}_{s1} values of 100% were noted in streams ranging from less than 10 to greater than 40 m (Figure 1).

Discussion

The removal model can be used when only two capture events (electrofishing passes) are available (Heimbuch et al. 1997). When using the removal model with two capture events, the initial probability of detection is assumed to be equal for all individuals in the population. When using the removal model with three or more capture events the probability of detection for each individual remains constant over time, but the probability of detection between individuals may vary. Because individuals with higher probabilities of detection tend to be removed first, this formulation implies that, between any two occasions, the average prob-

TABLE 4.—Number of fish species taken in the second but not the first pass for selected families of fishes and percent of the samples and study units in which the family was collected in the second but not the first pass, where all 183 samples were combined and all 10 study units were combined.

Family	Number of species	Percent of samples	Percent of study units
Cyprinidae	26	21.9	90
Centrarchidae	11	17.5	80
Percidae	6	7.1	60
Catostomidae	10	6.6	80
Ictaluridae	7	6.6	50
Salmonidae	5	6.0	60
Cottidae	1	0.5	10

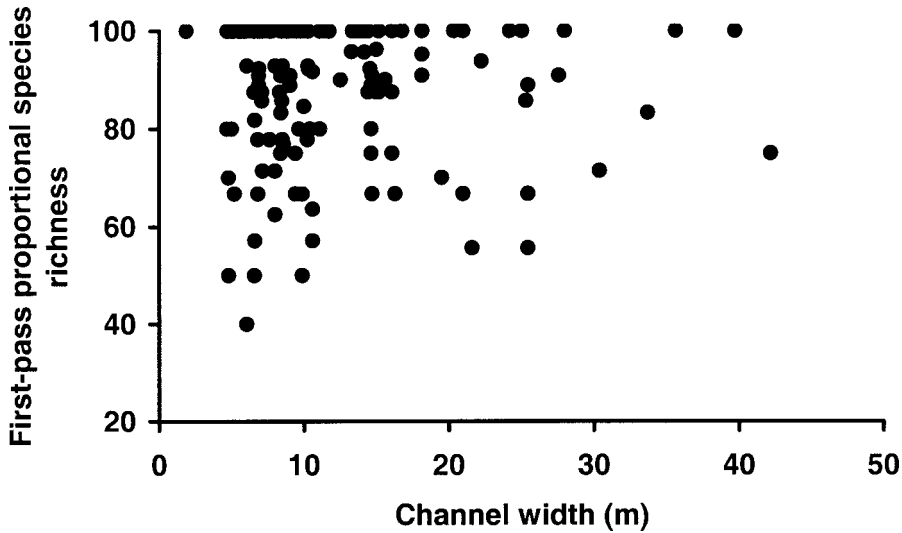


FIGURE 1.—Scatter plot of channel width (m) and proportional fish species richness of the first pass of backpack electrofishing ($\hat{p}_{1,1}$) based on National Water-Quality Assessment Program data (U.S. Geological Survey).

ability of detection for the remaining individuals in the population will decrease.

When using data from two-pass backpack electrofishing the assumption that probabilities of detection are constant between both individuals and samples cannot be tested. However, White et al. (1982) reported that if all animals have an average probability of detection of at least 0.80, two capture events will suffice because failure of the constant probability of detection assumption will not matter. White et al. (1982) also noted that to obtain useful results with the removal model, mean probabilities of detection should be at least 0.2. Even if all of the assumptions are valid, the simplest removal model can fail if n_2 is greater than or equal to n_1 .

Given the relatively high failure rate of the removal model when used to estimate probabilities of detection of individual species, significant heterogeneity of probabilities of detection may exist. For two capture events, if parameters are estimated with the removal model in the presence of heterogeneous probabilities of detection across individuals, then \hat{N} tends to be underestimated and \hat{p} tends to be overestimated (Seber 1982). This results in a deflated estimate of the population abundance and an inflated estimate of a constant probability of detection. Thus, probabilities of detection of species based on a two-pass removal model would overestimate probability of detection derived from single-pass backpack sampling, making it difficult to determine whether patterns of relative abun-

dance are real or spurious. However, when used to estimate proportional species richness, the two-pass removal model failure rate was relatively low (1%), and average proportional species richness estimates were relatively high (80.7% to 100%). This suggests that the two-pass removal model is sufficient for estimating proportional species richness of single-pass electrofishing when averaged across at least seven sites throughout a river basin.

Mean first-pass proportional species richness estimates based on two-pass sampling in our analysis were comparable to first-pass proportional species richness estimates based on three or more passes in other studies. Using five-pass backpack electrofishing for sampling two streams in Australia, Pusey et al. (1998) reported first-pass proportional species richness estimates of 89% (mean channel width, 6.9 m) and 82% (8.1 m). Using a towed electrofishing barge in Wisconsin, Simonson and Lyons (1995) captured an average of 10 species with three to four passes in streams less than 8 m wide versus 9 species with a single pass. Patton et al. (2000) evaluated the effort needed to estimate species richness in small streams (2.5–10.2 m wide) in Wyoming and reported that 90–100% of species richness could be collected by electrofishing with a shoreline generator. Overall, for all our 10 study units combined, we detected about 90% of the estimated total species during the first pass in streams that averaged 11.4 m in width. However, at individual sites, first-pass proportional species richness was as low as 40%.

Backpack electrofishing, particularly the single backpack electrofishing unit, may not be efficient in relatively wide streams. The data analyzed in this study reflect a wide range of stream sizes sampled as part of a national monitoring program; some of those streams may be wider than those typically sampled by backpack electrofishing in studies of smaller geographic scale. However, channel width was not related to \hat{p}_{s1} in 9 of the 10 study units. In the Hudson River basin where \hat{p}_{s1} increased significantly with decreasing channel width, \hat{p}_{s1} values ranged from 80% to 100%. At sites where \hat{p}_{s1} was 50% or less, channel widths ranged from 4.8 to 9.9 m. Thus, low proportional species richness detected in the first pass at some sites was not a function of channel width alone.

Smaller channel widths may support comparatively fewer species. One might expect \hat{p}_{s1} values to be lower where total species richness is relatively high. Because the estimated values of \hat{S} and \hat{p}_{s1} are not independent, direct statistical analysis of the relation between the two cannot be conducted. However, the highest and lowest values for \hat{p}_{s1} were collected at sites where estimated values of \hat{S} were among the lowest. Thus, it does not appear that there is a relation between high values of \hat{S} and low values of \hat{p}_{s1} .

Of the species collected that were unique to the second pass, cyprinids and centrarchids were collected most frequently across at least 8 of the 10 study units, which is not surprising for cyprinids. That is, in addition to fish population and fish community characteristics and physical factors such as stream size, electrofishing efficiency is also influenced by characteristics of fish species and individual fish. For example, electrofishing tends to be selective for larger fish, both intraspecifically and interspecifically (Reynolds 1996). Also, fish with fine scales (e.g., salmonids) tend to be more vulnerable to detection by electrofishing than fish with coarse scales (e.g., cyprinids). Thus, it would seem unlikely that single-pass backpack electrofishing would be efficient in collecting cyprinid species occurring at a site.

The relatively frequent occurrence of centrarchids unique to second-pass samples may not seem likely. However, largemouth bass, bluegills, and other species may be able to detect and avoid the electrical field. In a study using two-pass pooled abundance data to estimate probabilities of fish detection for streams in Maryland, Heimbuch et al. (1997) reported relatively low probabilities of detection for largemouth bass and bluegills. These species tend to be associated with deeper areas and

cover, such as aquatic vegetation and submerged woody debris. Such areas may not allow for efficient single-pass backpack electrofishing.

Standardized sampling of fish on a large geographic scale has many benefits (Bonar and Hubert 2002). Decisions regarding standardized sampling effort and whether to conduct one or more electrofishing passes must be based on study objectives. Standardized sampling protocols as part of regional and national monitoring programs vary. For example, the U.S. Environmental Protection Agency's (USEPA) Environmental Monitoring and Assessment Program design utilizes single-pass electrofishing within a reach blocked off with nets placed at both ends of the reach (Lazorchak et al. 1998). By comparison, the NAWQA Program sampling methods use two-pass electrofishing without block nets. The USEPA Rapid Bioassessment Protocols are based on electrofishing as the recommended technique, with sufficient effort to collect 80–90% of the expected number of fish species (Plafkin et al. 1989). Multiple-pass electrofishing at a large number of sites as part of a standardized sampling protocol across a large geographic area may not be cost-effective. Our analysis of NAWQA data and use of the removal model suggest that, for projects with a large geographic scale and wide range of stream sizes, single-pass backpack electrofishing data collected without block nets may generally represent 80–100% of estimated total species richness. However, single-pass data may underrepresent species richness (by as much as 60%) in some streams, particularly for cyprinids and centrarchids, because of a number of factors such as stream size, fish size, and fish behavior.

Recent studies suggest that a thorough sample to characterize species richness in streams may be obtained with single-pass sampling (Paller 1995; Simonson and Lyons 1995) but that data from a single-pass alone may compromise the ability to relate fish community structure to environmental conditions (Pusey et al. 1998). Data collected by single-pass sampling alone provides little opportunity to assess the effectiveness of sampling for species richness and the relative abundances of individual species. Whereas the removal model can be used with data collected by two-pass sampling to assess the effectiveness of sampling for species richness, it probably is of limited value in adequately assessing probabilities of detection for individual species and, thus, assessment of relative abundance information. To better evaluate the ad-

equacy of single-pass sampling, some multiple-pass sampling may be necessary.

With multiple-pass sampling the general removal model that allows for heterogeneity can be used to determine mean probabilities of detection. Compared with two-pass data, multiple-pass sampling provides less biased estimates of \hat{N} and \hat{p} . By dividing single-pass individual species abundance data by a mean probability of detection for that species, possible bias in rank abundances based on single-pass data can be assessed (Mitro and Zale 2000). If rank abundances are biased, these biases can be adjusted by using such an approach. A combination of multiple-pass and single-pass sampling across broad geographic areas provides opportunities to reduce overall data-collection effort and to better assess the precision of fish community characterizations.

Acknowledgments

We thank Ken Burnham, Jim Reynolds, Gary White, three anonymous reviewers, and the associate editor for their helpful comments and suggestions. We also thank the biologists, hydrologists, and technicians, too numerous to name individually, who spent their time and effort collecting fish community samples as part of the NAWQA Program.

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