USING A RESTRICTED ADAPTIVE CLUSTER SAMPLING TO ESTIMATE PACIFIC HAKE LARVAL ABUNDANCE

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ABSTRACT

In adaptive sampling the procedure for selecting sample sites and allocating effort depends on data collected during the survey. From March 9 to 27, 1995, stratified adaptive sampling was used to survey Pacific hake larvae because the spatial distribution of the larvae is highly patchy and because adaptive sampling is an efficient means of surveying such a population.

The survey, conducted between Los Angeles and San Francisco and covering an area of 202,115 km^2 (59,540 n mi^2), was designed to test the feasibility of adaptive sampling. Because of limited survey time, we used a restricted design imposing a maximum number of stations in each stratum. A stratified, two-stage cluster Horvitz-Thompson (HT) estimator and a simple stratified (SS) sample mean were used to determine mean catch per tow. The variance of the HT estimate included the variance resulting from subsampling within a cluster and was high. The mean density from SS sampling was biased downward, but its variance was a 2-fold reduction over what it would have been if the same number of samples had been allocated proportional to the area size within strata. Nonetheless, our adaptive sampling was relatively easy to implement, and it provided biological information within patches.

INTRODUCTION

The more patchy egg and larval distribution becomes, the larger a sample size is needed to maintain the same level of precision. Thus large sample sizes are needed to precisely estimate the abundance of eggs or larvae with a highly patchy distribution (Smith 1981). Of the fishes that have been studied in the California Current, the Pacific hake (*Merluccius productus*) has by far the most patchy egg and larval distribution. The standard deviation for hake larvae counts/10 m^2 is about 10 times the mean value (Smith 1995); i.e., the coefficient of variation (CV) = 10, whereas the standard deviation of anchovy and sardine larval counts is only 3 times the mean value. Owing to their highly contagious distribution, it may be impractical to achieve a reasonable level of precision (CV = 20%) for an estimate of hake larval abundance with conventional simple random sampling (SRS), because too many samples would be required (Stauffer 1985).

When a population has a patchy spatial distribution, the precision of abundance estimates may be improved by using adaptive sampling rather than SRS (Seber 1986). In an adaptive sampling design, the selection of sample sites and the allocation of sampling effort depends upon data collected during the survey. Adaptive sampling designs have been used for trawl surveys (Francis 1984; Thompson and Seber 1996) and forest surveys (Roesch 1993), and have been evaluated for waterfowl (Smith et al. 1995) and plant surveys (Brown 1996a, b), but they have not been evaluated for ichthyoplankton surveys.

The purpose of this paper is to examine the feasibility of using adaptive sampling to estimate abundance of the highly aggregated larval Pacific hake (Smith 1995). We empirically compare the relative efficiency of estimates based on adaptive sampling to estimates based on simple random sampling and conventional stratified sampling schemes. Because patch size may be estimated from clustered samples, we also provide an estimate of the size of patches of larval hake. The size of larval patch not only serves as a guide for future adaptive sampling strategies, but is also a useful early life-history parameter (Hewitt 1981).

THEORY OF ADAPTIVE CLUSTER SAMPLING

The conceptual basis of adaptive sampling was developed in the late 1960s (Basu 1969), and the theory has been improved considerably in recent years (Thompson 1992; Brown 1994, 1996a, b; Thompson and Seber 1996). Adaptive cluster sampling starts with a random sample of n units (net-tow stations in our application). If any of the initial observations exceeds or is equal to a predetermined critical value (number of larvae), sampling units in the neighborhood of that observation are also sampled.

The *neighborhood* can be any arbitrary pattern. The neighborhood relationship is symmetric; e.g., if unit a is in the neighborhood of unit b, then unit b is in the neighborhood of unit a. However, the units in the neighborhood could be noncontiguous (Thompson 1992; Thompson and Seber 1996). If any one of the additional observations meets the condition, then observations in its neighborhood are taken. This procedure continues until no observations meet the condition.

All contiguous observations that meet the condition constitute a *network*, and observations that do not meet

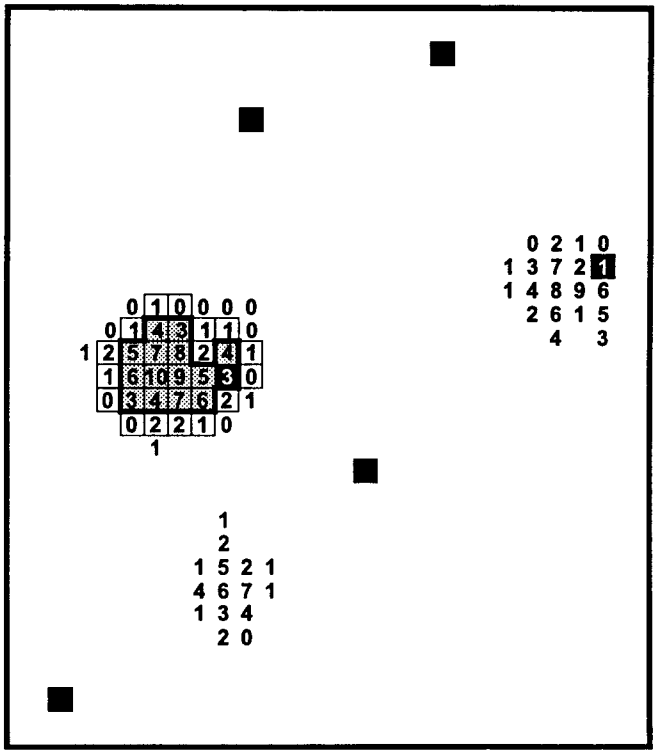

Figure 1. An example of adaptive sampling with a complete enumeration of network encountered: dark squares are the initial random sample size of 6. There are three patches. Numbers in each square indicate the number of larvae. The critical value is 3. The neighborhood of a unit is four units each in the north-south and east-west directions. Two observations in the initial sample intersect with two patches. One observation was 3. The resulting network was outlined in bold. The edge units are units with fewer than 3 larvae, indicated by open squares. Notice that in this patch 3 larvae were not sampled. Another initial observation was 1, therefore no further observations were taken in its neighborhood.

the condition are called *edge units*. A network plus edge units makes up a *cluster*. A *patch*, in this paper, is a group of fish larvae. Therefore a network or a cluster can be a patch of different scale and a cluster may be a subset of a large patch. Edge units are not used in the computation unless they are part of the initial sample. A sampling unit that does not meet the condition but was included in the initial sample is considered as a network of size 1 (figure 1).

The estimators we used for larval density were a stratified, adaptive two-stage cluster Horvitz-Thompson (HT) estimator modified from the adaptive single-stage cluster estimator (Thompson 1990, 1991), even though our adaptive sampling design is a restricted one, and a simple stratified (SS) mean. The adaptive cluster sampling procedures proposed by Thompson (1992) require continuous sampling in the neighborhood until observations no longer meet the criteria. This approach will not be practical for population-scale studies of hake larvae in the open ocean if the neighborhood consists of adjacent sampling units, because ship time is limited and the potential spawning habitat is vast.

In this study, we did not use a single definition of *neighborhood*, and the neighborhood was not symmetric, as shown in figure 1. We considered that the sampling units which met the criteria were a random sample from a network, and we therefore used them to estimate the mean density per tow in the network. We then estimated the area covered by a network by measuring the area surrounding a group of stations where the catch was at least as great as a critical value.

TABLE 1

Mean, Standard Deviation (SD), and Number of Stations (*n*) from Initial Stations, Stratum Area, Stations Allocated (*n*) for Optimal Stratified (OSS), Proportional Stratified (PSS), and Unbiased Adaptive Stratified (UASS) Sampling; Mean and Standard Error (SE) for Horvitz-Thompson (HT) and Simple Stratified (SS) Sampling, March 9–15, 1995

	Initial A-stations				Number of stations (*n*)				HT		SS	
Stratum	Mean	SD	*n*	Area (km^2)	OSS	PSS*	UASS	HT or SS	Mean	SE	Mean	SE
1	2	2.65	3	15,635	3	4	3	3	2	1.53	2	1.53
2	4	5.29	3	13,764	5	3	2	3	4	3.05	4	3.06
3	9	12.73	2	10,952	9	3	5	2	9	8.98	9	9.00
4	4.5	2.12	2	10,952	2	2	5	2	4.5	1.50	4.5	1.50
5	0	0.00	2	10,952	0	3	2	2	0	0.00	0	0.00
6	0	0.00	2	10,952	0	3	2	2	0	0.00	0	0.00
7	0	0.00	2	10,952	0	2	2	2	0	0.00	0	0.00
8	1	1.41	2	10,952	1	3	2	2	1	1.00	1	1.00
9	16.5	23.30	2	13,764	17	3	2	8	19.19	19.75	10.75	6.05
11	0.33	0.58	3	13,764	1	3	5	3	0.33	0.33	0.33	0.33
12	4.5	6.36	2	10,952	5	3	2	2	4.5	4.50	4.5	4.50
13	0.5	0.71	2	10,952	1	2	2	2	0.5	0.50	0.5	0.5
14	0	0.00	2	10,952	0	3	2	2	0	0.00	0	0.00
15	2	1.41	2	10,952	1	3	2	2	2	1.00	2	1.00
16	12.5	0.71	2	10,952	1	2	2	6	6.43	6.11	6.5	2.20
17	5.5	0.71	2	10,952	1	3	5	2	5.5	0.50	5.5	0.50
18	0.67	1.15	3	13,764	1	3	3	3	0.66	0.66	0.66	0.38
Total or mean			38	202,115	48	48	48	48	3.61	1.51	3.04	0.73

*Number of stations was reduced from 3 to 2 for four strata, so that the total number of stations = 48.

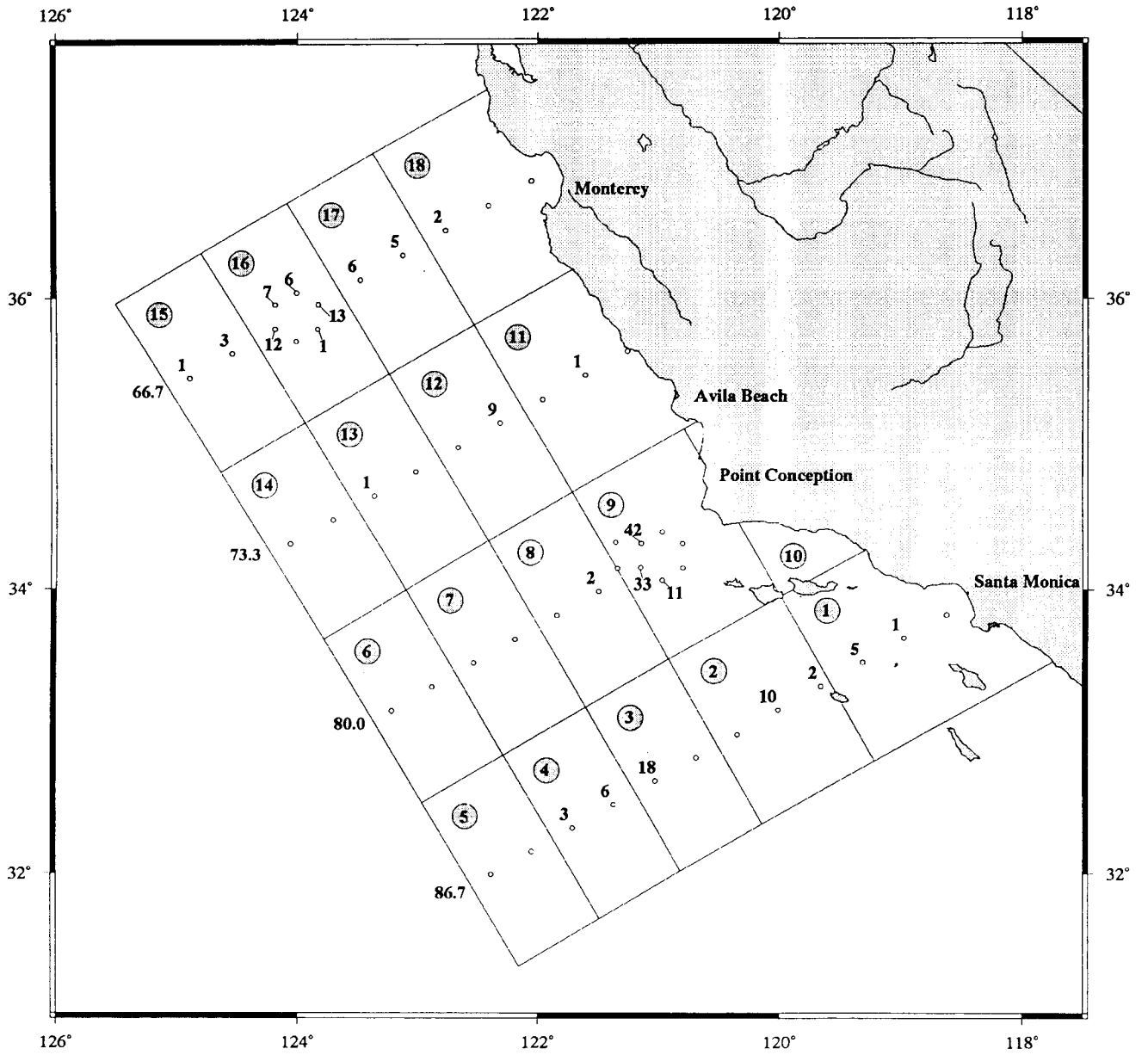

Figure 2. Stations occupied within each of 18 strata in the survey for Pacific hake larvae, March 9–15, 1995. Small numerals indicate the number of larvae caught at each station. Circled numbers identify strata. Decimal numbers identify CalCOFI lines.

MATERIALS AND METHODS

Survey Design

In order to test the adaptive sampling technique, a survey was conducted during March 9–27, 1995, covering an area of 202,115 km^2 (59,540 n mi^2), from California Cooperative Oceanic Fisheries Investigations (CalCOFI) survey line 66.7 south to line 86.7. Each line extended to 200 n mi offshore (table 1 and figure 2). The survey area was divided into 18 rectangular strata with two initial stations in each stratum except for strata 1, 2, 11, and 18, which had three initial stations each (stratum 10 was excluded from analyses because only one station was occupied). The initial stations were on CalCOFI lines 86.7, 80.0, 73.3, and 66.7. Each stratum was approximately 10,952 km^2 (3,200 n mi^2). The initial stations (points A in figure 3) were 37 km (20 n mi) apart. Ichthyoplankton samples were taken at the initial stations in each stratum with bongo nets (71-cm-dia. opening with 505-μm-mesh nets) towed to a nominal depth of 212 meters (depth permitting) and retrieved obliquely (Smith and Richardson 1977). The Pacific hake larvae in each tow were identified and counted before the ship departed from the sampling station.

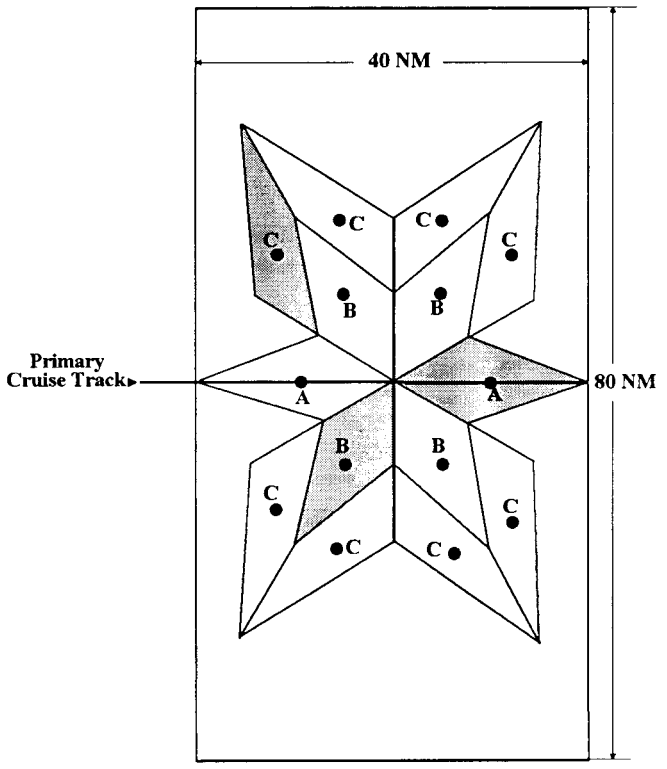

Figure 3. Diagram of survey pattern under adaptive sampling for Pacific hake larvae within a stratum. A-stations are the initial stations. B- and C-stations are added when catch in the previous station exceeds a critical value. Distance is 37 km (20 n mi) from A to A and is 18.5 km (10 n mi) from A to B, B to C, B to B, and C to C. *Shading* indicates the area represented by each station. Area for A and B is 312.47 km^2 (91.3 n mi^2); area for C is 388.45 km^2 (113.5 n mi^2).

If any of the samples from the initial stations (A-samples) contained a number of larvae more than or equal to a critical value, two additional B-stations (B-samples) were added to the north and south from each A-station (figure 3) to form a polygon. If any of the four B-stations contained more than or equal to the critical value, then two C-stations (C-samples) were added to the nearby area of a B-station (figure 3) so that the distance between adjacent stations was 18.5 km (10 n mi), except that the distance between two A-stations was 37 km (20 n mi). The distance between additional stations (18.5 km; 10 n mi) was our best guess of the maximum diameter of spawning hake schools from data provided by Stauffer (1985) and Mark Saunders (pers. comm.).

Adaptive cluster sampling (Thompson 1992) requires this procedure to continue until catches no longer meet the criterion, but in this study sampling stopped at C-stations. Such a stopping rule limits the number of unscheduled samples, thereby limiting the ship time required to complete the survey. This restricted sampling design (Brown and Manly, in press) may bias the estimates of density (the extent of this bias could be estimated by simulation).

Selecting a Critical Value

Selecting a critical value (number of larvae needed for adding extra stations) required a consideration not only of the expected densities of hake larvae, but also of the time that could be devoted to taking extra samples while still completing all scheduled samples. We decided that we might not be able to complete the survey in the scheduled two weeks if more than four strata with extra stations were allowed. To estimate the critical value that would fill this requirement, we first divided the survey area of 1993 and 1994 CalCOFI surveys into strata. Each stratum had 2 to 4 stations, similar to the 1995 survey (figure 2).

Mean and standard deviation of larval hake catch for each stratum were obtained from data collected during the two CalCOFI surveys. We then followed the adaptive sampling procedures of increasing the number of samples by four each time the maximum larvae within a stratum exceeded or equaled a predetermined critical value. Applying critical values from 2 to 20, we obtained the total number of strata with maximum catch greater than or equal to a given critical value and the variance of the grand mean.

The final critical values were determined so that a maximum of five strata could include extra stations. Since the mean larval densities were different between 1993 (1.081/tow) and 1994 (6.61/tow), the final critical values differed. A critical value of 6 resulted in five strata with extra stations when 1993 data were used, while a critical value of 20 resulted in three strata with extra stations when 1994 data were used. For 1994 data, if the critical value was reduced from 20 to 15, the variance of the grand mean decreased only slightly. Assuming that the larval density in 1995 was close to the level of 1994, we decided to use a critical value of 20.

Actual results required us to change the critical value midway in the survey. After occupying half of the survey pattern (CalCOFI lines 86.7 and 80.0) we had taken only one set of additional samples (figure 2). Consequently, we lowered the critical value from 20 to 10. With the lower value, one additional set of samples was taken in stratum 16; the total number of samples used in our analyses was 48, taken from March 9 to 15.

Estimating Hake Larval Density

We estimated larval density with the two-stage cluster Horvitz-Thompson estimator (HT) and a simple stratified (SS) sample mean from the resulting stations within each stratum, recognizing that both are biased for the restricted adaptive sampling. We chose HT because it was designed to reduce the bias resulting from nonrandom sampling. The HT estimates were computed only for strata in which the number of larvae caught in at least one of the initial stations exceeded or was equal to

the critical value. For other strata, we used simple sample means. For comparison purposes, we also computed an unstratified SRS mean density from all initial stations.

Horvitz-Thompson (HT) estimator. The adaptive sampling procedure allocates larger sample sizes to strata where a large catch is observed at one of the initial stations. Therefore the probability that a station will be occupied depends on the catch at stations nearby; the probability is a function of the patch size and larval density. Each station does not have equal probability of being selected. This sampling procedure constitutes a probability sampling design (Overton and Stehman 1995). An unbiased estimator was first introduced by Horvitz-Thompson (1952; see also Cochran 1977). The original HT estimator for the population total, T, is

$$\hat{T}_y = \sum_{i \in s} \frac{y_i}{p_i}$$

where p_i is the inclusion probability for each observation y_i (e.g., the larval count from each station, or the total larvae from a network), and the summation is over the sample observed. The HT estimator downweights observations that are more likely to be observed than others. Since the observations are overrepresented in the sample, they are divided by their inclusion probability to reduce overrepresentation.

For adaptive sampling, Thompson (1992) modified the HT estimator to make use of observations that are less than the critical value only when they are included in the initial sample. In Thompson's procedure, the network in which one initial station is located is enumerated completely, so there is no sampling error in the total count of the network; this is a single-stage cluster sampling design.

In the case of hake larval sampling, without a single definition of neighborhood, when the number of larvae was equal to or greater than a predetermined value, two stations 10 n mi away from each initial station were sampled. Therefore the sampling scheme is an adaptive two-stage cluster sampling. A-stations are used to locate patches (stage 1), and B-stations and C-stations are used to subsample the patches (stage 2; figures 1, 3).

Any station where the larval count was equal to or greater than the critical value is denoted as a "G-station." The area surrounding adjacent G-stations was used to estimate the area of a network (network size). G-stations can be considered as a random sample from a network[1], and the average of number of larvae from G-stations is used to estimate the mean larvae per tow for that network. The probability that any of the initial stations intersect a network is called the intersection probability (α; equation A2, appendix) rather than the inclusion probability, because stations that do not meet the condition will be included in the computation only if they are initial stations (Thompson 1992). The mean density of larvae per tow, $\hat{y}_i$, in the ith stratum is computed from equation A3 (appendix) as

$$\hat{y}_i = \frac{1}{A_i} \sum_{j=1}^{K} \frac{\bar{y}_j a_j z_j}{\alpha_j} = \frac{1}{A_i} \sum_{j=1}^{k} \frac{\bar{y}_j a_j}{\alpha_j} \quad (1)$$

where K is the number of total patches in the ith stratum, which may never be known, and k is the total patches sampled. In the jth patch observed,

$$\bar{y}_j = \sum_{u=1}^{m_j} \frac{y_{ju}}{m_j}$$

is the sample mean per tow from m_j tows, and m_j is the number of G-stations sampled in the network, including the jth A-station. On the population level, z_j is equal to 1 if the jth network was sampled, and zero otherwise. Therefore $\alpha_j = p(z_j = 1)$ is the intersection probability for the jth network (equation A2 in appendix); A_i is the area for ith stratum; and a_j is the network size (km^2), estimated by the total area represented by adjacent G-stations including the jth A-station.

The area size represented by A- and B-stations was determined so that A- and B-stations would represent equal areas, as indicated by the inner star in figure 3. We then defined the area for C-stations in a symmetric fashion. The area for one C-station, 388.45 km^2 (113.5 n mi^2), was slightly larger than that for each A- and B-station, 312.47 km^2 (91.3 n mi^2; figure 3).

The variance of $\hat{y}_j$ (equation 1) did not include the variance of estimated network size (equation A5), therefore the variance of $\hat{y}_j$ would be underestimated. For detailed derivation and the variance, see appendix.

We used the general formula for stratified sample mean to compute the overall mean density for the survey area. The stratified sample mean is

$$\bar{y} = \sum_{i=1}^{I} \bar{y}_i \frac{N_i}{\sum_{i=1}^{I} N_i} = \sum_{i=1}^{I} \bar{y}_i \frac{A_i}{\sum_{i=1}^{I} A_i} \quad (2)$$

[1]*Network* in this paper refers to a patch of units with larval counts greater than or equal to the critical value.

where in the ith stratum, $\bar{y}_i$ is the estimate of mean density per tow; e.g., $\bar{y}_i = \Sigma y_{ij}/n_i$ is the sample mean under simple random sample (SRS). N_i is the total possible sample size. A_i is the area of the ith stratum. The standard error (SE) of stratified sample mean for a sample size $n = \Sigma n_i$ is

$$SE = \sqrt{\sum_{i=1}^{I} se^2_i \left[\frac{A_i}{\sum_{i=1}^{I} A_i}\right]^2} \qquad (3)$$

$$= \sqrt{\sum_{i=1}^{I} \frac{\sigma^2_i}{n_i} \left[\frac{A_i}{\sum_{i=1}^{I} A_i}\right]^2} \quad \text{if } \bar{y}_i \text{ is simple sample mean}$$

where σ_i is the standard deviation in the ith stratum, and can be estimated by the sample standard deviation s_i from the initial stations.

Simple stratified (SS) sample mean. For simple stratified sampling, the sample mean ($\bar{y}_i$) and standard deviation (s_i) were computed from all stations occupied in the ith stratum from the adaptive procedure. This estimate is biased for any adaptive sampling (Francis 1984; Thompson 1992) because sampling is not random and because extra samples are taken from areas of high abundance. Nevertheless, the simple stratified sample mean can be used as a relative index of mean density, and its variance can be compared with the variance of other stratified sample means (table 2).

Comparison of Adaptive Sampling with Standard Conventional Sampling

The standard approach to survey design requires the allocation of sample size to individual strata according to the area (A_i), the standard deviation (σ_i), and the cost of sampling within strata. Such statistical design, termed optimal stratified sampling (Cochran 1977), is seldom used in pelagic surveys because one rarely can anticipate what the variance may be in a given stratum. Nevertheless, we compared the results of adaptive sampling with those of optimal stratified sampling (OSS), proportional stratified sampling (PSS), and simple random sampling (SRS). We also included an unbiased adaptive stratified sampling (UASS) proposed by Thompson et al. (1992; table 2) in the relative efficiency comparison (see below).

Because the cost of sampling is the same among strata, the sample allocation for optimal stratified sampling is $n_i \sim \sigma_i A_i$, and for proportional stratified sampling it is $n_i \sim A_i$. For standard deviation within strata, we used sample standard deviation, s_i, computed from A-samples.

The UASS is a variation of a stratified adaptive sampling procedure for animal populations in which sample size in a given stratum depends on the observations obtained in the previous stratum. The conventional stratified sample mean is unbiased under such a sampling scheme (table 2). Under UASS, if in the previous stratum one of the A-samples exceeded or was equal to the critical value, we would add three extra stations randomly in space (table 1). The variance of the estimate was computed according to equation 3, where standard deviation was computed from A-stations. Therefore, except for HT, SS, and SRS, the difference in variances among sampling schemes was primarily due to the different sample size allocated to each stratum.

To compare the relative efficiency of any two estimates, say X_1 to X_2, we computed the ratio of the variance of X_2 to variance of X_1:

$$\text{RE}(X_1 \text{ TO } X_2) = \text{var}(X_2)/\text{var}(X_1) = (SE(x_2)/SE(x_1))^2 \qquad (4)$$

TABLE 2

Estimates of Hake Larval Density and Their Standard Errors (SE) from Horvitz-Thompson (HT), Simple Stratified (SS), and Unbiased Adaptive Stratified Sampling (UASS) under Adaptive Sampling, and Proportional Stratified Sampling (PSS), Optimal Stratified Sampling (OSS), and Simple Random Sampling (SRS)

Sampling design	Criteria of sample allocation	Density estimate (number/tow)	SE	Relative efficiency $(SE(PPS)/SE)^2$	n
Adaptive					
HT	Catch within stratum	3.61	1.51	0.48	48(39[a])
SS	Sample size from HT	3.04	0.732	2.06	48
UASS	Catch in previous stratum	—[b]	1.226	0.73	48
Conventional					
PSS	Area	—	1.051	1.00	48
OSS	Area and standard deviation	—	0.693	2.30	48
SRS		3.50	1.066	0.97	38
			0.948	1.23	48

Except HT and SS, the variances of estimates were computed from the within-stratum variance based on data collected at initial A-stations and allocated sample size in each stratum.

[a]Number of stations used in calculation.

[b]No actual survey took place. Only standard error was computed (see text).

For example, the relative efficiency of the HT estimate to a proportional stratified sampling estimate is Var(PSS)/Var(HT). Except for HT and SS, a total resulting sample size of 48 was allocated to each stratum according to each sampling scheme, and we then computed the variances of the stratified sample mean for each sampling scheme (equation 3).

RESULTS

Hake Larval Mean Density per Tow

The mean and standard deviation for the number of hake larvae per tow, computed from initial stations (A-samples) in each stratum (columns 2 and 3 of table 1), indicated that strata 9 and 16 had a high abundance of larvae. The HT adaptive sampling procedures were followed in strata 9 and 16, although a single high catch of 18 larvae occurred in stratum 3.

In stratum 9, the critical value was 20. At the first A-station, 33 larvae were caught, so a total of four B-stations were occupied (figure 2). The four B-samples each had catches of 42, 0, 0, and 11. Therefore two C-samples were taken 10 n mi away from one B-station with catch = 42. Two C-stations had zero catch. The other three B-stations were edge units, because catches were less than the critical value of 20.

We assumed that two stations with catches of 33 and 42 were from a single patch, and we computed the network size, a_1, as the total area represented by these two stations: 91.3 n mi^2 × 2 × (1.85 km/n mi)^2 = 624.94 km^2 (figures 2 and 3). The mean density of larvae in the first network, $\overline{y}_{9,1}$, is (33+42)/2 = 37.5. The catch of the second A-sample, $\overline{y}_{9,2}$, is zero ($\overline{y}_{9,2}$ = 0). Therefore, we sampled one patch from the first A-station in stratum 9.

For the HT estimate, the intersection probability for the one network was $\alpha_1 = 1 - (1 - 624.94/13764)^2 = 0.0887$ (equation A2). The HT mean density for the stratum, $\hat{y}_9$, is (37.5 × 624.94/0.0887/13764) + 0 = 19.19 (equation 1 and table 1). The sample variance of mean density was reduced to one term since there was only one nonzero network (equation A5): $SE(\hat{y}_9) = 19.75$.

In stratum 16, the critical value was set at 10. Two A-samples contained 12 and 13 larvae, respectively, which exceeded the critical value, so four B-samples were taken, resulting in catches of 7, 6, 1, and 0 (figures 2, 3). Since the number of larvae in B-samples was less than 10, these samples were treated as edge units, and no C-samples were taken. In this stratum, we assumed that the two A-samples came from one patch, therefore the area of the network is the area represented by two A-stations: a_1 = 624.94 km^2. The intersection probability, α_1, was 0.1108 (equation A2). The modified HT mean density, $\hat{y}_{16}$, for the stratum is 12.5 × 624.94/0.1108/10952 = 6.43 (equation A3) with $SE(\hat{y}_{16})$ = 6.11 (equation A5).

The modified two-staged HT estimate of larval mean density for the entire survey area was 3.61 (SE = 1.51; equation 2 and table 1) calculated from 39 stations. The other two estimates of mean density were 3.04 (SE = 0.732) for simple stratified (SS) sampling, where within-stratum variance was computed from resulting stations by means of the restricted adaptive sampling design (columns 12 and 13 of table 1), and 3.50 (SE = $s/\sqrt{48}$ = $6.57/\sqrt{48}$ = 0.948) for unstratified SRS where the standard deviation (s = 6.57) was computed from 38 A-samples (table 2 and figure 2).

Relative Efficiency

An estimated relative efficiency (equation 4) with respect to proportional stratified sampling (PSS) was computed for unstratified simple random sampling (SRS; n = 48), optimal stratified sampling (OSS), Horvitz-Thompson (HT), simple stratified (SS), and unbiased adaptive stratified sampling (UASS) designs (table 2). The standard error for OSS, PSS, and UASS was computed on the basis of sample standard deviation from initial A-stations and the sample size allocated to each stratum (tables 1, 2). The standard error was 1.051[2] for PSS, and 1.226 for UASS (table 2). The SE for the OSS estimate was 0.693, the lowest of all estimates. Standard errors for SRS with n = 38, HT and UASS were higher than proportional stratified sampling. The relative efficiency (HT to PSS) was 0.48. This means that HT was less efficient than proportional stratified sampling. The relative efficiency (SS to PSS) was 2.06, and the sample size for PSS had to be two times the sample size for SS to achieve the same precision.

If the UASS (Thompson et al. 1992) had been used, it would have produced unbiased estimates. The variance of UASS was high in this example because allocated sample size was small in strata 9 and 16, where the variance was high; and the allocated sample size was large in strata 11 and 17, where variance was low (table 1). If we had used a lower critical value, then additional stations would have been allocated to strata 9 and 16, and the variance of the estimate would be lower.

DISCUSSION

An important application of this restricted adaptive ichthyoplankton sampling would be to improve the precision of estimates of adult spawning biomass from daily or annual egg production methods, or from larval production methods (Hunter and Lo 1993) and to obtain biological information within patches. Improving the

[2]Sqrt((2.65^2/4 × 15635^2 + 5.29^2/3 × 13764^2 + . . . + 1.15^2/3 × 13764^2)/20211^2) (columns 3, 5, and 7 of table 1)

precision of a larval or egg production estimate of biomass with adaptive sampling requires (1) that eggs or larvae of the target species can be identified rapidly on shipboard; (2) that the distributions of the egg or larval stages are sufficiently patchy to be worth the extra effort of adaptive sampling; (3) the computation of a suitable critical value; (4) minimization of the bias of sample mean estimates; (5) selection of an appropriate survey design; and (6) an estimate of the optimal distance between adaptive samples. The first two conditions require no elaboration, but the latter four warrant further discussion.

Critical Value

If we had set our critical value at 10 instead of 20 before starting our survey, we would have been able to include four instead of two patches in the survey. We expect this would have reduced the variance of the estimate both by increasing sample size and by sampling two more clusters. Fearing that we would use up all the available ship time without completing the pattern, we used our estimate from the 1994 survey (20 larvae) rather than the mean of the two critical values from the 1994 and 1993 surveys (13 = {20+6}/2).

Although we set our critical value too high, our mid-survey revision of the critical value did not affect the accuracy of the estimate of larval density because we used a stratified design. Thus critical value selection is important but not an irrevocable choice as long as a stratified design is used. Brown (1996a, b) suggested that a large critical value would increase the precision of an estimate, but only (we would add) as long as the value is not so high that it substantially reduces the chance of sampling patches.

An alternative to selecting a critical value prior to the survey is to use an order statistic from the initial random sample (Thompson and Seber 1996). The adaptive sampling will be performed in the neighborhood of initial sites whose observations have values greater than or equal to, say, the 90th percentile of the initial observations. This order statistic method was used for a terrestrial pollution survey (Thompson and Seber 1996) and may not be practical for marine surveys.

Bias

Although restricted adaptive sampling produces a biased estimate, in our example the mean densities from HT and SRS (n = 38) were very close: 3.61/tow and 3.5/tow. If, in stratum 16, two A-samples were assumed to belong to two separate patches, the mean density from HT would have been 3.91. Thus HT appears to reduce the bias under the restricted adaptive sampling. The simple stratified (SS) mean under the adaptive sampling was 3.04, lower than both the HT and SRS estimates (an apparent underestimate of the mean density). However, the SE of the SS mean was lower than that of the HT estimate (table 2). The results of the study demonstrated that the variance of HT under restricted sampling was higher than for other conventional sampling designs. Simulations are being done to verify our conclusions and to estimate the biases for HT and SS, and their variances.

Since the variance of the HT estimate includes the variance due to subsampling but not the variance for estimating network size, the variance of HT is underestimated and the magnitude of underestimation is unknown. Although 48 stations were occupied in leg 1 of the survey, for the HT estimate, only initial stations and one station that had met the conditions were included in the computation. As a result, the total number of stations used in HT was 39.

Survey Design

The retrospective comparison of relative efficiency indicated that SS was more efficient than most sampling designs, even though SS was biased downward. This still speaks well for adaptive sampling of ichthyoplankton, since the optimal sampling design (stratified sampling weighted by the mean and variance in each stratum) is unrealistic for pelagic species. The bias of SS can be estimated by simulation.

Our adaptive sampling plan was easy to implement because the location of each station was predetermined. We assumed that larval patches are randomly distributed in the ocean and that their locations are unknown prior to the survey. Fish larvae move much more slowly than the research vessel (Smith and Hewitt 1985); therefore a larval patch can be considered as stationary when it is sampled.

In our survey, B-stations were located between two A-stations to save survey time. Alternatively, B-stations can be centered around a single A-station with a catch equal to or greater than the critical value, which was the original intention of the adaptive sampling.

The restricted sampling plan is more practical to implement than one-stage cluster sampling when the neighborhood consists of adjacent sampling units (Thompson and Seber 1996), since the time required to completely enumerate each patch encountered may prevent sampling of more than one or two strata. But subsampling patches increases the variance of the HT estimate. In our example, the relative efficiency of the estimates from the restricted two-stage sampling is lower than for other stratified sampling. If an unrestricted adaptive cluster sampling procedure is to be used, the neighborhood should consist of stations with an optimal distance from stations where the catch is greater than or equal to the critical value, so that patches can be adequately sampled and the survey can be completed within a fixed time frame.

The unbiased adaptive stratified sampling (UASS; Thompson et al. 1992) might be a practical alternative to our sampling plan, because within a stratum, simple random sampling of a fixed number of stations should ensure that the survey is finished within a fixed time, and that means and variances are unbiased. This method requires taking additional samples in a stratum when the catches in the previous stratum meet or exceed the critical value. It is important to recognize that for UASS to be effective the stratum size must be smaller than the patch size, because high catch in the previous stratum must be linked to a high catch in the adjacent stratum. The critical value should be lower than in our restricted adaptive sampling, to ensure that additional stations are allocated to the strata with high abundance.

Patch Size

An important benefit of sampling adaptively is that one may use the data to estimate patch size. The sizes of egg and larval patches are an interesting biological characteristic of a species (Smith 1973, 1981; Hewitt 1981), as well as a property of their distributions that one needs to know in order to sample adaptively.

The distance between adjacent stations with catches greater than or equal to 10 larvae provides an estimate of the patch size of larval hake averaging 7.5 mm long (Cass-Calay, pers. comm.) and about 40 days old (Butler 1997). In stratum 9, one A-station and two B-stations had larval counts greater than 10. The distance between A- and B-stations was 10 n mi, and the distance between two B-stations was 15 n mi, so the diameter of the patch could be, say, 20 n mi. In stratum 16, we assumed that two A-stations were from one patch 20 n mi apart, each with larval counts greater than 10, so the diameter of the patch could be, say, 30 n mi. Thus the diameters of the patches of 40-day-old hake larvae were 37–55 km (20–30 n mi; figure 2). It seems remarkable that such distinct hake larval patches persist for 40 days in the open sea.

Patch diameter also dictates the optimal spatial interval between stations in an adaptive sampling design. The preferred distance is less than half of the diameter of patches. Too short a distance between stations may result in excessive time spent in one patch. If the distance is greater than half of the patch diameter, patches will not be adequately sampled. We selected 10 n mi as our interval; it seems to be a good guess, but there is room for improvement. If the survey were carried out on a regular basis we could greatly improve our estimates of patch size, and thereby improve the efficiency of subsequent adaptive sampling surveys.

CONCLUSIONS

Although it is an information-rich approach, requiring prior knowledge of density and patch size to be effective (Brown 1994, 1996a, b), adaptive cluster sampling is a way to improve the precision of pelagic egg and larval surveys while holding the maximum sample size constant. In our survey, adaptive cluster sampling of two patches of hake larvae resulted in a 2-fold reduction in the variance over the proportional stratified sampling. Adaptive ichthyoplankton sampling has several biological benefits in addition to the issue of precision. Increasing sampling effort in the area where catch was high not only provided an estimate of the dimension of the patch, but also yielded more specimens for biological studies (Moser et al. 1997; Cass-Calay 1997; Mullin 1997) than would have been obtained from other designs.

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APPENDIX

Two-Stage Cluster Horvitz-Thompson Estimator and Its Variance

Following Thompson (1990), the unbiased estimator for total larvae summed over networks observed in a stratum is:

$$\hat{T} = \sum_{j=1}^{K} \frac{y^{\star}_j z_j}{\alpha_j}$$

$$= \sum_{j=1}^{K} \frac{\frac{\bar{y}_j}{0.4} a_j z_j}{\alpha_j}$$

$$= \sum_{j=1}^{k} \frac{\frac{\bar{y}_j}{0.4} a_j}{\alpha_j} \qquad \text{(A1)}$$

where K is total number of patches, which was not observed in a stratum, and k is number of patches sampled in a stratum. z_j is 1 if the jth patch is sampled, and zero otherwise.

$$\bar{y}_j = \sum_{u=1}^{m_j} \frac{\bar{y}_{ju}}{m_j}$$

is the sample mean per tow from m_j tows; m_j is the number of G-stations sampled in the network, including the jth A-station. $Ez_j = \alpha_j(1-\alpha_j)$. 0.4 m^2 is the surface area covered by a bongo tow with 71-cm diameter. a_j is the area of the jth network. The estimator of network total, $y^{\star}$, is computed from catch at G-stations:

$$y^{\star}_j = \frac{\bar{y}_j}{0.4} a_j \text{ and}$$

$$\alpha_j = 1 - C^{N-x_j}_{q} / C^{N}_{q} = 1 - \frac{(N-x_j)!}{(N-x_j-q)!q!} \frac{(N-q)q!}{N!} \qquad \text{(A2)}$$

where q is the number of the initial stations and A is the total area for a given stratum. $N = A/0.4$ is the total number of tows in the stratum; $x_j = a_j/0.4$ is the total number of tows in the jth network. If q/N is small (p. 274 in Thompson 1992), then $\alpha_i \sim 1-(1-a_j/A)^q$. For example, for $q = 2$, we have

$$\alpha_j = 1 - C^{N-x_j}_{q} / C^{N}_{q} = 1 - \frac{(N-x_j)(N-x_j-1)}{N(N-1)}$$

$$\doteq 1 - \left(1 - \frac{x_j}{N}\right)^2 = 1 - \left(1 - \frac{a_j}{A}\right)^2$$

The estimated mean number of larvae per tow from (equation A1) is

$$\hat{y} = \frac{\hat{T}}{A/0.4} = \frac{1}{A/0.4} \sum_{j=1}^{K} \frac{\frac{\bar{y}_j}{0.4} a_j z_j}{\alpha_j}$$

$$= \frac{1}{A} \sum_{j=1}^{K} \frac{\bar{y}_j a_j z_j}{\alpha_j} \qquad \text{(A3)}$$

The variance of $\hat{y}$ (var($\hat{y}$)) is

$$\text{var}(\hat{y}) = \frac{1}{A^2}\text{var}\left(\sum_{j=1}^{K}\frac{a_j}{\alpha_j}\overline{y}_j z_j\right) \tag{A4}$$

$$\text{var}(\hat{y}) = \frac{1}{A^2}\left(\sum_{j=1}^{K}\frac{a_j^2}{\alpha_j^2}\text{var}[\overline{y}_j z_j] + \sum_{i<j}2\frac{a_i a_j}{\alpha_i \alpha_j}\text{cov}[\overline{y}_i z_i, \overline{y}_j z_j]\right)$$

The unbiased estimate of var($\hat{y}$) is (Thompson 1992)

$$\hat{\text{var}}(\hat{y}) = \frac{1}{A^2}\left[\sum_{j=1}^{K}\frac{a_j^2}{\alpha_j^2}\frac{z_j}{\alpha_j}\hat{\text{var}}(\overline{y}_j z_j) + \sum_{i<j}2\frac{a_i a_j}{\alpha_i \alpha_j}\frac{z_i z_j}{\alpha_{ij}}\hat{\text{cov}}(\overline{y}_i z_i, \overline{y}_j z_j)\right] \tag{A5}$$

where

$$\hat{\text{var}}(\overline{y}_i z_i) = \overline{y}_i^2\text{var}(z_i) + z_i^2\hat{\text{var}}(\overline{y}_i) - \hat{\text{var}}(\overline{y}_i)\text{var}(z_i)$$

(Goodman 1960).

$$\text{var}(z_i) = Ez_i^2 - [Ez_i]^2 = \alpha_i(1-\alpha_i)$$

and

$$\hat{\text{var}}(\overline{y}_i) = \frac{s_i^2}{m_i}.$$

Assuming $\text{cov}(\overline{y}_i, z_j) = 0$ for $I \neq j$, we have

$$\text{cov}(\overline{y}_i z_i, \overline{y}_j z_j) = E\overline{y}_i E\overline{y}_j \text{cov}(z_i, z_j) + Ez_i Ez_j \text{cov}(\overline{y}_i, \overline{y}_j) + \text{cov}(\overline{y}_i, \overline{y}_j)\text{cov}(z_i, z_j)$$

$$\hat{\text{cov}}(\overline{y}_i z_i, \overline{y}_j z_j) = \overline{y}_i \overline{y}_j(\alpha_{ij} - \alpha_i \alpha_j) \quad \text{if } \text{cov}(\overline{y}_i\, \overline{y}_j) = 0$$

where

$$\text{cov}(z_i, z_j) = (\alpha_{ij} - \alpha_i \alpha_j)$$

and

$$\alpha_{ij} = E(z_i z_j) = 1 - \left[\left(1 - \frac{a_i}{A}\right)^q + \left(1 - \frac{a_j}{A}\right)^q - \left(1 - \frac{a_i + a_j}{A}\right)^q\right]$$

(p. 274 in Thompson 1992).