



Stopping Rule Sampling to Monitor and Protect Endangered Species

Lara MITCHELL[✉], Leo POLANSKY[✉], and Ken B. NEWMAN[✉]

Ecological science and management often require animal population abundance estimates to determine population status, set harvest limits on exploited populations, assess biodiversity, and evaluate the effects of management actions. However, sampling can harm animal populations. Motivated by trawl sampling of an endangered fish, we present a sequential adaptive sampling design focused on making population-level inferences while limiting harm to the target population. The design incorporates stopping rules such that multiple samples are collected at a site until one or more individuals from the target population are captured, conditional on the number of samples falling within a predetermined range. With this application in mind, we pair the stopping rules sampling design with a density model from which to base abundance indices. We use theoretical analyses and simulations to evaluate inference of population parameters and reduction in catch under the stopping rule sampling design compared to fixed sampling designs. Density point estimates based on stopping rules could theoretically be biased high, but simulations indicated that the stopping rules did not induce noticeable bias in practice. Retrospective analysis of the case study indicated that the stopping rules reduced catch by 60% compared to a fixed sampling design with maximum possible effort.

Supplementary materials accompanying this paper appear online.

Key Words: Abundance index; Adaptive sampling; Allowable take; Delta smelt; *Hypomesus transpacificus*; Negative binomial.

1. INTRODUCTION

Abundance estimates are important population metrics for ecological science, being integral for population ecology (Krebs 1999) and modeling (Newman et al. 2014), species status assessments (Smith et al. 2018), and conservation and management (Morris and Doak 2002).

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Abundance estimates, or indices of abundance, are often based on data collected through a statistical sampling procedure, including, for example, stratified random sampling of areas or volumes (Hankin et al. 2019), capture–recapture methods (McCrea and Morgan 2014), distance sampling (Buckland et al. 2015), and presence–absence sampling (MacKenzie et al. 2017). For a species that is at risk and increasingly rare, there can be pressure to increase monitoring in order to optimize management decisions, especially if the species has not been observed for some time (Chadès et al. 2008).

In ecology, it is recognized that many if not most species have spatial distributions leading to rarity at different scales (recently reviewed at the intersection of conservation, monitoring, and modeling by Jeliaskov et al. (2022)). This has led to sampling designs to address populations that are clustered in space, such as adaptive cluster sampling (Thompson 1990) which increases sampling in areas where the target species is encountered, and analysis using statistical models capable of addressing zero inflation (Cunningham and Lindenmayer 2005).

However, when the species is also at risk and ongoing monitoring further harms the individuals, referred to as “take” in the context of biological opinions (USFWS 2006), it is important to consider whether sampling may negatively impact the population (McGowan and Ryan 2009; Gezon et al. 2015; Hope et al. 2018). While statistical sampling theory generally indicates that more samples are better than fewer samples for population inference, when take must be considered or the cost of sampling is consequentially high in some other way, then a sampling design limiting overall effort may be of interest.

To address these challenges as they relate to threatened populations, we describe an adaptive sampling design with the objective of generating an index of population size, which necessarily involves frequent sampling with good spatial coverage due to rarity and patchiness, while limiting take. Achieving this objective leads to a tension between a need for multiple samples at each site to reduce negative bias by incorrectly concluding there are no individuals at a site (and which may also allow quantification of imperfect detection), and a desire to cap effort and minimize take. In the proposed design, referred to as a *stopping rule* sampling design, multiple samples are collected at a sampling site until one or more individuals from the target population are successfully sampled, conditional on the number of samples falling within a predetermined range. Because sampling at a site beyond the minimum stops after the species is found, the sampling design limits the handling of target species and reduces field time by minimizing the number of samples taken at a site once the species has been found. Bounding sample effort at the site level is important for achieving a sufficient number of sites across a species’ range for making robust population-level inference. At the same time, collecting multiple samples per site increases the amount of data available for modeling variability in observed counts, though in practice the effects of increasing total sample size in this way may be affected by pseudo-replication at the site level. This design is in contrast to more commonly used adaptive sampling designs in environmental and ecological sampling where samples are added in an area around a site after a nonzero detection (Thompson 2003).

The stopping rule sampling design described here was motivated by the need to monitor delta smelt (*Hypomesus transpacificus*), a finger-length fish that has experienced severe population declines and is susceptible to harm during sampling, but remains a high priority

for active monitoring (Sect. 2). With this application in mind, we present a density model from which to base abundance indices (Sect. 3). Potential effects of the stopping rules on inference about density and comparisons of the performance of the stopping rule sampling design are examined in general using both theoretical analyses and simulation experiments (Sect. 4). We derive delta smelt abundance indices and use a simulation study to estimate the reduction in their take based on stopping rule sampling (Sect. 5). We close with a discussion that includes comparing our approach to other adaptive designs along with some limitations and future research needs (Sect. 6).

2. BACKGROUND ON THE MOTIVATING CASE STUDY

Delta smelt are endemic to the San Francisco Estuary (SFE) in California, USA. Human activity has substantially altered the SFE (Nichols et al. 1986; Whipple et al. 2012), resulting in reduced habitat quality for native fishes. These changes have coincided with the long-term decline of delta smelt (Sommer et al. 2007; Moyle et al. 2016), which are included in both state (CFGC 2009) and federal (USFWS 1993) government endangered species lists. There is ongoing interest in contemporary determinants of the distribution and abundance of the delta smelt population, despite the species becoming increasingly rare.

In December 2016, the Enhanced Delta Smelt Monitoring (EDSM) program was initiated by the U.S. Fish and Wildlife Service to provide near real-time and year-round information on the population distribution and abundance of delta smelt through trawl sampling. However, collection and handling of delta smelt can result in harmful levels of stress and injury (Swanson et al. 1996), leading to a conflict between two goals, continued population monitoring and minimizing take. Furthermore, because of their small size compared to the volume of potential habitat, and varying density at multiple spatial scales (Polansky et al. 2018), there is an additional conflict between the need for (1) multiple samples per site while also (2) visiting enough sites to enable population-level inference. EDSM attempts to achieve both of these goals while minimizing take by employing stopping rules.

3. METHODS

3.1. SAMPLING DESIGN

Suppose sampling is to take place at a set of n sites and that at each site $k = 1, \dots, n$ a set of Q_k independent samples is to be collected. We assume the number of individuals of the target species observed or captured in sample i , denoted $Y_{k,i}$, is recorded along with a measure of sampling effort, denoted $v_{k,i}$. This measure of effort is needed because the sample unit is not precisely definable. Under the stopping rule sampling design, the number of samples collected at a site is constrained to fall within a predetermined range denoted q_{\min} to q_{\max} . Sampling stops after q_{\min} samples if any of the first q_{\min} samples results in a positive count of the target species. Otherwise, sampling proceeds until a positive count is observed, after which sampling at the site stops, or until q_{\max} samples have been taken.

The number of samples collected at a given site k , Q_k , is a random variable taking on integer values from q_{\min} to q_{\max} . Its value depends on which of the following three sets of conditions occur.

$$Q_k = \begin{cases} q_{\min}, & \text{if } \sum_{i=1}^{q_{\min}} Y_{k,i} > 0 \\ q \in \{q_{\min} + 1, \dots, q_{\max} - 1\}, & \text{if } \sum_{i=1}^{q-1} Y_{k,i} = 0 \text{ and } Y_{k,q} > 0 \\ q_{\max}, & \text{otherwise} \end{cases} \quad (1)$$

Q_k 's probability distribution is thus determined by q_{\min} , q_{\max} , and the probability of observing a zero count in a given sample, $P(Y_{k,i} = 0)$ (Supplemental Information (SI) Section S1.1). When sampling effort is constant, Q_k can be interpreted as following a doubly truncated non-homogeneous geometric distribution with lower truncation at q_{\min} , upper truncation at q_{\max} , and success defined as observing a positive count.

At each site, the expected total number of samples $E(Q_k)$ and the expected total count $E(Y_{k,\cdot})$ are

$$E(Q_k) = q_{\min} + \sum_{q=q_{\min}}^{q_{\max}-1} \prod_{i=1}^q P(Y_{k,i} = 0) \quad (2)$$

$$E(Y_{k,\cdot}) = \sum_{i=1}^{q_{\min}} E(Y_{k,i}) + \sum_{q=q_{\min}+1}^{q_{\max}} E(Y_{k,q}) \prod_{i=1}^{q-1} P(Y_{k,i} = 0), \quad (3)$$

respectively (SI Sections S1.2 and S1.3). These equations can be used in conjunction with preliminary estimates of parameters defining the distribution of $Y_{k,i}$ to inform decisions about setting survey design parameters and anticipate take. For example, if r_1 is the average travel time between sites and r_2 is the average time required to collect a single sample, then values of q_{\min} , q_{\max} , and n can be found that constrain (1) total sample time, $T = r_1(n-1) + r_2 \sum_{k=1}^n Q_k$, and (2) total catch across sites, $C = \sum_{k=1}^n Y_{k,\cdot}$. The corresponding expected values are $E(T) = r_1(n-1) + r_2 n E(Q_k)$ and $E(C) = n E(Y_{k,\cdot})$.

A density model given stopping rule data is developed next in Sect. 3.2, but here we note that the stopping rules do not influence the probability that a given count will be observed during a given sample. The joint distribution for all random variables associated with site k can therefore be written as the product of the count probabilities (SI Section

$$S1.4): P(Y_{k,1}, \dots, Y_{k,Q_k}, Q_k) = \prod_{i=1}^{Q_k} P(Y_{k,i}).$$

Because stopping depends only on the observed counts and not the parameters to be estimated, the stopping rule is “non-informative” for likelihood inference (Roberts 1967) and the likelihood is the same with regard to model parameters whether the stopping rules are followed or broken (SI Section S1.5; see Roberts (1967) for examples of informative stopping rules). We also note that the non-informative design with regard to the likelihood does not mean that parameter estimates will be unbiased given data collected under a stopping rule sampling design (Sect. 4).

3.2. DENSITY MODEL

A goal of the stopping rule sampling design is to provide data for fitting models to estimate population densities, abundance indices, or other similar population metrics. Here we present a generalized linear mixed model (GLMM) for estimating relative density using count data collected with the stopping rule sampling design and demonstrate how the fitted model can be used to calculate indices of abundance.

Suppose sampling takes place over $t = 1, \dots, T$ time periods in $h = 1, \dots, H$ spatial strata with $k = 1, \dots, n_{t,h}$ sites in a given time period and stratum. We consider the general model

$$\begin{aligned}
 y_{t,h,k,i} &\sim \text{D}(\mu_{t,h,k,i}, [\theta_{t,h,k,i}]) \\
 \log(\mu_{t,h,k,i}) &= \beta_{0,t,h} + \mathbf{x}_{t,h,k,i}^T \boldsymbol{\beta} + \alpha_{t,h,k} + \log(v_{t,h,k,i}) \\
 \alpha_{t,h,k} &\sim \text{N}(0, \sigma_\alpha) \\
 \log(\theta_{t,h,k,i}) &= \gamma_0 + \mathbf{w}_{t,h,k,i}^T \boldsymbol{\gamma}
 \end{aligned} \tag{4}$$

where $y_{t,h,k,i}$ is the count from the i^{th} sample at site k in stratum h and time period t , and D is a probability distribution with expected count $\mu_{t,h,k,i}$ and optional dispersion parameter $\theta_{t,h,k,i}$. The expected count is a log-linear combination of (1) time- and stratum-specific intercepts $\beta_{0,t,h}$, (2) a site- and sample-specific covariate matrix $\mathbf{x}_{t,h,k,i}$ multiplied by coefficient vector $\boldsymbol{\beta}$, (3) a normally distributed site random effect (RE) $\alpha_{t,h,k}$ with standard deviation σ_α , and (4) sampling effort offset, $\log(v_{t,h,k,i})$. The intercepts reflect large-scale spatiotemporal changes in density (number of organisms per unit of sampling effort) while site random effects account for variability between sites as well as correlation between samples at a site. The covariates reflect finer-scale patterns in availability or detection or both. We assume that a new set of sites is sampled within each time period and stratum (e.g., subscripts t , h , and k are needed to denote a unique site), though the site effect could be simplified. For example, if the same set of sites was visited over time, the site effect could be time invariant, $\alpha_{h,k} \sim \text{N}(0, \sigma_\alpha)$.

We consider models where the distribution D is either Poisson, in which case $\theta_{t,h,k,i}$ is not needed, or negative binomial with variance $\text{Var}(Y_{t,h,k,i}) = \mu_{t,h,k,i} + \mu_{t,h,k,i}^2 / \theta_{t,h,k,i}$. The dispersion parameter $\theta_{t,h,k,i}$ controls the level of aggregation of organisms with smaller values corresponding to increased aggregation (Stoklosa et al. 2022). We treat the log of $\theta_{t,h,k,i}$ as a linear combination of covariates $\mathbf{w}_{t,h,k,i}$ with coefficients $\boldsymbol{\gamma}$ to allow the level of aggregation to change, for example with changes in habitat quality.

One alternative to the GLMM approach is N-mixture models, which separate out patterns in abundance and detection using replicate samples per site (Royle 2004). Such models require, among other things, that replicates are unambiguous re-samples of a closed population at the site, and it is generally recognized that many empirical data sets likely violate this closure assumption (Barker et al. 2018; Goldstein and de Valpine 2022). We expect our motivating case study, which involves sampling of a mobile organism with trawls in a highly dynamic habitat, to fall into this category. The exact boundaries of a site and the amount of overlap in habitat sampled between samples (tows of the trawl) at a site are not easily definable, and the degree to which the movement of fish and water may violate the

closure assumption at a site is generally unknown. For this reason, we keep our focus on GLMMs, acknowledging that this class of models produces estimates of relative density or abundance rather than absolute abundance (Dénes et al. 2015; Barker et al. 2018).

Estimates of relative abundance can be calculated using parameter estimates from a fitted model if sampling effort $v_{t,h,k,i}$ represents a measure of habitat quantity such as water volume sampled for aquatic species or area sampled for terrestrial species, and estimates of total habitat quantity, $V_{t,h}$, are available. Let $\hat{\delta}_{t,h} = \exp(\hat{\beta}_{0,t,h} + \bar{\mathbf{x}}_{t,h}^T \hat{\boldsymbol{\beta}})$ be the estimated density given average covariate values $\bar{\mathbf{x}}_{t,h}$. Then a relative abundance index $\hat{I}_{t,h}$ is given by $\hat{I}_{t,h} = \hat{\delta}_{t,h} V_{t,h}$. Standard error estimates $\widehat{\text{SE}}(\hat{I}_{t,h})$ can be calculated with model parameter standard errors using the delta method (Rao 1973). Assuming independence between strata, a total index and its variance for a given time period are given by the sum of stratum-specific estimates: $\hat{I}_t = \sum_{h=1}^H \hat{I}_{t,h}$ and $\widehat{\text{Var}}(\hat{I}_t) = \sum_{h=1}^H \widehat{\text{Var}}(\hat{I}_{t,h})$. Further assuming that the sampling distribution for the total estimate \hat{I}_t is approximately lognormally distributed with log-scale mean $\mu = \log(\hat{I}_t / \sqrt{1 + (\widehat{\text{Var}}(\hat{I}_t) / \hat{I}_t^2)})$ and log-scale standard deviation $\sigma = \sqrt{\log(1 + \widehat{\text{Var}}(\hat{I}_t) / \hat{I}_t^2)}$, a confidence interval (CI) for \hat{I}_t can be constructed using the quantiles from this lognormal distribution.

3.3. MODEL FITTING

A range of tools are available for fitting GLMMs (Bolker et al. 2009). All analyses presented in this paper were carried out in R (R Core Team 2023), and models were fit within a frequentist framework using the glmmTMB package (Brooks et al. 2017), with covariates standardized to have mean zero and standard deviation one. The DHARMA package (Hartig 2022) was used for residual analyses in the case study (Sect. 5).

4. INVESTIGATION OF PARAMETER ESTIMATION UNDER THE STOPPING RULES

The use of stopping rules to collect count data may affect inferences based on the data. Brown and Manly (1998), for example, discuss bias in the context of adaptive cluster sampling with a different stopping rule than the one considered here. We used a combination of analytic and simulation approaches to investigate properties of model parameter estimates given data collected according to the stopping rule sampling design.

4.1. INVESTIGATION 1: POISSON COUNT DISTRIBUTION

4.1.1. Methods

Here we consider a highly simplified scenario in which there is a single time period and stratum, sites share a constant mean density of organisms (δ), sampling effort (v) is constant, and counts follow a Poisson distribution. Dropping non-varying subscripts, the model can be written as $y_{k,i} \sim \text{Poisson}(\delta v)$ for all samples at all n sites. We analytically derived the maximum likelihood estimate (MLE) of density, $\hat{\delta}$, and an approximation of the theoretical bias, $\text{Bias}(\hat{\delta}) = E(\hat{\delta}) - \delta$, based on a Taylor series expansion of $\hat{\delta}$ (SI Section S2.1). We

investigated how bias in $\hat{\delta}$ changes as a function of q_{\min} , q_{\max} , and the number of sites n . For this, we used $v = 1$ and let true density δ range from 0.001 to 4, allowing the probability of observing a zero to vary from 0.018 to 0.999. We set $q_{\min} = 2, 4, 6, \text{ or } 8$, $q_{\max} = 4, 6, 8, \text{ or } 10$, and $n = 2 \text{ or } 4$. The ranges of values considered for q_{\min} and q_{\max} are generally based on the case study where q_{\min} has consistently been 2 and q_{\max} has ranged from 4 to 10 (Sect. 5); we allowed q_{\min} to be larger than 2 for investigative purposes. For each combination of inputs, we used the bias approximation to calculate percent relative bias as $100 \times \text{Bias}(\hat{\delta})/\delta$ and graphically summarized the results.

4.1.2. Results

An approximation of the theoretical bias in the density MLE is given by

$$\text{Bias}(\hat{\delta}) \approx \frac{\delta \sum_{q=q_{\min}+1}^{q_{\max}} (q-1) \exp(-\delta v(q-1))}{n \left(q_{\min} + \sum_{q=q_{\min}+1}^{q_{\max}} \exp(-\delta v(q-1)) \right)^2}. \quad (5)$$

The theoretical bias approximation is positive and decreases as total sample effort is increased by increasing n , increasing v , or increasing q_{\min} while q_{\max} is held constant (Fig. 1a). We note that with a fixed number of samples per site, i.e., with no stopping rules, the estimate $\hat{\delta}$ would be unbiased (SI Section S2.1).

The bias may be associated with the stopping rules that allow data collectors to “quit while ahead,” i.e., stop sampling after the first positive catch after sample q_{\min} and before sample q_{\max} . This is supported by the observation that relative bias generally increases as density decreases (Fig. 1): In the lower density range, the stopping rules are more likely to be invoked after sample q_{\min} while at larger densities the stopping rule sampling design appears more like a fixed sampling design with the number of samples fixed at q_{\min} . Furthermore, the bias may depend on the difference between q_{\min} and q_{\max} , with larger differences allowing the stopping rules to have more of an effect on bias and smaller differences again bringing the stopping rule sampling design closer to a fixed sampling design. This is supported by the finding that at lower densities, increasing the difference between q_{\min} and q_{\max} by holding $q_{\min} = 2$ constant and increasing q_{\max} could result in increased relative bias (Fig. 1b).

Relative bias ranged from 0 to 27.1% across the complete sets of inputs considered here. For an example of the magnitude of bias, when $\delta = 0.5$ with $q_{\min} = 2$, $q_{\max} = 6$, $n = 2$, the expected value of $\hat{\delta}$ is $E(\hat{\delta}) = 0.575$, a 15% positive bias. A bias-adjusted estimate of density could theoretically be calculated as $\hat{\delta}_{\text{adj}} = \hat{\delta} - \text{Bias}(\hat{\delta})$. However, we note that the expression for $\text{Bias}(\hat{\delta})$ depends on the maximum possible number of samples, q_{\max} , and all associated sample volumes. In practice, it is likely that not all q_{\max} samples will be realized and sample effort will vary, making application of the bias correction factor unrealistic.

4.2. INVESTIGATION 2: NEGATIVE BINOMIAL COUNT DISTRIBUTION

4.2.1. Methods

Here we consider a negative binomial model (Eq. 4) with site- and sample-specific covariates, random site effect, and constant dispersion parameter. We simulated data sets that

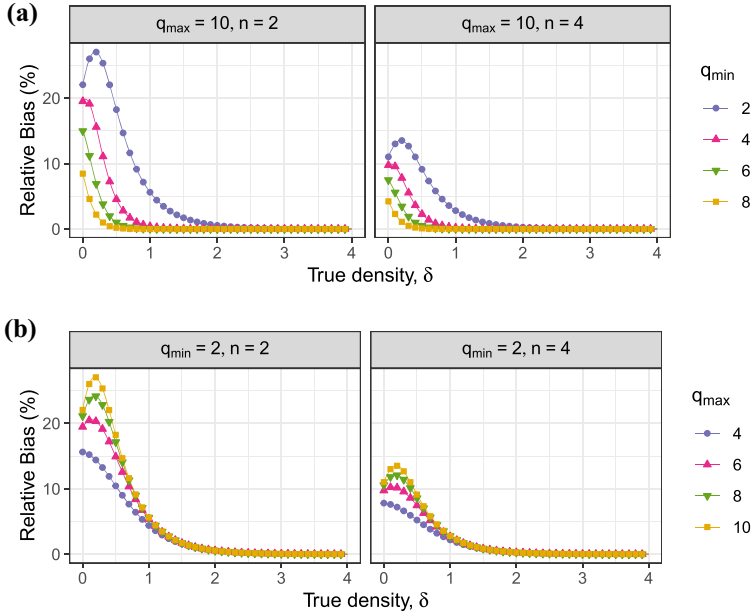


Figure 1. Percent relative bias in density estimates ($\hat{\delta}$) based on stopping rule data as described in Investigation 1 in Sect. 4.1. Panel **a** reflects the effects of fixing the maximum number of samples (q_{\max}) and varying the number of sites (n) and the minimum number of samples (q_{\min}). Panel **b** reflects the effects of fixing q_{\min} and varying n and q_{\max} . Quantities indicated in sub-panel titles are held constant at the indicated values.

applied the stopping rules as well as three alternative sampling designs and fit the model to these data sets. Our goals were twofold: to compare parameter estimates based on the different sampling designs, looking for bias in estimates based on the stopping rules, and to investigate trade-offs between the number of organisms caught and parameter estimate quality.

We selected $T = 10$ time periods, $H = 1$ stratum, $n = 40$ new sites per time period and set $q_{\min} = 2$ and $q_{\max} = 10$. The “true” parameter values used for data generation were $\beta_{0,t} = \log(0.0002 \exp(-0.07(t - 1)))$, $\beta_1 = 0.4$ for a site-specific covariate coefficient, $\beta_2 = 0.2$ for a sample-specific covariate coefficient, $\sigma_\alpha = 0.8$, and $\theta = 0.4$. Values of sampling effort, $v_{t,k,i}$, were drawn from a gamma distribution with shape parameters 11.86 and expected value 3100, and were similar to values from the case study (Sect. 5). Site- and sample-specific covariate values were generated from a Uniform $(-1, 1)$ distribution. Inputs were chosen so counts were relatively low with high variability as this is a scenario where the stopping rule sampling design is likely to be relevant. In time period $t = 1$, for example, the expected count in a sample was approximately 0.46 with coefficient of variation 2.16 and probability of observing a zero count equal to 0.74.

Data sets were generated according to the following process. We first generated a single data set according to Eq. 4 with 10 samples per site, designating this the “max” effort data set because sample size is fixed at the value q_{\max} . We then created three additional versions of the data, starting with the max data set each time. First, a “min” effort data set was created by retaining only the first $q_{\min} = 2$ samples from each site. Next, a “stopping rule” data set

was created by applying the stopping rules. Finally, a “randomized” data set was created by taking the numbers of samples that would be retained under the stopping rules, randomly reassigning those numbers across sites, and then retaining the assigned number of samples from each site. The max, min, and randomized data sets represent sampling designs where there is no potential effect of stopping rules on model inference and no effort is made to limit catch. The randomized data set keeps the total number of samples equal to that of the stopping rules data set so that potential differences in parameter estimates are less affected by differences in sample size. This complete data generation process was carried out 10,000 times.

We fit the model to each of the 40,000 data sets using restricted maximum likelihood (REML). Although the true log intercepts $\beta_{0,t}$ were related in time through an exponential function for convenience, we note that this time dependence was not reflected in the model (Eq. 4). We checked to ensure that all models converged.

For each sample design, parameter estimates were summarized using the mean, 95th (2.5–97.5) quantile range, and mean squared error. Additionally, total catch in each data set (total number of organisms caught across time, sites, and samples) was summarized using the mean and 95th quantile range. To determine how well the proposed lognormal-based CI performed, we calculated abundance indices and CIs from the fitted models using habitat volume $V_t = 10,000$ for all t , and determined the proportion of times the CI contained the value $I_t = \exp(\beta_{0,t})V_t$.

4.2.2. Results

The average number of samples collected under the stopping rule design, across time periods, ranged from 2 to 10 with mean 4.2. Accuracy and precision of the parameter estimates generally improved as the total number of samples increased across sampling designs (Figs. 2a, b and 3; SI Section S2.2), consistent with expected patterns. The stopping rule sampling design fit within this pattern and did not show systematic bias in parameter estimates or unusually high uncertainty compared to the min and randomized designs. All four sampling designs generally estimated the coefficient parameters β_1 and β_2 comparably. The parameters σ_α and θ were more likely to be underestimated than overestimated regardless of sampling design, with the bias worst with q_{\min} . Increasing the number of samples beyond q_{\min} through application of the stopping rules was particularly beneficial in estimating σ_α and θ and reducing bias in estimates of $\beta_{0,t}$ compared to the min sampling design. Overall, the stopping rule and randomized designs performed equally, though the extra catch allowed under the randomized design resulted in a marginal decrease in uncertainty in estimates of β_2 and θ .

The stopping rule sampling design reduced average total catch by 22.8% and 67.9% relative to the randomized and max sampling designs, respectively, and increased average total catch by 60.3% relative to the min sampling design (Fig. 2c). The lognormal-based CIs had coverage between 94.1% and 95.7%, consistent with the target coverage of 95% (SI Section S2.2).

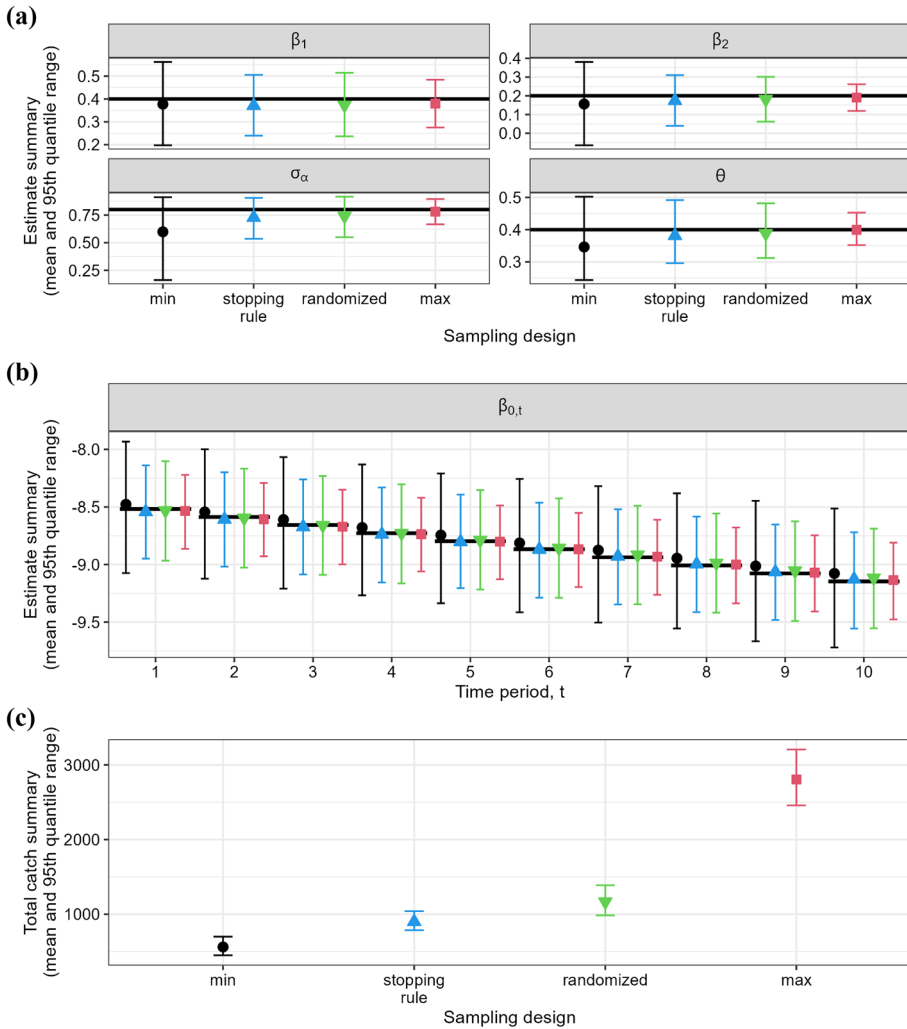


Figure 2. Summary (mean and 95th quantile range) of parameter estimates (panels **a** and **b**) and total catch (panel **c**) under the four sampling designs from Investigation 2 in Sect. 4.2. Parameters are covariate effect coefficients β_1 and β_2 , site random effect standard deviation σ_α , dispersion θ , and log densities $\beta_{0,t}$, $t = 1, \dots, 10$. Sampling design is indicated by order (min, stopping rule, randomized, and max) as well as color and point shape across all sub-panels. In panels **a** and **b**, thick horizontal black lines reflect true values.

5. CASE STUDY

5.1. DATA COLLECTION

The EDSM program uses trawls to sample delta smelt from the beginning of July, when individuals reach the juvenile life stage, through the subsequent March, by which time they have developed into mature adults and the majority of spawning is thought to have occurred. The habitat range has been stratified into between 4 and 10 strata throughout the life of the program (2016 to present, SI Figures S3.1, S3.2) to account for geographically varying

STOPPING RULE SAMPLING TO MONITOR

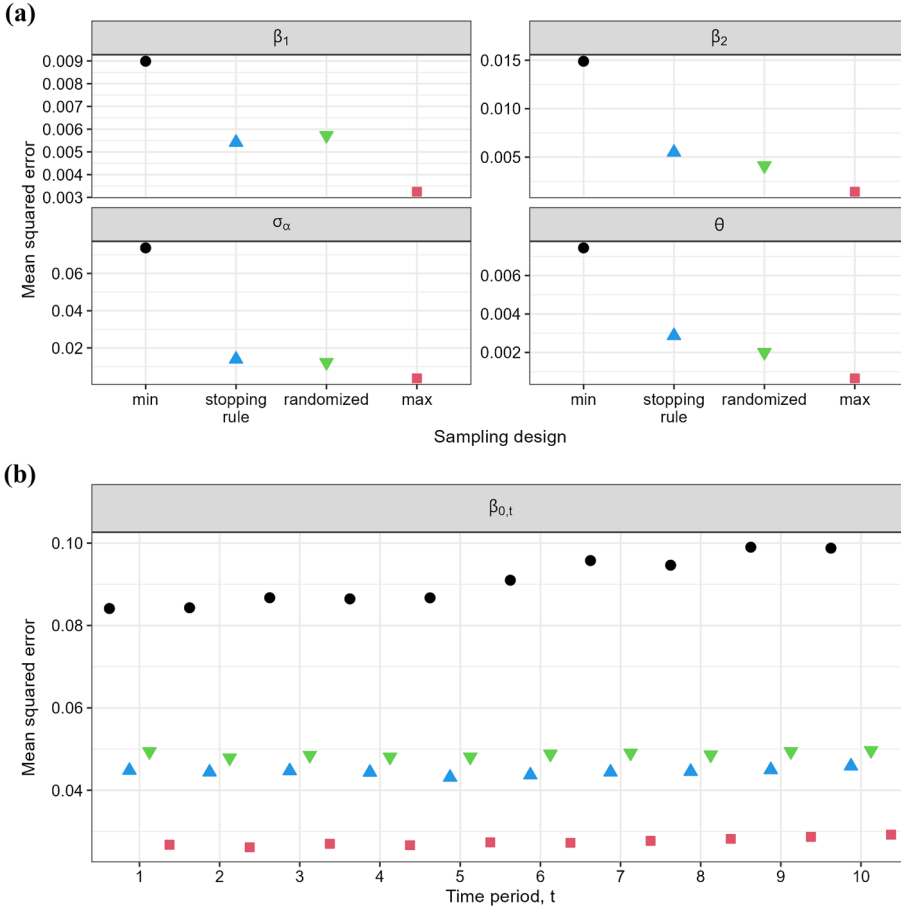


Figure 3. Parameter estimate mean squared errors from Investigation 2 in Sect. 4.2. Parameters are covariate effect coefficients β_1 and β_2 , site random effect standard deviation σ_α , dispersion θ , and log densities $\beta_{0,t}$, $t = 1, \dots, 10$. Sampling design is indicated by order (min, stopping rule, randomized, and max) as well as color and point shape across all sub-panels.

habitat types and densities. Sampling occurs weekly in all strata. Within each stratum, sites are defined by a set of coordinates generated using a generalized random tessellation stratified design (Stevens and Olsen 2004). The target number of sites per stratum per week, $n_{t,h}$, has varied over time but generally ranges from 2 to 6.

A tow of the trawl constitutes a single sample and a flow meter is used to estimate the volume (m^3) of water sampled in a tow as a measure of sampling effort. Delta smelt are identified and enumerated after each tow. The stopping rules are applied July–March, a period when individuals are typically large enough to be identified in the field. The value of q_{\min} has remained at 2 while q_{\max} has varied between 4 and 10 depending on the year and the availability of sampling resources. Auxiliary data on environmental conditions are also collected with each tow including Secchi depth (m; a measure of water clarity), specific conductance ($\mu S/cm$ at $25^\circ C$, a measure of water electrical conductivity subsequently

referred to as EC), water temperature (°C), and tide stage (ft, see below). See SI Section S3.1 for program history and sampling details.

5.2. MODEL FITTING, INDEX CALCULATIONS, AND THEORETICAL TAKE CALCULATIONS

We used data collected between December 2016 and March 2021 to fit negative binomial models with a weekly time step, geographic stratification, and site random effect. We included four sample-level environmental covariates (Secchi depth, EC, water temperature, tide) and a categorical variable s_t representing spawning season (winter, approximately December–March) or non-spawning season (summer/fall, approximately July–November). The full model can be written as

$$\begin{aligned} \log(\mu_{t,h,k,i}) &= \beta_{0,t,h} + \sum_{u=1}^4 \left(\beta_{u,1} x_{(u),t,h,k,i} + \beta_{u,2} x_{(u),t,h,k,i}^2 \right) \times s_t + \alpha_{t,h,k} + \log(v_{t,h,k,i}) \\ \alpha_{t,h,k} &\sim \text{N}(0, \sigma_\alpha) \\ \log(\theta_{t,h,k,i}) &= \gamma_0 + \gamma_1 \times s_t \end{aligned} \tag{6}$$

where the u th environmental covariate is represented with the notation $x_{(u)}$. Catch densities of delta smelt have previously been associated with environmental conditions (Feyrer et al. 2007; Polansky et al. 2018; Hendrix et al. 2023), and we hypothesized that the nature of this association may change during the spawning season. We also hypothesized that the level of aggregation would be higher in winter when spawning occurs.

Because EDSM did not record tide data in the early months of the program, we used hourly mean tide level (ft) at Port Chicago, CA (station ID 9415144; NOAA (2024)) as the tide variable throughout the modeled time period. We joined the two data sets by rounding the start time for a tow to the nearest hour and assigning the corresponding mean tide level to that tow. We excluded weeks with no catch from the model data set. Following the assumption that delta smelt are distributed between 0.5 and 4.5 m depth, we adjusted tow volumes to account for the fraction of sampling carried out within this depth stratum (Polansky et al. 2019). See SI Section S3.2 for further details on data processing.

We relied primarily on an information-theoretic approach based on Akaike information criteria (AIC) to arrive at a final model structure (Mundry and Nunn 2009; Zuur et al. 2009). We first found an optimal random structure (site RE or no RE) given the full fixed effects structure using restricted maximum likelihood estimation (REML), then carried out a backward elimination procedure on the fixed effects using maximum likelihood estimation (ML). Results presented here are based on REML.

We examined relationships between environmental covariates and relative catch to verify that these relationships appeared biologically plausible. For each covariate retained in the selected model, we used parameter estimates $\hat{\beta}_{u,1}$ and $\hat{\beta}_{u,2}$ to calculate and plot the quantity $\exp(\hat{\beta}_{u,1} x_{(u)} + \hat{\beta}_{u,2} x_{(u)}^2)$ over the observed range of values of $x_{(u)}$. This effectively fixes the intercept parameter, random effect, log sample volume, and remaining covariate values at zero to allow inspection of the general relationship between μ and x_u . We note that

combinations of covariate values used in these calculations do not necessarily represent combinations that were observed in the data.

Using the selected model, we calculated $\hat{I}_{t,h}$ and $\widehat{SE}(\hat{I}_{t,h})$ using estimates of the volume of water between 0.5 and 4.5 m depth in each stratum (SI Section S3.3). To investigate the effects of the stopping rules on delta smelt catch, we used the selected model to generate catches in additional tows that would have been conducted if there were no stopping rules and sample size was fixed at q_{\max} . For each additional, hypothetical tow i^* , we used site-level covariate averages (standardized in accordance with the model) and site-level sample volume averages to calculate estimates $\hat{\mu}_{t,h,k,i^*}$ and $\hat{\theta}_{t,h,k,i^*}$, generated the additional counts from negative binomial distributions using these parameters, and added these catches to the realized total catch of delta smelt to estimate a hypothetical total catch across the study period. We carried out this procedure 10,000 times and summarized the distribution of the resulting total catches by calculating the mean and 95th quantile range.

5.3. RESULTS

A total of 23,168 tows were collected from a total of 5,394 sites over the sampling period used in this analysis. At least one delta smelt was caught in 407 (1.76%) of the samples and at 354 (6.6%) of the sites. A total of 888 individual delta smelt were caught with 29% caught in the first sample at a site, 29.7% in the second sample, 16.2% in the third, 14.5% in the fourth, 6.9% in the fifth, 2.2% in the sixth, 0.5% in the seventh, and 1% in the eighth sample.

The selected model retained the site random effect as well as linear and quadratic terms for Secchi depth, EC, and temperature (Table 1; SI Sections S3.4, S3.5). One of the three residual tests did not pass, indicating possible deviation from the expected distribution (SI Section S3.6). However, all tests passed for the same model refit with ML.

Relative catch density decreased with increasing Secchi depth (increasing water clarity) and increasing EC (increasing salinity; Fig. 4), consistent with patterns found previously (Nobriga et al. 2008; Hendrix et al. 2023). The relative effect of temperature was generally highest between 15 and 20 °C. Lack of support for a tide effect is in contrast to other studies (Feyrer et al. 2013; Bennett and Burau 2015; Polansky et al. 2018), but may be due in part to the lack of spatial resolution in the tide data. The estimated standard deviation for the site random effect was $\hat{\sigma}_{\alpha} = 1.31$, and the estimated dispersion parameter was $\hat{\theta} = 1.22$. Estimates of relative density, $\exp(\hat{\beta}_{0,t,h})$, ranged from 1.65×10^{-6} to 4.87×10^{-2} , and total indices ranged from 0 to 625,986 with high uncertainties (Fig. 5).

Under the hypothetical scenario in which q_{\max} samples were collected at every site (without stopping rules), the simulated total catches had mean 2220, 150% higher than the actual number caught, and 95th quantile range 1902 to 2618. Based on the mean, this corresponds to a 60% (1332/2220) decrease in catch under the stopping rule sampling design relative to a design with the maximum number of samples per site.

Table 1. Estimates and standard errors of environmental covariate coefficients from the final model from the case study (Sect. 5)

Parameter	Estimate	Std. Error
$\beta_{1,1}$ (Secchi)	- 3.6129	0.3963
$\beta_{1,2}$ (Secchi ²)	- 1.2448	0.4435
$\beta_{2,1}$ (EC)	- 0.2491	0.4044
$\beta_{2,1}$ (EC ²)	- 0.1715	0.1252
$\beta_{3,1}$ (Temp)	0.7203	1.0109
$\beta_{3,1}$ (Temp ²)	- 1.2293	0.4810

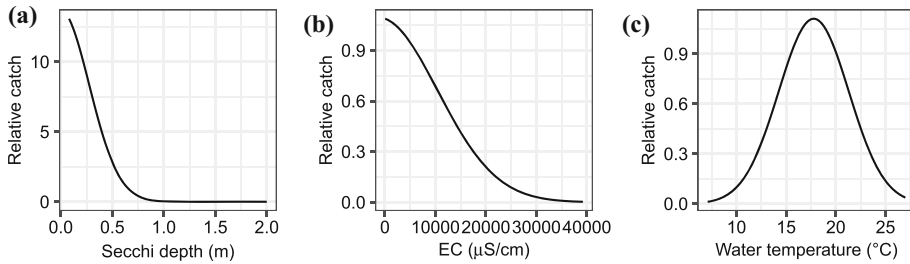


Figure 4. Relationships between each environmental covariate (**a** Secchi depth, **b** EC, **c** water temperature) and relative catch of delta smelt based on the selected case study model (Sect. 5). In each panel, the indicated covariate is allowed to vary while other terms in the log expected count are fixed at zero. Covariate values shown on the horizontal axes are on their original scales (not standardized).

6. DISCUSSION

Ecological field sampling involves balancing the objective of estimating one or more quantities of interest (to a desired level of accuracy and precision) with the cost of sampling. For rare species, this cost can include harm to individuals in the population of interest. We presented an adaptive sampling design developed to provide data for making population-level inferences while aiming to limit the handling or take of the target population, and illustrated how these data can be used to calculate abundance indices via a GLMM that is fit using readily available software. Through an analytic investigation, we found that maximum likelihood estimates of population density based on stopping rule data have increased positive bias as densities decline. Through a simulation-based investigation intended to more closely reflect real data collection processes, we found that the stopping rule sampling design can improve accuracy and precision of parameter estimates through increased data collection while simultaneously reducing catch without noticeable bias. In practice, what constitutes an acceptable trade-off between take-related costs of sampling and quality of estimates of population parameters will be situation specific.

An important consideration of the stopping rule sampling design is the trade-off between the number of sites sampled and the number of samples collected per site. The stopping rules can help achieve good spatial balance and coverage by allowing a high number of sites, particularly when positive counts are observed and time saved at one site can be used

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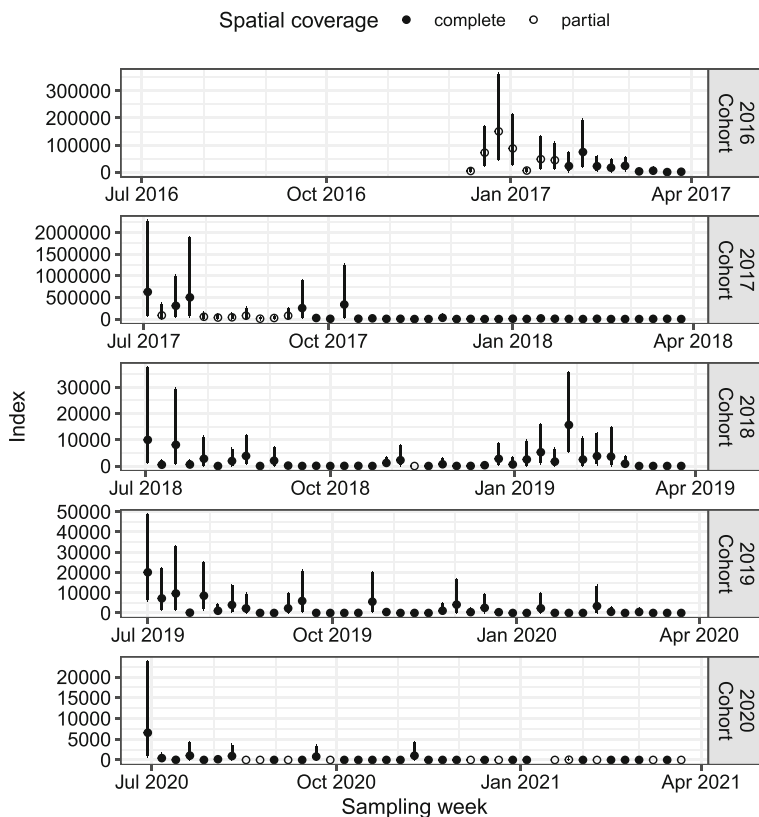


Figure 5. Delta smelt abundance index time series for 5 cohorts from July through March, the period over which a cohort of delta smelt develop through the juvenile to spawning adult life stages. Circles represent point estimates and vertical lines represent 95% confidence intervals. Point type reflects spatial coverage (complete=all strata were sampled; partial=at least one stratum was not sampled).

to visit one or more additional sites. At the same time, collecting multiple samples per site may allow for modeling of imperfect detection when model assumptions are met (Royle 2004) or exploration of alternative density models.

There are both similarities and differences between the adaptive design described here and some others used in ecology. Sequential sampling aims to sample until some decision can be made with some amount of certainty (Krebs 1999). In mark–recapture studies, sequential analysis has been used to determine the number of recaptures needed to estimate population size with a given level of precision (Mukhopadhyay and Bhattacharjee 2018; Silva et al. 2023). Such methodology did not apply to our case study because there were no marked delta smelt in the SFE at the time (though see next paragraph) and the bound on sampling effort for recaptures would likely apply to total sites, not number of samples per site or necessarily with the aim of minimizing take. Removal design, whereby surveying stops at a site on first detection, has been developed within an occupancy modeling framework (Azuma et al. 1990; MacKenzie and Royle 2005) where the goals are to estimate species occurrence and detection probabilities, but not abundance. Adaptive cluster sampling does aim to acquire

data for estimating abundance, but increases rather than decreases effort upon detection (Thompson 1990). Adaptive cluster sampling has perhaps received the most attention within ecology (see, e.g., the special issue in *Environmental and Ecological Statistics* edited by Thompson (2003)). Such research has included adding a stopping rule by fixing a maximum number of adaptive sample iterations (Su and Quinn 2003), different than the condition-based rule described here that aims to minimize positive counts.

To maximize generality and applicability, we used a common but relatively simple GLMM to analyze the data. This model could be extended by adding complexity to the fixed effect structure to include explicit spatial, temporal, or spatiotemporal terms. Extension to the probabilistic structure of the model allowing for zero inflation at the sample level (currently available in the `glmmTMB` package) or site level are some additional ways for building on the model considered here. For example, if no fish are within the water associated with a given site the density at that site may be considered a structural zero. As noted previously, explicitly modeling imperfect detection might be considered.

The delta smelt case study provides insight into the application of the stopping rule sampling design to a species that embodies the challenge of balancing monitoring and take. The stopping rules likely reduced overall take of delta smelt while providing indices of abundance on a weekly basis, whereas other monitoring programs deploying less effort have by in large ceased to detect any delta smelt at all. In recent years, cultured adult delta smelt marked with tags or fin clips have been released into the SFE as part of experimental efforts to supplement the decreasing wild population (USFWS 2020). In addition to potentially bolstering the population, this opens new avenues for mark–recapture modeling and additional efforts to quantify population size and vital rates. As the research community enters this new phase in delta smelt science and management, we expect the question of how to balance take considerations with monitoring objectives to remain relevant.

When species status assessments indicate a population is at risk, the importance of indices increases to uncover mechanisms driving the decline and evaluate the effectiveness of management actions. As a result, pressure to monitor may also increase, but this can impact the larger objective of protecting the population. Pressure for increased monitoring to assess conservation actions can become particularly intense when actions involve significant cost to humans, as is the case with delta smelt. As more species decline (IUCN 2022), it will become increasingly important to develop and apply methods of reducing the harmful impacts of sampling.

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Data Availability Statement The data that support the findings of the case study are available in the supplementary material of this article. R code supporting the article is also available in the supplementary material.

Declarations

Conflict of interest We have no conflict of interest to disclose.

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