

10

SAMPLING DESIGN

9608
9609
9610
9611 Statistical design is recognized as an important component of animal population studies
9612 (Morrison et al., 2008; Williams et al., 2002). Many biologists have ~~probably~~ been in a
9613 situation where some problem with their data could be traced back to a flaw in study
9614 design. Commonly, design is thought of in terms of number of samples to take, when to
9615 sample, methods of capture, desired sample size (of individuals), power of tests, and related
9616 considerations. In the context of spatial sampling problems, where populations of mobile
9617 animals are sampled by an array of traps or devices, there are a number of critical design
9618 elements. Two of the most important ones are the spacing and configuration of traps
9619 (or sampling devices) within the array. For traditional capture-recapture, conceptual and
9620 heuristic design considerations have been addressed by a number of authors (e.g., Nichols
9621 and Karanth, 2002, Chapt. 11), but little formal analysis focused on spatial design of
9622 arrays has been carried out. Bondrup-Nielsen (1983) investigated the effect of trapping
9623 grid size (relative to animal home range area) on capture-recapture density estimates
9624 using a simulation study and some authors have addressed trap spacing and configuration
9625 by sensitivity “re-analysis” (deleting traps and reanalyzing; Wegge et al., 2004; Tobler
9626 et al., 2008). The scarcity of simulation-based studies looking at study design issues is
9627 surprising, as it seems natural to evaluate prescribed designs by Monte Carlo simulation in
9628 terms of their accuracy and precision. In the past few years, however, a growing number of
9629 simulation studies addressing questions of study design in the context of spatial capture-
9630 recapture have come out (e.g., Marques et al. (2011); Sollmann et al. (2012); Efford and
9631 Fewster (2012); Efford (2011b)), the results of which we will discuss throughout this
9632 chapter.

9633 In this chapter we recommend a general framework for evaluating design choices for
9634 SCR studies using Monte Carlo simulation of specific design scenarios based on trade-offs
9635 between available effort, funding, logistics and other practical considerations – what we
9636 call *scenario analysis*. Many study design related issues can be addressed with preliminary
9637 field studies that will give you an idea of how much data you can expect to collect with a
9638 unit of effort (a camera trap day or a point count survey, for example). But it is also always
9639 useful to perform scenario analysis based on simulation before conducting the actual field

where the expectation is with respect to the sample of 100 grid cells. For example, if we repeatedly draw samples of size 100 then, over many such samples, the expected value of the estimator may be unbiased. Classical design-based sampling does not tell us anything about the specific 100 sample units that we obtained in our sample. However, in the SCR modeling framework, properties of our estimators are distinctly model-based. We evaluate estimators (usually) or care only about a fixed sample of spatial locations, averaged over realizations of the underlying process and data we might generate. Although sometimes we might condition on the data for purposes of inference (if we have our Bayesian hat on), the probability model for the data is fundamental to inference, and the spatial sample of trap locations is always fixed.

10.1.2 Sampling space or sampling individuals?

A fundamental question in any sampling problem is what is the sample frame – or the population we are hoping to extrapolate to. In the context of capture-recapture studies, it is tempting to think of the sample frame as being spatial (the space within “the study area”, tiled into quadrats perhaps). Clearly SCR models involve a type of spatial sampling – we have to identify spatial locations for traps, or arrays of traps. However, unlike conventional natural resource sampling the attribute we measure is *not* directly relevant to the *sample location*, such as where we place a trap and, therefore, it may not be sensible to think of the sample frame as being comprised of spatial units. On the other hand, capture-recapture studies clearly obtain a sample of *individuals* and SCR models are models of *individual* encounter and space use. Therefore, it is more natural to think of the sample frame as a list of N individuals, determined by the definition of the state-space, or a subset of the state-space, i.e., the study-area, but the number N is unknown. The purpose of the SCR study is to draw a sample of these N individuals and learn about an individual attribute – namely, where that individual lives. *That* is the sampling context of SCR models. SCR models link the observed data (encounter histories) to this individual attribute via a model (with parameters) which we need to “fit”. Once we fit that model, we usually use it to make a prediction or estimate of the attribute for individuals that did not appear in the sample.

Spatial sampling in SCR studies is important, but only as a device for accumulating individuals in the sample from which we can learn about their inclusion probability. That is, we’re not interested in any sample unit attribute directly but, rather, we use spatial units as a means for sampling individuals and obtaining individual level encounter histories. It makes sense in this context that we should want to choose a set of spatial sample units that provides an adequate sample size of individuals, perhaps as many as possible. The key technical consideration as it relates to spatial sampling and SCR is that arbitrary selection of sample units has a side-effect that it induces unequal probabilities of inclusion into the sample (i.e., an individual exposed to more traps is more likely to be included into the sample than an individual exposed to few traps) and so we must also learn about these unequal probabilities of sample inclusion as we obtain our sample.

The fact that SCR sampling induces unequal probabilities of sampling is consistent with the classical sampling idea of Horvitz-Thompson estimation which has motivated capture-recapture models similar to SCR (Huggins, 1989; Alho, 1990). In the Horvitz-Thompson framework, the sample inclusion probabilities are usually fixed and known.

10.2 STUDY DESIGN FOR (SPATIAL) CAPTURE-RECAPTURE

The importance of adequate trap spacing and overall configuration of the trapping array has long been discussed in the capture-recapture literature. A heuristic based on recognizing the importance of typical home range sizes (Dice, 1938, 1941) and thus being able to obtain information about home range size from the trap array is that traps should be spaced such that the array of available traps exposes as many individuals as possible but, at the same time, individuals should be captureable in multiple traps. Thus, good designs should generate a high sample size n (i.e., the number of individuals captured) and a large number of spatial recaptures. These two considerations form a trade-off in building designs. On one hand, having a lot of traps very close together should produce the most spatial recaptures but produce very few unique individuals captured (assuming that studies are limited in the total number of sampling devices they can deploy). On the other hand, spreading the traps out as much as possible, in a nearly systematic or regular design, should yield the most unique individuals, but probably few spatial recaptures. We will formalize this trade-off later, when we consider formal model-based design of SCR studies.

Traditional CR models require that all individuals in the study area have a probability > 0 of being captured, which means that the trap array must not contain “holes” large enough to contain an animal’s entire home range (Otis et al., 1978). The reason why “holes” cause a problem in non-spatial models is that they induce heterogeneity in capture probability. If an animal’s home range lies in or partially in a hole, then it will have a different probability of being captured than an individual whose home ranges is peppered with traps. As a consequence, trap spacing is recommended to be on the same order as the radius of a typical home range (e.g., Dillon and Kelly (2007)). For example, imagine a camera trap study implemented in South America with the objective to survey populations of both jaguars (*Panthera onca*) and the much smaller ocelots (*Leopardus pardalis*). Ocelots also have much smaller home ranges and therefore should require closer trap spacing than the large wide-ranging jaguars. The “no holes” assumption entails some strong restrictions with respect to study design. Although we need not cover an area systematically with traps, there has to be some consistent coverage of the entire area of interest. Often, this is achieved by dividing the study area into grid cells, the size of which approximates an average home range (or possibly the smallest home range recorded for the study species in the study area or a similar area; e.g. Wallace et al. (2003)), and then place (at least) one trap within each cell. In many field situations, especially when dealing with large mammals and accordingly large study areas, achieving this consistent coverage can be extremely challenging or even impossible. Depending on local environmental conditions, parts of the study area can be virtually inaccessible to humans, because of dense vegetation cover, or unsuitable for setting up detectors, because of flooding. Even when accessible, setting up traps in difficult habitat conditions can consume disproportional amounts of time, manpower and other resources. Moreover, even when the trap spacing does not result in holes, the problem of spatial heterogeneity in capture probability will still exist because individuals with home ranges near the borders of the trap array will have a different probability of being captured than individuals that spend all their time within the trap array.

Where approaches such as MMDM (mean maximum distance moved) are used in combination with traditional CR models to obtain density estimates (see Chapt. 4), trap

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make a prediction across distances even when these are latent, including distances larger than the extent of the trap array. When there is enough data across at least some range of distances, the model will do well at making predictions at unobserved distances. The key here is that there needs to be ‘enough data across some range of distances’, which induces some constraint on how large our overall trap array must be to provide this range of distances (e.g., Marques et al., 2011; Efford, 2011b). We will review the flexibility of SCR models in terms of trap spacing and trapping grid size in the following section.

10.3 TRAP SPACING AND ARRAY SIZE RELATIVE TO ANIMAL MOVEMENT

Using a simulation study, Sollmann et al. (2012) investigated how trap spacing and array size relative to animal movement influence SCR parameter estimates and we will summarize their study here. They simulated encounter histories on an 8×8 trap array with regular spacing of 2 units, using a binomial observation model with Gaussian hazard encounter model, across a range of values for the scale parameter σ^* . We refer to the scale parameter as σ^* here, because Sollmann et al. (2012) use a slightly different parametrization of SCR models, in which σ^* corresponds to $\sigma \times \sqrt{2}$.

In Sec. 5.4 we pointed out that under the Gaussian (or half-normal) detection model σ can be converted into an estimate of the 95% home range or “use area” around s_i . Based on this transformation, values for σ^* were chosen so that there was a scenario where the trap array was smaller than a single individual’s home range, i.e. trap spacing was small relative to individual movements ($\sigma^* = 5$), a scenario where spaces between traps were large enough to contain entire home ranges ($\sigma^* = 0.5$), and two intermediate scenarios and where sigma was smaller ($\sigma^* = 1$ unit) and larger ($\sigma^* = 2.5$ units) than the trap spacing, respectively. N was 100, the baseline trap encounter rate λ_0 was 0.5 (on the cloglog scale) for all four scenarios and trap encounters were generated over 4 occasions. Table 10.1 shows the results as the average over 100 simulations.

All model parameters were estimated with relatively low bias ($< 10\%$) and high to moderate precision (relative root mean squared error, RRMSE $< 25\%$) for all scenarios of σ^* , except $\sigma^* = 0.5$ units, under which model parameters were mostly not estimable (therefore excluded from Table 10.1). Data for the latter case mostly differed from the other scenarios in that fewer animals were captured and very few of the captured animals were recorded at more than 1 trap (Table 10.2). For $\sigma^* = 0.5$, abundance (N) was not estimable in 88% of the simulations, and when estimable, was underestimated by approximately 50%. This shows that a wide trap spacing that is considerably too large relative to animal movement may be problematic in SCR studies.

Estimates (posterior means) of N were least biased and most precise under the $\sigma^* = 2.5$ scenario, and in general, all parameters were estimated best under the $\sigma^* = 2.5$ or the $\sigma^* = 5$ scenario. All estimates had the highest relative bias and the lowest precision under the $\sigma^* = 1$ scenario. These results clearly demonstrate that SCR models can successfully handle a range of trap spacing to animal movement ratios, and even when using a trapping array smaller than an average home range: at $\sigma^* = 5$, the home range of an individual was approximately 235 units², while the trapping grid only covered 196 units². Still, the model performed very well.

An important consideration in this simulation study is that all but the $\sigma^* = 0.5$ units

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trap spacing, whereas the latter goes down. In summary, in small trap spacing scenarios, the small sample size leads to imprecise estimates, whereas in large trap spacing scenarios, lack of spatial recaptures leads to imprecise and biased estimates.

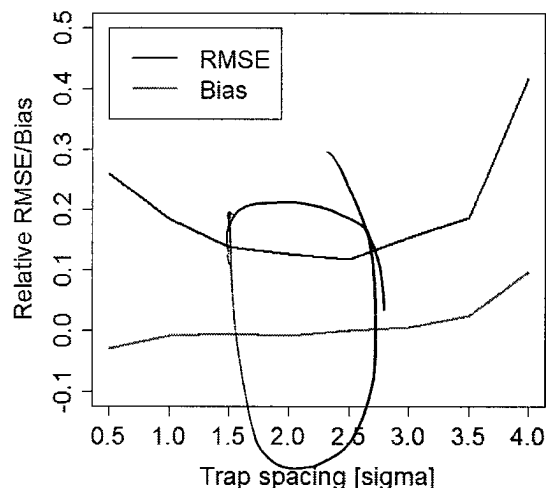


Figure 10.1. Relative bias and RRMSE of estimates of N from an SCR model for a range of trap spacing scenarios.

10.3.1 Black bears from Pictured Rocks National Lakeshore

To see how trap array size influences parameter estimates from spatial capture-recapture models in the real world, Sollmann et al. (2012) also looked at a black bear data set from Pictured Rocks National Lakeshore, Michigan, collected using 123 hair snares distributed over an area of 440 km² along the shore of Lake Superior in May-July 2005 (Belant et al., 2005). The SCR model for the bear data included sex-specific encounter rate parameters, and an occasion-specific baseline encounter rate. This was motivated by a) the lower average number of detections for male bears, b) the decreasing number of detections over time in the raw data, and c) the fact that male black bears are known to move over larger areas than females (e.g., Gardner et al., 2010b; Koehler and Pierce, 2003).

To address the impact of a smaller trap array on the parameter estimates, models fitted to the full data set were compared to models fitted to data subsets. The first subset retained only those 50% of the traps closest to the grid center. In the second, only the southern 20% of the traps were retained 10.3.

Reducing the area of the trap array by 50% created a grid polygon of 144 km², which was smaller than an estimated male black bear home range and only 50% larger than a

are useful in practice, either by themselves or combined: Sampling based on *clusters* of traps and sampling based on *rotating* groups of traps over the landscape.

Karanth and Nichols (2002) describe 3 strategies for moving traps to achieve coverage of a larger study area, geared toward traditional capture-recapture analysis. Suppose that sampling the entire area of interest requires sampling G sites, then the 3 strategies are:

- (1) For every day/sampling occasion, randomly choose x out of your G sites, where x is the number of trapping devices you have at hand. Obviously, this requires that it be relatively easy to move traps around.
- (2) Move blocks of traps that are close to each other in space daily. For example, if you divide your total study area into 4 blocks, sample block 1 for a day, then move traps to block 2 for a day, and so forth, and repeat until each block has been sampled for a sufficient amount of time.
- (3) If moving blocks of traps daily is too challenging logistically, then you can sample each block for a certain number of days/occasions before moving cameras to the next block. In this fashion, you only need to move traps to each block once.

In traditional CR we collapse data across traps and assume all individuals in the study area have some probability > 0 of being detected. For our data that means that, under scenario (2) the first occasion is defined as the time it takes to sample all 4 blocks once, the second occasion consists of the second round of sampling all blocks, etc. Under scenario (3), we have to combine data from day 1 in each of the blocks to form occasion 1, data from day 2 in each of the blocks forms occasion 2, and so on. Especially scenario 3 makes modeling time-dependent detection difficult, since occasion 1 does no longer refer to an actual day or continuous time interval. We do not have that problem in SCR, where accounting for sampling effort at each trap is straight forward, as we first demonstrated for the wolverine example in Sec. 5.9. Because we are dealing with detection at the trap level, even for design (3) in a spatial framework, we can still look at variation in detection over time. As such, we don't think that one of the above designs is superior for SCR models than the other, but rather, all of them may produce adequate SCR data, as long as overall sample size requirements are met.

Efford and Fewster (2012) looked at the performance of different spatial study designs for abundance estimation from traditional and spatial capture-recapture models, including a clustered design, where groups of detectors are spaced throughout the larger region of interest. They found that in a spatial framework this design performed well, although there were indications of a slight positive bias in estimates of N . Such a clustered design enables researchers to increase area coverage without having to increase the number of traps. Efford and Fewster (2012) note that distribution of clusters has to be spatially representative – for example, systematic with a random origin. The issue of spatially representative designs is not limited to SCR and an extensive treatment of the topic can be found in the distance sampling literature (Buckland et al., 2001). Further, the authors stress that, if distances among clusters are large and individuals are unlikely to show up in several clusters, then the method relies on spatial recaptures *within* clusters, meaning that spacing of detectors within clusters has to be appropriate to the movements of the species under study. A clustered type of design is also suggested by Efford et al. (2009b) for acoustic detectors (see Chapt. 9.4) with small groups of such detectors (e.g., 2×2) being distributed in a probabilistic fashion across the region of interest.

and Sloane, 1993; Fedorov and Hackl, 1997) to develop a framework for designing spatial trapping arrays for capture-recapture studies. Müller (2007) provides a recent monograph level treatment of the subject that is very accessible.

In the following sections, we adapt these classical methods for constructing optimal designs to obtain the configuration of traps (or sampling devices) in some region (the design space, \mathcal{X}), that minimizes some appropriate objective function based on the variance of model parameters, α , or N , for a prescribed state-space. We show that this criterion – based on the variance of an estimator of N – represents a formal compromise between minimizing the variance of the MLEs of the detection model parameters and obtaining a high expected probability of capture. Intuitively, if our only objective was to minimize the variance of parameter estimates then all of our traps should be in one or a small number of clusters where we can recapture a small number of individuals many times each. Conversely, if our objective was only to maximize the expected probability of encounter then the array should be highly uniform so as to maximize the number of individuals being exposed to capture.

10.5.1 Statement of the design problem

Let \mathcal{X} , the *design space*, denote some region within which sampling could occur and let $\mathbf{X} = \mathbf{x}_1, \dots, \mathbf{x}_J$ denote the *design*, the set of sample locations (e.g., of camera traps), normally we just call these “traps.” The design space \mathcal{X} must be prescribed (a priori). Operationally, we could equate \mathcal{X} to the study area itself (which is of management interest) but, in practical cases, there will generally be parts of the study area that we cannot sample. Those areas need to be excluded from \mathcal{X} . While \mathcal{X} may be continuous, in practice it will be sufficient to represent \mathcal{X} by a discrete collection of points which is what we do here. This is especially convenient when the geometry of \mathcal{X} is complicated and irregular, which would be the case in most practical applications. The technical problem addressed subsequently is how do we choose the locations \mathbf{X} in a manner that produces the “optimal” (lowest variance) for estimating population size or density, or some other quantity of interest.

As usual, we regard the population of N individual “activity centers” as the outcome of a point process distributed uniformly over the state-space \mathcal{S} . The relevance and importance of \mathcal{S} has been established repeatedly in this book, as it defines a population of individuals (i.e., activity centers) and, in practice, it is not usually the same as \mathcal{X} due to the fact that animals move freely over the landscape and the location of traps is typically restricted by policies, ownership, logistics and other considerations. The objective we pursue here is: Given (1) \mathcal{X} , (2) a number of design points, J ; (3) the state-space \mathcal{S} , (4) an SCR model, and (5) a design criterion $Q(\mathbf{X})$, we want to choose *which* J design points we should select in order to obtain the *optimal* design under the chosen model, where the optimality is with respect to $Q(\mathbf{X})$.

What types of functions make reasonable objective functions, $Q(\mathbf{X})$? We will describe some possible choices for $Q(\mathbf{X})$ below, but it makes sense that they should relate to the variance of estimators of one or more parameters of the SCR model.

We motivate the basic ideas of model-based design with a simple model that proves to be an effective caricature of the SCR model that we’ll use shortly. Suppose \mathbf{s} is the activity center of a single individual, and \mathbf{s} is known with certainty. Then, for an array

10109 over all possible values of \mathbf{s}_i , and for *each* \mathbf{s}_i , which is an N -fold summation: *(one for each N)*

$$E_{\mathbf{s}_1, \dots, \mathbf{s}_N} \mathcal{I}(\boldsymbol{\alpha}, \mathbf{X}) = \sum_{i=1}^N \sum_{\mathbf{s} \in \mathcal{S}} (\mathbf{M}'_i(\mathbf{s}_i) \mathbf{M}_i(\mathbf{s}_i))$$

10110 which is just N copies of the integrated (spatially averaged) information: *assuming independence?*

$$E_{\mathbf{s}_1, \dots, \mathbf{s}_N} \mathcal{I}(\boldsymbol{\alpha}, \mathbf{X}) = N \sum_{\mathbf{s} \in \mathcal{S}} (\mathbf{M}'_i(\mathbf{s}_i) \mathbf{M}_i(\mathbf{s}_i)).$$

10111 It therefore seems sensible to base design of SCR studies on some criterion that is
 10112 a function of this expected information matrix. E.g., find the design that maximizes
 10113 the diagonals, or the determinant, or minimizes the trace of the *inverse* (the variance-
 10114 covariance matrix based on N individuals). This can be done for any number of design
 10115 points $\mathbf{x}_1, \dots, \mathbf{x}_J$ using standard exchange algorithms (see Müller, 2007, Chapt. 3) and
 10116 we discuss this below in Sec. 10.5.5. However, our SCR models are not normal linear
 10117 models but, rather, more like Poisson or binomial GLMs. We see in the next section that
 10118 we can adapt these ideas for such models.

10119 10.5.2 Model-based Design for SCR

10120 Following our development of the normal linear model above, suppose for the moment
 10121 that we know \mathbf{s} for a single individual. In this case, its vector of counts of encounter in
 10122 each trap \mathbf{y} are either binomial or Poisson counts, and the linear predictor has this form:

$$g(\mathbb{E}(\mathbf{y})) = \alpha_0 + \alpha_1 \|\mathbf{x} - \mathbf{s}\|^2.$$

10123 for the Gaussian encounter probability model, or any other model could be used. In vector
 10124 form, we write this as:

$$g(\mathbb{E}(\mathbf{y})) = \mathbf{M}'\boldsymbol{\alpha} \quad \text{for an individual.}$$

10125 where \mathbf{M} is the $J \times 2$ design matrix where the 2nd column contains the squared pairwise
 10126 distances between each individual i and trap j , and thus it depends on both \mathbf{X} and \mathbf{s} .

10127 The asymptotic formula for $\text{Var}(\boldsymbol{\alpha})$ can be cooked up for any type of GLM. As an
 10128 example (we use this below), for the Poisson GLM, the asymptotic variance-covariance
 10129 matrix of $\hat{\boldsymbol{\alpha}}$, considering a single individual having location \mathbf{s} , is¹

$$\text{Var}(\hat{\boldsymbol{\alpha}}|\mathbf{X}, \mathbf{s}) = (\mathbf{M}(\mathbf{s})'\mathbf{D}(\boldsymbol{\alpha}, \mathbf{s})\mathbf{M}(\mathbf{s}))^{-1}. \quad (10.5.2)$$

10130 This is a function of the design \mathbf{X} as well as \mathbf{s} , both of which are balled-up in the re-
 10131 gression design matrix \mathbf{M} , and the matrix \mathbf{D} which is a diagonal matrix having elements
 10132 $\text{Var}(y_j|\mathbf{s}) = \exp(\mathbf{m}'_j\boldsymbol{\alpha})$ for y_j = the frequency of encounter in trap j and where \mathbf{m}'_j is the
 10133 j^{th} row of $\mathbf{M}(\mathbf{s})$. We can compute the expected information under the Poisson model with
 10134 known N using this modified formulation. These ideas are meant to motivate technical
 10135 concepts related to model-based design, where we know N , and therefore have a convenient
 10136 variance or information expression to work with. However, in all real capture-recapture
 10137 applications we won't know N , and so we need to address that issue, which we do in the
 10138 next section.

¹ This is basic GLM theory that derives from the fact that the Poisson is a member of the natural exponential family of distributions, e.g., see McCullagh and Nelder (1989) or Agresti (2002).

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To make use of any of these criteria in a particular design problem, we need to decide on values of N , and the model parameters for computing \bar{p} , and then think about optimizing the criterion over all possible designs (see below).

10.5.4 Too much math for a Sunday afternoon

Here we discuss calculation \bar{p} and variance expressions required to compute the design criteria above.

Characterizing \bar{p}

In SCR models, an individual with activity center \mathbf{s}_i is captured if it is captured in *any* trap and therefore, under the Bernoulli (passive detector) observation model,

$$\bar{p}(\mathbf{s}_i, \mathbf{X}) = 1 - \prod_{j=1}^J (1 - p_{ij}(\mathbf{x}_j, \mathbf{s}_i))$$

where p_{ij} here is the Gaussian (or other) encounter probability model that depends on distance between traps and activity centers, say d_{ij} for the distance between individual activity center \mathbf{s}_i and trap \mathbf{x}_j . Under the Poisson observation model, with a Gaussian hazard model:

$$\bar{p}(\mathbf{s}_i, \mathbf{X}) = 1 - \exp(-\lambda_0 \sum_j \exp(\alpha_1 * d(\mathbf{x}_j, \mathbf{s}_i)^2))$$

use same notation
or add
= above

where here we emphasized that this is conditional on \mathbf{s}_i and also the design – the trap locations \mathbf{x}_j . The *marginal* probability of encounter, averaging over all possible locations of \mathbf{s} is:

$$\bar{p}(\mathbf{X}) = 1 - \int_{\mathbf{s}} \bar{p}(\mathbf{s}_i, \mathbf{X}) d\mathbf{s}. \quad (10.5.4)$$

It is important to note that this can be calculated directly *given* the design \mathbf{X} , and parameters of the model. This is handy because we see that it is used in the variance formulae given subsequently and therefore it is used directly in evaluating any of the criteria described above.

Characterizing $\text{Var}(\hat{\bar{p}})$

Developing an expression for $\text{Var}(\hat{\bar{p}})$ depends on the observation model. We work here with the Poisson observation model, and we do that because the technical argument that follows is somewhat easier for that case compared to the Bernoulli model for passive detection devices (but see Huggins (1989) and Alho (1990) for additional context). We first express the integral in Eq. 10.5.4 as a summation over a fine mesh of points so that:

$$\bar{p}(\mathbf{X}) = \sum_{\mathbf{s}} 1 - \bar{p}(\mathbf{s}_i, \mathbf{X})$$

which under the Poisson observation model is, in a simplified notation:

$$\bar{p}(\mathbf{X}) = \sum_{\mathbf{s}} \left\{ 1 - \exp\left(-\sum_j \exp(\alpha_0 + \alpha_1 d(\mathbf{x}_j, \mathbf{s})^2)\right) \right\}$$

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10.5.5 Optimization of the criterion

To compute spatial designs that optimize a given criterion, we need to come up with a ballpark guess of the model parameters so that the criterion can be evaluated for any design. i.e., what are the values of α and N we expect in our study? If we do that, and specify the state-space \mathcal{S} then, we can, in theory, optimize the variance criterion over all possible configurations of J traps. In formulating the optimization problem note that we have J sample locations corresponding to rows of \mathbf{X} . The problem is therefore a $2J$ dimensional optimization problem which, for J small, could be solved using standard numerical optimization algorithms as exist in almost every statistical computation environment. However, J will almost always be large enough so as to preclude effective use of such algorithms. This is a common problem in experimental design, and spatial sampling in general, for which sequential exchange or swapping algorithms have been fairly widely adopted (e.g., Wynn, 1970; Fedorov, 1972; Mitchell, 1974; Meyer and Nachtsheim, 1995; Nychka et al., 1997; Royle and Nychka, 1998). The basic idea is to pose the problem as a sequence of 1-dimensional optimization problems in which the objective function is optimized over 1 or several coordinates at a time. In the present case, we consider swapping out \mathbf{x}_j for some point in \mathcal{X} that is nearby \mathbf{x}_j (e.g., a 1st order neighbor). Beginning with an initial design, chosen randomly or by some other method, the objective function is evaluated for all possible swaps (at most 4 in the case of 1st order neighbors) and whichever point yields the biggest improvement is swapped for the current value. The algorithm is iterated over all J design points and this continues until convergence is achieved. Such algorithms may yield local optima and optimization for a number of random initial designs can yield incremental improvements. We implemented such a swapping algorithm in **R**, and it is available as a function in the **scrbook** package with the function **SCRdesign**. The algorithm operates on a discrete representation of \mathcal{S} (an arbitrary matrix of coordinates). For each point in the design, \mathbf{X} , only the nearest neighbors (the number is specified by the user) are considered for swapping into the design during each iteration. For example, to compute `ndesigns = 10` putative optimal designs (each based on a random start) of size $J = 11$, we execute the function as follows:

```
> des<-SCRdesign(S,X,ntraps=11,ndesigns=10,nn=15,sigma=1)
```

Where the state-space \mathcal{S} , the candidate set \mathbf{X} are provided as matrices, `nn` is the number of nearest neighbors to inspect for each design point change, and `sigma` is the scale parameter of, in this case, a Gaussian hazard model. See the help file **SCRdesign** for examples and analysis of the output.

While swapping algorithms are convenient to implement, and efficient at reducing the criterion in very high dimensional problems, they do not always yield the global optimum. In practice, as in the examples below, it is advisable to apply the algorithm to a large number of random starting designs. Our experience is that essentially meaningless improvements are realized after searching through a few dozen random starts.

The design criteria we developed above bear a striking resemblance to design criteria used to construct so-called space-filling designs (Nychka et al., 1997). Such criteria are based on inter-point distances, and space-filling designs seek to optimize some function of distance alone, instead of a variance-based objective function. The benefit of this approach is that one doesn't have to specify the model to produce a design, and space-filling designs have been shown to provide reasonable approximations to designs based on

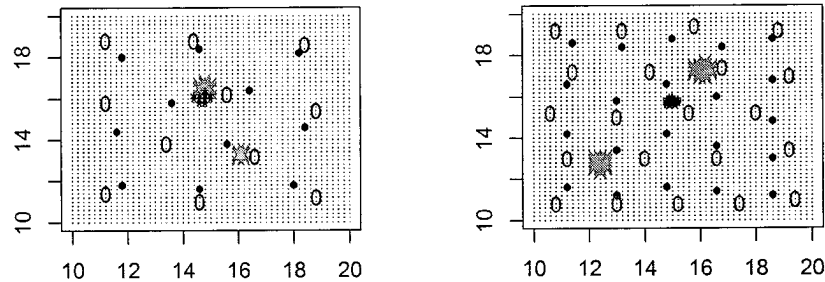


Figure 10.3. Best designs for each of 4 design criteria, produced using the exchange algorithm with 15 nearest-neighbors and based on 10 random starting designs. The left panel shows the best $J = 11$ point designs, and the right panel shows the best $J = 21$ point designs. The solid black dots correspond to the best design for Q_1 , 0 marks the design for Q_3 , "X" for Q_2 and the tightly clustered "*" corresponds to Q_4 .

10.5.7 Density covariate models

Many capture-recapture studies will involve one or more landscape or habitat covariates that are thought to affect density, with the idea of using the methods described in Chapt. 11 for modeling and inference. We imagine that it should be possible to extend the model-based framework described previously to accommodate uncertainty due to having to estimate β , and this could be included as a feature of the design criterion.

In this case, we can think of the captures in a trap being Poisson random variables with mean $\mu(\mathbf{x}, \mathbf{s}) * D(\mathbf{s})$ and we think the same arguments as given above can be used to devise design criteria and optimize them. However, in this case we might not only care about estimating N but also (or instead) inference about the parameters β . Thus, we might choose designs that are good for N or perhaps only good for estimating β or perhaps both. Intuitively, we think these two design objectives conflict with one another to some extent. Model-based approaches should favor areas of higher density, but the design points need to realize variation in the landscape covariates too.

10.6 TEMPORAL ASPECTS OF STUDY DESIGN

The spatial configuration of traps is one of the most important aspects of sampling design for capture-recapture studies. Indeed, as we discussed in the previous section, design under SCR models can be thought of as being analogous to classical model-based spatial design, and the concepts and methods from that field can be brought to bear on the design

Add reference to Coarsenet al in prep?

Will send graph

10380 have to strive for a compromise between collecting enough data while still approximating
 10381 a closed population. For some species we may be able to avoid seasons where violation
 10382 of demographic closure is particularly likely – for example migration seasons in migratory
 10383 birds, or specific breeding seasons (or collective suicide season in lemmings). But for many
 10384 species such biological seasons might be less clear cut. For example, in warm climates tigers
 10385 and other large cats can breed year round (Nowak, 1999). As a consequence, guidelines
 10386 as to what time frame adequately approximates a closed population are generally vague
 10387 and arm-wavy. Unfortunately, we do not have much more to offer on the subject of how
 10388 to decide on the length of a study, other than to urge you to think about the biology of
 10389 your study species *before the study* and choose a time window that seems appropriate for
 10390 that purpose.

*This exactly parallels traditional ~~SCR~~ CR
 (implies same decision
 I think?)*

10391 10.6.2 Diagnosing and dealing with lack of closure

10392 Once a field study has been conducted, you may wonder whether the collected data contain
 10393 any evidence that the closure assumption has been met or violated. Relatively few tests
 10394 for population closure in traditional capture-recapture have been developed, mostly due
 10395 to the fact that behavioral variation in detection is indistinguishable from violation of
 10396 demographic closure (Otis et al., 1978; White et al., 1982). Otis et al. (1978) developed
 10397 a test for population closure that can handle heterogeneity in detection probability, but
 10398 does not perform well in the presence of time or behavioral variation in p . Stanley and
 10399 Burnham (1999) developed a closure test for model M_t (time variation in detection), which
 10400 works well when there is permanent emigration and a large number of individuals migrate.
 10401 Both tests are implemented in the program **CloseTest** (Stanley and Richards (2013)).

10402 There are no specific population closure tests for SCR models, for the same reasons that
 10403 violation of other model assumptions cannot necessarily be distinguished from a lack of
 10404 population closure. If you are worried that closure might have been violated in your study,
 10405 one approach of dealing with this problem is to fit an open population model. You can
 10406 subdivide your study into several periods and fit a spatial version of Pollock's robust design
 10407 capture-recapture model, which can estimate population size/density for each of these
 10408 periods (in this context also called primary periods) using models of demographic closure.
 10409 Alternatively, we may consider fully dynamic models which contain explicit parameters
 10410 of survival and recruitment (Chapt. 16). These models can be quite time consuming,
 10411 and if you wanted a faster check you could alternatively fit a spatial Cormack-Jolly-Seber
 10412 model that only estimates survival. The magnitude of the survival estimates gives you
 10413 some partial information about population closure in your study – if survival is close
 10414 to 1 ~~at least~~ there is little evidence of losses of individuals, either through permanent
 10415 emigration or death. These and other open population models are presented in detail in
 10416 Chapt. 16. Finally, if your data are too sparse to fit a full-blown open population model,
 10417 you can subdivide your study into $t = 1, 2, \dots, T$ primary periods and estimate abundance
 10418 separately for each period's worth of data, possibly sharing the detection parameters across
 10419 periods, if you can safely assume they remain constant. You can do that by either letting
 10420 N_t be independent from each other, or by specifying an underlying distribution for all N_t
 10421 in a multi-session framework as described in Chapt. 14.

10467 in ecology. In our view, model-based design under SCR models has great potential due
 10468 to its coherent formulation and flexibility. On this topic, we have just barely scratched
 10469 the surface here, showing how to formulate a criterion that is a function of the design,
 10470 and then optimizing the criterion over all possible designs. Our cursory analysis of model-
 10471 based design in a single situation did reveal an important aspect of design that has not
 10472 been discussed in the literature. That is, the optimal spacing of traps in an array depends
 10473 on the *density* of traps in the state-space. In our analysis, the spacing of 11 and 21 trap
 10474 optimal designs was quite different. Therefore, this should be considered in practical SCR
 10475 design exercises.

10476 Conceptually, the information in SCR studies comes in two parts: Recaptures of in-
 10477 dividuals at different traps (spatial recaptures) and the total sample size of individuals.
 10478 Maximizing both of these things as objectives induces an explicit trade-off in the construc-
 10479 tion of capture-recapture designs. We need designs that are good for estimating \bar{p} and
 10480 also designs that obtain a high sample size of n . Designs that are extremely good only for
 10481 one or the other will produce bad SCR designs – estimators of density with low precision
 10482 – or designs in which N is not estimable due to a lack of spatial recaptures. One possible
 10483 exception is when telemetry data are available (or other auxiliary data). In Chapt. 13 we
 10484 discuss SCR models that integrate auxiliary information on resource selection obtained
 10485 by telemetry. Telemetry data are directly informative about the coefficient of the distance
 10486 term (σ or α_1) and, in fact, can be estimated from telemetry data alone. It stands to
 10487 reason that, when telemetry data are available, this should affect considerations related to
 10488 trap spacing. Conceivably even, one might be able to build SCR designs that don't yield
 10489 any formal spatial recaptures because all of the information about σ is provided by the
 10490 telemetry data. We have done limited evaluations of the trap spacing problem in the pres-
 10491 ence of telemetry data, and the results suggest that, while efficient designs have a larger
 10492 trap spacing than without telemetry data, the realization of some spatial recaptures is
 10493 important even when telemetry data are available. With the **R** code we provide in Chapt.
 10494 13, you should be able to carry out your own custom evaluation of these types of design
 10495 problems.

Someone
 should
 say
 really
 well
 file to
 var(N)