A comparison of design-based and model-based approaches for spatial data.

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Abstract

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Potential Journals:

- Ecological Applications
- Methods in Ecology and Evolution
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- Environmetrics
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1. Introduction

There are two general approaches for using data to make statistical inferences about a population: design-based approaches and model-based approaches. When data cannot be obtained for all units in a population (population units), data on a subset of the population units is collected in a sample. In the design-based approach, inferences about the underlying population are informed from a probabilistic process in which population units are selected to be in the sample. Alternatively, in the model-based approach, inferences are made from specific assumptions about the underlying process that generated the data. Each paradigm has a deep historical context (Sterba, 2009) and its own set of general advantages (Hansen et al., 1983).

Though the design-based and model-based approaches apply to statistical inference in a broad sense, we focus on comparing these approaches for spatial data. We define spatial data as variables measured at specific geographic locations. De Gruijter and Ter Braak (1990) give an early comparison of design-based and model-based approaches for spatial data, quashing the belief that design-based

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approaches could not be used for spatially correlated data. Thereafter, several comparisons between design-based and model-based for spatial data have been considered, but they tend to compare design-based approaches that ignore spatial locations to model-based approaches (Brus and De Gruijter, 1997; Ver Hoef, 2002, 2008). Cooper (2006) review the two approaches in an ecological context before introducing a "model-assisted" variance estimator that combines aspects from each approach. In addition to Cooper (2006), there has been substantial research and development into estimators that use both design and model-based principles (see e.g. Cicchitelli and Montanari (2012), Chan-Golston et al. (2020) for a Bayesian approach, and Sterba (2009)). More recent overviews include Brus (2020) and Wang et al. (2012), but no numerical comparison has been made between design-based approaches that incorporate spatial locations and model-based approaches.

The rest of this paper is organized as follows. In Section 2, we compare sampling and estimation procedures between the design-based approach and the model-based approach. In Section 3, we use simulated and real data to study the the behavior of both approaches. And in Section 4, we end with a discussion and provide directions for future research.

2. Background

The design-based and model-based approaches incorporate randomness in fundamentally different ways. In this section, we describe the role of randomness and its effects on subsequent inferences. We then discuss specific inference methods for the design-based and model-based approaches for spatial data.

2.1. Comparing Design-Based vs. Model-Based

The design-based approach assumes the data are fixed. Randomness is incorporated in the selection of population units according to a sampling design. A sampling design assigns a positive probability of inclusion in the sample (inclusion probability) to each population unit. Some examples of commonly used sampling designs include independent random sampling (IRS), stratified random sampling, and cluster sampling. The goal is to use the sampling design and the sampled data to estimate population parameters like means and totals. These population parameters are typically assumed to be fixed but unknown.

Treating the data as fixed and incorporating randomness through the sampling design yields estimators having very few other assumptions. Confidence intervals for these types of estimators are typically derived using limiting arguments. Means and totals, for example, are asymptotically normally distributed by the Central Limit Theorem. Särndal et al. (2003) and Lohr (2009) provide thorough reviews of the design-based approach.

The model-based approach assumes the data are a random realization of a data-generating process. Randomness is often incorporated through distributional assumptions on this process. Instead of estimating fixed but unknown parameters (as in the design-based approach), the goal of model-based inference

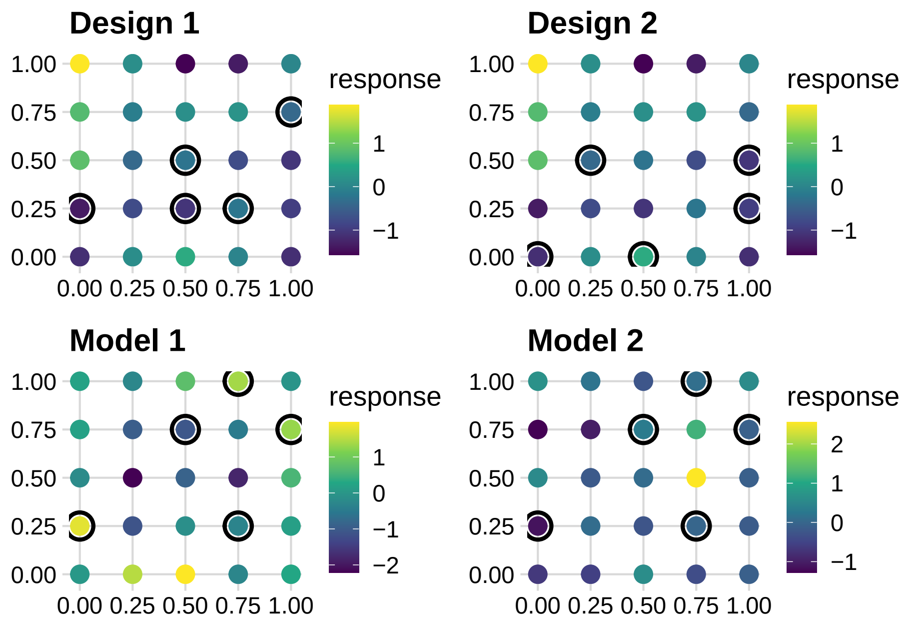

Figure 1: A comparison of sampling under the design-based and model-based frameworks. In the top row, we have one fixed population, and two random samples. In the bottom row, we have two realizations of the same spatial process sampled at the same locations.

in the spatial context is often *prediction* of an unknown quantity. For example, suppose the realized mean of all population units is the quantity of interest. Instead of *estimating* a fixed unknown mean, we are *predicting* the value of the mean, a random variable. We know that if we sampled all population units, we would have an exact prediction for the mean of our one realized process, without any uncertainty. But we are typically not interested in the true, unknown mean of the underlying process.

Assuming the data is a realization of a specific data-generating process yields predictors that are linked to distributional assumptions. These distributional assumptions are used to derive prediction intervals. The distributional assumptions allow the prediction intervals to be more precise. Cressie (1993) and Schabenberger and Gotway (2017) provide reviews of model-based approaches for spatial data.

Description of Figure 1 goes here.

2.2. Spatially Balanced Design and Analysis

The design-based approach can use spatial locations to obtain spatially balanced samples. First we discuss spatial balance with respect to the population (Stevens Jr and Olsen, 2004). A sample is spatially balanced with respect to the population if the sampled population units are a miniature of the population units. A sample is a miniature of the population if the distribution of the sampled population units mirrors the density of all population units. Spatial balance with respect to the population is different than spatial balance with respect to geography. A sample that is spatially balanced with respect to geography is spread out in some type of equidistant manner over geographical space and is not meant to be miniatures of the population. When we refer to spatial balance henceforth, we mean spatial balance with respect to the population.

Spatially balanced samples are useful because they tend to yield estimates that have lower variance than estimates constructed from sampling designs lacking spatial balance (Barabesi and Franceschi, 2011; Benedetti et al., 2017; Grafström and Lundström, 2013; Robertson et al., 2013; Stevens Jr and Olsen, 2004; Wang et al., 2013). To quantify spatial balance, Stevens Jr and Olsen (2004) proposed loss functions based on Voroni polygons. The first spatially balanced sampling algorithm that saw widespread use was the Generalized Random Tessellation Stratified (Stevens Jr and Olsen, 2004). Since GRTS was developed, several other spatially balanced sampling algorithms have emerged, including the Local Pivotal Method (Grafström et al., 2012; Grafström and Matei, 2018), Spatially Correlated Poisson Sampling (Grafström, 2012), Balanced Acceptance Sampling (Robertson et al., 2013), Within-Sample-Distance (Benedetti and Piersimoni, 2017), and Halton Iterative Partitioning (Robertson et al., 2018). We focus on the Generalized Random Tessellation Stratified (GRTS) algorithm to select spatially balanced sampling because it has several attractive properties detailed by Stevens Jr and Olsen (2004) and Dumelle et al. (2021).

The GRTS algorithm is used to sample from finite and infinite populations and works by utilizing a mapping between two-dimensional and one-dimensional space. The population units in two-dimensional space are divided into cells using a hierarchical index. Population units are then mapped to a one-dimensional line via the hierarchical indexing. The line length of each population unit equals its inclusion probability. A systematic sample is conducted on the line and these samples are linked to a population unit in two-dimensional space, which results in the desired sample. Stevens Jr and Olsen (2004) provide and Dumelle et al. (2021) provide further details.

After collecting a sample using the GRTS algorithm, the data are used to estimate population parameters. The Horvitz-Thompson estimator (Horvitz and Thompson, 1952) yields unbiased estimates of population means and totals. For example, if τ is a population total, then the Horvitz-Thompson estimator of τ (denoted by $\hat{\tau}_{ht}$), is given by

$$\hat{\tau}_{ht} = \sum_{i=1}^{n} Z_i \pi_i^{-1}, \tag{1}$$

where Z_i and π_i are the observed value and inclusion probability of the ith population unit selected in the sample. A similar formula exists for estimating the mean, μ. Horvitz and Thompson (1952) and Sen (1953) provide variance estimators for $\hat{\tau}_{ht}$, but they have two drawbacks. First, they rely on calculating π_{ij}, the probability that population unit i and population unit j are included in the sample, and this can be very difficult to calculate. Second, they ignore the spatial locations of the population units. To address these drawbacks, Stevens Jr and Olsen (2003) proposed a local neighborhood variance estimator. The local neighborhood variance estimator does not rely on π_{ij}, and it incorporates spatial locations by assigning higher weights to nearby observations. Stevens Jr and Olsen (2003) show this variance estimators tends to reduce the estimated standard error of $\hat{\tau}$, yielding narrower confidence confidence intervals for τ.

2.3. Finite Population Block Kriging

Finite Population Block Kriging (FPBK) is a model-based approach that expands the geostatistical Kriging framework to the finite population setting (Ver Hoef, 2008). Instead of basing inference off of a specific sampling design, we assume the data are generated by a spatial process. Ver Hoef (2008) gives details on the theory of FPBK, but some of the basic principles are summarized below. Let $\mathbf{z} \equiv \{\mathrm{z}(s_1), \mathrm{z}(s_2), ..., \mathrm{z}(s_N)\}$ be a response variable that can be measured at the N population units and is represented as an $N \times 1$ vector. Suppose we want to predict some linear function of the response variable, $f(\mathbf{z}) = \mathbf{b}'\mathbf{z}$, where $\mathbf{b}$ is a $1 \times N$ vector of weights. For example, if we want to predict the population total across all population units, then we would use a vector of 1's for the weights.

Typically, however, we only have a sample of the N population units. Denoting quantities that are part of the sampled population units with a subscript s and quantities that are part of the unsampled population units with a subscript u,

$$\begin{pmatrix} \mathbf{z}_s \\ \mathbf{z}_u \end{pmatrix} = \begin{pmatrix} \mathbf{X}_s \\ \mathbf{X}_u \end{pmatrix} \boldsymbol{\beta} + \begin{pmatrix} \boldsymbol{\delta}_s \\ \boldsymbol{\delta}_u \end{pmatrix}, \tag{2}$$

where $\mathbf{X}_s$ and $\mathbf{X}_u$ are the design matrices for the sampled and unsampled population units, respectively; β is the parameter vector of fixed effects; and $\boldsymbol{\delta}_s$ and $\boldsymbol{\delta}_u$ are random errors for the sampled and unsampled population units, respectively. Denoting $\boldsymbol{\delta} \equiv [\boldsymbol{\delta}_s \ \boldsymbol{\delta}_u]'$, we assume the expectation of $\boldsymbol{\delta}$ equals $\mathbf{0}$.

We also typically assume that there is spatial correlation in $\boldsymbol{\delta}$, which can be modeled using a covariance function. It is common to assume the covariance function is second-order stationary and isotropic (Cressie, 1993), and that the spatial covariance decreases as the separation between population units increases. Many spatial covariance functions exist, but the primary function we use throughout the simulations and applications in this manuscript is the exponential covariance function: the i, j^{th} entry for $\mathrm{cov}(\boldsymbol{\delta})$ is

$$\mathrm{cov}(\delta_i, \delta_j) = \theta_1 \exp(-3h_{i,j}/\theta_2) + \theta_3 \mathbb{1}\{\mathbf{h}_{i,j} = 0\}, \tag{3}$$

where $h_{i,j}$ is the distance between population units i and j, and $\boldsymbol{\theta}$ is a vector of spatial covariance parameters of the partial sill θ_1, the range θ_2, and the nugget θ_3, and $\mathbb{1}$ is an indicator function. However, any spatial covariance function could be used in the place of the exponential, including functions that allow for non-stationarity or anisotropy (Chiles and Delfiner, 1999, pp. 80–93).

With the above model formulation, the Best Linear Unbiased Predictor (BLUP) for $f(\mathbf{b}'\mathbf{z})$ and its prediction variance can be computed. While details of the derivation are in (Ver Hoef, 2008), we note here that the predictor and its variance are both moment-based.

We note that we only use FPBK in this paper in order to focus more on comparing the design-based and model-based approaches. However, k-nearest-neighbors (Fix and Hodges, 1951; Ver Hoef and Temesgen, 2013), random forest (Breiman, 2001), Bayesian models (Chan-Golston et al., 2020), among others, can also be used to obtain predictions for a mean or total from spatially correlated responses in a finite population setting.

3. Numerical Study

Sample Simulation

For the following simulation results, we simulated 1040 different gridded populations, each of size 900 (on the unit square) with sample size 150. For the design-based approach, population units were selected via GRTS, the Horvitz-Thompson estimator was used,and the local mean variance was used. For the model-based approach (FPBK), population units were selected via Independent Random Sampling (IRS) and the appropriate prediction and prediction variance formulas were used.

The response was normally distributed with an exponential covariance function with partial sill of 0.9, effective range of $\sqrt{2}$, and a nugget of 0.1. For model-based, we assumed the correct form of the covariance function (exponential), but estimated the spatial parameters with REML.

Approach	Bias	RMSE	MedAE	Coverage	PClose	MedIL
Design	0.0003	0.0353	0.0251	0.9461	0.4889	0.1362
Model	-0.0001	0.0362	0.0253	0.9480	0.5111	0.1430

Table 1: Approach, mean bias (Bias), root-mean-squared error (RMSE), median absolute error (MedAE), 95 percent interval coverage (Coverage), proportion of times the approach was closer to the true value (PClose), and median interval length (MedIL)

Base Simulations

- both good: correctly specified model with high correlation (we did this in Table 1)
- break model: highly non-normal errors with small sample size
- break design: small area estimation

Simulation Discussion Questions

- model-based: how should sample be drawn? should locations be fixed?
- change n or sampling fraction?

Other Base Settings?

- both good?: misspecified covariance model with high correlation
- break both? non-gaussian areas with smaller sample size

3.1. Software

The GRTS algorithm and the local neighborhood variance estimator are available in the **R** package `spsurvey` (Dumelle et al., 2021). FPBK can be readily performed in R with the `sptotal` package (Higham et al., 2020). We use `sptotal` for both the simulation analysis and the application, estimating parameters with Restricted Maximum Likelihood (REML).

3.2. Applied Example

Potential Data Sets:

- National Lakes Assessment
- Moose in Alaska
- Temperature Data from NOAA

4. Discussion

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