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

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Abstract

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1. Introduction

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Several comparisons between model-based and design-based for spatial data have been considered, but they tend to compare spatial models to IRS or SIRS (stratified IRS). No comparison has been made between spatial models and spatially balanced design-based approaches.

2. Background

2.1. Design-Based Philosphy

Design-Based Overview

Design-based inference uses characteristics of the sampling design to to estimate parameters of interest Typically, there are few assumptions involved because intervals are derived using the sampling design itself...........

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2.2. Model-Based Philosphy

Model-Based Overview

On the other hand, model-based inference imposes additional assumptions on the data with a potential to provide more precise estimates if the additional assumptions hold. Instead of estimating true but unknown parameters, the goal of model-based inference in the spatial context is often *prediction* of an unknown quantity. This is a fundamental philosophical difference between sampling-based and model-based approaches. 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 sites, we would have an exact prediction for the mean of our one realized spatial surface, without any uncertainty. But, the true mean of the spatial process that generated our realized data is still not known, and, in the prediction context, we typically do not care much about what value the mean of the underlying process takes.

Figure 1a. Data is fixed. In a finite population example, show a 3d surface that can be generated by anything. If we repeatedly sample the surface, then 95% of all 95% CIs will contain the true mean, which never changes.

Figure 1b. Spatial process is fixed. In a finite population example, show 10 3d surfaces that are generated from some model. If we repeatedly generate the surface and obtain a sample, then 95% of all 95% PIs will contain the realized means. The realized mean changes from surface to surface and it's not necessarily the case that 95% of all 95% PIs will contain the true, underlying mean.

2.3. Comparing Design-Based vs. Model-Based

Design-Based and Model-Based Comparisons

There have been many comparisons between the two paradigms. . . . . . .

2.4. Spatially Balanced Design and Analysis

Spatially balanced sampling algorithms use spatial information to obtain samples spread out in space. Spatially balanced samples are useful because they tend to yield estimators that are more precise than estimators constructed from an sampling algorithm that is not spatially balanced (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 statistics based on Voroni polygons. Many spatially balanced sampling algorithms exist, including the Generalized Random Tessellation Stratified (Stevens Jr and Olsen, 2004), 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) algorithms. Here we focus on the Generalized Random Tessellation Stratified (GRTS) algorithm, which has several attractive properties that we discuss next.

The GRTS algorithm is used to sample from finite and infinite sample frames. A finite sample frames contains a finite number of sampling units and is related

to a point geometry. An infinite sample frame contains an infinite number of sampling units and is related to linear and polygon geometries. Examples of point, linear, and polygon resources include lake centroids, stream networks, and wetland areas, respectively. In addition to its applicability for finite and infinite sample frames, the GRTS algorithm naturally accommodates stratified designs and designs with unequal selection probabilities. The algorithm has also been used to select replacement sites using reverse hierarchical ordering (Stevens Jr and Olsen, 2004). Replacement sites are used to replace sites in the original sample that cannot be sampled, often as a result of physical difficulty in reaching the site or landowner denial of access to the sites. More recently, the GRTS algorithm also accommodates legacy (historical) sites, minimum distance between sites, and nearest neighbor replacement sites. The GRTS algorithm is implemented in the **R** package `spsurvey` (Dumelle et al., 2021).

The GRTS algorithm works by mapping two-dimensional space into one-dimensional space while incorporating some elements of randomness. First a square bounding box is placed over the sample frame and divided into four equally sized squares randomly given an level-one address of 0, 1, 2, or 3. Then the inclusion probabilities of the sampling units in each square are summed. If this sum is at least one in any of the cells, a set of four sub-squares are placed within each square. Each set of four sub-squares are randomly given a second address (a level-two address) of 0, 1, 2, 3. Then the inclusion probabilities in each sub-square are summed, and if any of these sums are at least one, a third level of squares are added in the same manner. This hierarchical addressing continues until the inclusion probabilities in the smallest squares are all less than 1. The squares are then mapped to the one-dimensional line in order of their addresses. The length of this line equals n, the desired sample size (the sum of the inclusion probabilities). A uniform random variable, denoted by u_1 is simulated in $[0, 1]$ and placed on this line. The location of u_1 on the line can be linked to a sampling unit, denoted by s_1. Then $u_2 \equiv u_1 + 1$, which can be linked to another sampling unit, denoted by s_2. Because the GRTS algorithm requires the inclusion probabilities of the smallest sub-cells to be less than one, s_1 and s_2 must be distinct. This process continues until the n sampling units have been selected as part of the sample. Further details are provided by (Stevens Jr and Olsen, 2004) and (Dumelle et al., 2021).

The Horvitz-Thompson estimator (Horvitz and Thompson, 1952) and its continuous analog (Cordy, 1993) yield unbiased estimates of population totals (and means). If τ is a population total, then the Horvitz-Thompson estimator of τ, denoted by $\hat{\tau}_{HT}$, is given by

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

where Y_i is the observed value of the ith sampling unit, and π_i is the inclusion probability of the ith sampling unit. Estimating the variance of $\hat{\tau}_{HT}$ directly relies on knowing the probability that s_i and s_j are both included in the sample (second-order inclusion probability), which can be unfeasible to compute. Fur-

thermore, this variance estimator does incorporate spatial locations. To address these challenges, (Stevens Jr and Olsen, 2003) proposed an alternative variance estimator: the local neighborhood variance estimator. The local neighborhood variance estimator does not require second-order inclusion probabilities. It also incorporates spatial locations, which tends to reduce the estimated variance of compared $\hat{\tau}_{HT}$ to a variance estimator ignoring spatial location (Stevens Jr and Olsen, 2003).

2.5. Finite Population Block Kriging

Finite Population Block Kriging (FPBK) is an alternative to samipling-based methods (Ver Hoef, 2008). FPBK expands the geostatistical kriging framework to the finite population setting. Instead of basing inference off of a specific sampling design, we assume the data were generated by a spatial process with parameters that can be estimated using the framework of a model.

Ver Hoef (2008) gives details on the theory of FPBK, but some of the basic principles are summarized below. For a response variable $\mathbf{z}$ that can be measured on a finite number of N sites, we want to predict some linear function of the response variable, $\tau(\mathbf{z}) = \mathbf{b}'\mathbf{z}$, where $\mathbf{b}$ is a vector of weights. For example, if we want to predict the total abundance across all sites, then we would use a vector of 1's for the weights.

Typically, however, we only have a sample of the N sites. Denoting quantities that are part of the sampled sites with a subscript s and quantities that are part of the unsampled sites 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 sites, respectively, and $\boldsymbol{\delta}_s$ and $\boldsymbol{\delta}_u$ are random errors for the sampled and unsampled sites. Denoting $\boldsymbol{\delta} \equiv [\boldsymbol{\delta}_s \ \boldsymbol{\delta}_u]'$, we assume that $E(\boldsymbol{\delta}) = \mathbf{0}$.

We also typically assume that there is spatial correlation in $\boldsymbol{\delta}$, which can be modeled using a covariance function. Many common choices for this function assume that spatial covariance decreases with increasing Euclidean distance between sites. The primary function used throughout the simulations and applications of this manuscript is the Exponential covariance function: the i, j^{th} entry for var$(\boldsymbol{\delta})$ is

$$\text{cov}(\delta_i, \delta_j) = \theta_3 + \theta_1 \exp(-h_{i,j}/\theta_2), \tag{3}$$

$$\sigma^2[(1-v)\exp(-3\mathbf{h}_{i,j}/\phi) + v\mathbb{1}\{\mathbf{h}_{i,j} = 0\}], \tag{4}$$

where $h_{i,j}$ is the distance between sites 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. However, any spatial covariance function could be used in the place of the Exponential, including functions that allow for anisotropy [pg. 80 - 93](Chiles and Delfiner, 1999).

With the above model formulation, the Best Linear Unbiased Predictor (BLUP) for $\tau(\mathbf{b}'\mathbf{z})$ Did you mean to give the form of the BLUP here? $\tau(\mathbf{b}'\mathbf{z})$

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is vague 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. Neither require a particular distribution for **z**.

3. Numerical Study

3.1. Software

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).

4. Discussion

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