

# DRAFT

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Don L. Stevens, Jr.  
Department of Statistics  
Oregon State University  
Corvallis, Oregon 97331-4501

Anthony R. Olsen  
U, S, Environmental Protection Agency  
NHEERL Western Ecology Division  
200 S.W. 35<sup>th</sup> Street  
Corvallis, Oregon 97333

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# Spatially-Balanced Sampling of Natural Resources in the Presence of Frame Imperfections

Don L. Stevens, Jr,<sup>1</sup> and Anthony R. Olsen<sup>2</sup>

<sup>1</sup>Department of Statistics, Oregon State University, Corvallis, OR

<sup>2</sup>US EPA Western Ecology Division, Corvallis, OR

## **Abstract**

The spatial distribution of a natural resource is an important consideration in designing an efficient survey or monitoring program for the resource. Generally, sample sites that are spatially-balanced, that is, more or less evenly dispersed over the extent of the resource, will be more efficient than simple random sampling. We review a unified strategy for selecting spatially-balanced probability samples of natural resources. The technique is based on creating a function that maps 2-dimensional space into 1-dimensional space, thereby defining an ordered spatial address. We use a restricted randomization to randomly order the addresses, so that systematic sampling along the randomly-ordered linear structure results in a spatially well-balanced random sample. Variable inclusion probability, proportional to an arbitrary positive ancillary variable, is easily accommodated. The basic technique selects points in a 2-dimensional continuum, but is also applicable to sampling finite populations or 1-dimensional continua embedded in 2-space. An extension of the basic technique gives a way to order the sample points so that any set of consecutively-numbered points is in itself a spatially-well-balanced sample. This latter property is extremely useful in adjusting the sample for the frame imperfections common in environmental sampling.

## **1. Introduction**

Environmental studies invariably involve populations distributed over space. Traditionally, such studies tended to focus on relatively small and well-delimited systems. However, some of the environmental issues that we face today, such as global warming, long-range transport of atmospheric pollutants, or habitat alteration, are not localized. Understanding and quantifying the extent of symptoms of wide-spread concerns requires large-scale study efforts, which in turn needs environmental sampling techniques and methodology that are formulated to address regional, continental, and global environmental issues. Stehman and Overton (1994) give an overview of some statistical issues associated with environmental sampling and monitoring, and Gilbert (1987) has an extensive discussion of sampling methods for monitoring environmental pollution.

A resource property relevant to sampling design is the dimension of conceptual spatial representation of the resource. Resource populations may be represented as collections of points, lines, areas or volumes; that is, as 0-, 1-, 2- or 3-dimensional objects. For example, small to medium-sized lakes can be viewed as distinct, natural units. Treating the lakes as points in a 2-dimensional domain is appropriate for sampling purposes, where the point associated with a lake is some uniquely defined location in the lake, e.g., the lake centroid. Resources such as streams or riparian wetlands may be given a 1-dimensional representation in 2-dimensional space, and sampled as linear resources. Such resources are in fact 2-dimensional, but are much longer than they are wide, and do not have well-defined natural units. Resources that extend over large regions in a more or less continuous and connected fashion may be treated as 2-dimensional objects. As for a linear resource, an extensive resource does not have distinct natural units. For example, the Southern

California Bight, Puget Sound, and large wetlands such as salt marshes or the Everglades fall into this category. In some instances, we may also need to consider the depth dimension of an extensive resource. For example, if we wished to estimate the total contaminant loading of Lake Ontario, we would need to view and sample the lake as a 3-dimensional object.

One of the more prominent features of many environmental populations is the arrangement of the population units throughout space. Nearby units interact with one another, and tend to be influenced by the same set of natural and anthropogenic factors. For example, neighboring trees in a forest interact by competing for energy and nutrients, and are influenced by the same set of physical and meteorological conditions, the same level of air- or water-borne pollutants, and the same set of landscape disturbances. Sampling designs that capitalize on this spatial aspect of environmental populations tend to be more efficient than simple random sampling. A related advantageous property is having the sample points well-dispersed over the extent of the resource domain. The advantages of this property could be established from a super-population perspective by introducing spatial correlation. Such studies have concluded that regularly-spaced design points are optimal for a variety of reasonable spatial correlation functions, (See, for example, Munholland and Borkowski (1996), Breidt (1995), Iachan (1985), Olea (1984), Bellhouse (1977), Dalenius *et al*, (1961), Matérn (1960), Das (1950), Quenouille (1949), Cochran (1946)), A drawback, of course, is that a design-based variance estimator is not available for a strict systematic sample point arrangement.

Over repeated sampling, a simple random sample (SRS) from a list frame is guaranteed to preserve and reflect all attributes of the population. The repeated sampling will faithfully reveal varying spatial density, clusters of elements, or voids. However, any single realization of an SRS may result in substantial distortion of spatial pattern. Our efforts are directed towards structuring the sample so as to ensure that a single realization will have sample spatial pattern that has strong resemblance to the population pattern, i.e., so that clusters and voids are picked up and reflected in the sample, to the resolution of the sample. Of course, the resolution depends on both the sample size and the extent of the population domain. A sample of size 100 from a population spread over 1000 km<sup>2</sup> (a sample density of 1 point/100 km<sup>2</sup>) has no chance of discerning 1 km<sup>2</sup>-size patches. The property that we would like to have is that the achieved sample size in any arbitrary subregion of the population domain has much smaller variance than under an SRS sample with the same first-order inclusion probability (and thus the same expected sample size).

The consideration of sample density versus population density is complicated by another consideration that invariably arises in designing a sample: some population elements are perceived to be more important than others. For example, in sampling lakes, one might wish to select large lakes with a greater probability than small lakes because large lakes are less numerous than small, or because they contribute disproportionately to total surface area, total water volume, or total recreational usage. For a second example, one might wish to increase the sampling rate for lakes in an arid region of the population domain to get enough samples to reliably describe lake characteristics for the region. These two examples illustrate two very different scenarios for which variable probability sampling might be required. In the first, the probability varies element-wise, and depends on an attribute (in this case, size) of the element. In the second case, the probability varies on a geographical region basis, but is the same for every element within the region.

Moreover, the two scenarios can occur in combination, so that we have a need to conform to both element-wise and region-wise variation in inclusion probability.

There are several paradigms for incorporating the spatial aspect of an environmental population into a sample. Area sampling partitions the domain of the population into polygons, which can either be treated as strata, or as population units themselves. Systematic sampling using a regular grid is often applied, as are several variants that perturb the strict alignment (Olea, 1984). Along the same lines, Munholland and Borkowski (1996) have used a Latin square with a single additional independent sample to achieve a spatially balanced sample. Breidt (1995) used a Markov process to generate a one-unit-per-stratum spatially distributed sample. Both of these techniques select cells in a regular grid, although they can be adapted to other populations. A third approach is to use space to order a list frame of the population, then use the order of the list to structure the sample, say by defining strata as successive segments of the ordered list, or by systematic random sampling. For example, Saalfeld (1991) drew on graph theory to define a tree that leads to a spatially articulated list frame, and the National Agricultural Statistics Service has used serpentine strips (Cotter and Nealon, 1987) to order their primary sample units within a state. A related idea that originated in geography is the General Balanced Ternary (GBT) spatial addressing scheme (Gibson and Lucas, 1982). The concept behind a GBT address is related to the concept of space-filling curves, such as first constructed by Peano (1890), or the Hilbert curve (Simmons, 1963). Stevens and Olsen (1999) used a similar concept, recursive partitioning, together with hierarchical randomization, to distribute sample points through space and time. Wolter and Harter (1990) have used a construction similar to Peano's to construct a "Peano key" to maintain the spatial dispersion of a sample as the underlying population experiences births or deaths. Saalfeld (1992) has also used the Peano key to maintain spatial dispersion of a sample.

In the design discussed here, several of these concepts are synthesized to create a very powerful and flexible technique for selecting a spatially-well-distributed probability sample. The technique is based on creating a function that maps 2-dimensional space into 1-dimensional space, thereby defining an ordered spatial address. We use a restricted randomization called hierarchical randomization (HR) to randomly order the address, and then apply a transformation that induces an equi-probable linear structure. Systematic sampling along the randomly ordered linear structure is analogous to sampling a random tessellation of 2-dimensional space, and results in a spatially well-balanced random sample. We call the resulting design a Generalized Random Tessellation Stratified (GRTS) design. Some of the properties of the design are discussed in Stevens and Olsen (2000).

A practical complication encountered in applying a spatially-balanced environmental sample is the difficulty in obtaining an accurate frame. In many instances, critical properties of the environmental resource are not known prior to field visit. For example, a frame for sampling streams might be blue line traces on USGS quadsheets. Unfortunately, many of the traces turn out to represent ephemeral or intermittent streams, rather than perennial streams, especially in the more arid sections of the Western U.S. An even more serious problem is that much of the resource we might like to sample is privately owned. Access permission from the owner is required before a sample can be collected. It is impractical to obtain access for the entire

frame, so we only seek access to the selected sample points. Our experience has been that we can lose 50% or more of our target sample points because of lack of access. In either case, we would like to have a procedure that allows us to add points to the sample as we discover non-target or inaccessible points, at the same time maintaining a spatially-well-balanced sample. In this paper, we show how to order the points resulting from an  $M$ -point GRTS sample so that the first  $m$  points, for  $m \leq M$ , are a spatially-well-balanced sample.

## 2. Generalized Random Tessellation Stratified Design

Three generic situations arise when sampling environmental resources that occur in a spatially defined region. First is the situation of a continuous population existing within a bounded area. Examples are the pH of soil, biomass density, and concentration of total phosphorus near the surface of a lake. Second is a continuous population that exists only on a linear network within a bounded area. Attributes that can be defined at all points of a stream or river network, such as water chemistry, are examples. Third is a discrete (finite) population that occupies fixed locations within a bounded area. Examples are basal area of trees and eutrophication status of a collection of lakes. In all three situations, the elements of the populations can be labeled by their spatial location.

We can cover all three cases with the same development if we work in the context of general measure and integration theory. Let  $R$  be the domain of the population we wish to sample, that is, the set of points occupied by elements of the population. We require that  $R$  be a bounded subset of  $\mathbb{R}^2$ . Thus,  $R$  can be enclosed in a bounded square, so that by scaling and translation, we can define a 1-1 map from  $R$  into  $(0, \frac{1}{2}] \times (0, \frac{1}{2}]$ , the lower left quadrant of the unit square. Clearly, every point in the image is associated with a unique point in  $R$  and vice versa, so henceforth, we will identify  $R$  with its image in the unit square.

A measure space is a triplet  $(X, \mathcal{B}, \mu)$ , where  $X$  is a set called the universe,  $\mathcal{B}$  is a  $\sigma$ -field of subsets of  $X$  called the measurable sets, and  $\mu$  is a measure. We take our 2-dimensional universe as the unit square  $I^2 = (0, 1] \times (0, 1] \subset \mathbb{R}^2$  and consider functions  $f(\bullet)$  that map  $I^2$  into the unit interval  $I = (0, 1]$ . The underlying  $\sigma$ -fields are  $\mathcal{B}(I)$  and  $\mathcal{B}(I^2)$ , the  $\sigma$ -fields of the Borel subsets of  $I$  and  $I^2$ , respectively.

Stevens (1997) derived inclusion and joint inclusion functions for several grid-based designs that were precursors to GRTS designs, and share some of their properties. The designs are all generalizations of the Random Tessellation Stratified (RTS) design (Overton and Stehman (1993), Olea (1984), Dalenius *et al.* (1961)). The RTS design selects random points in space via a 2-step process. First, a regular tessellation coherent with a regular grid is randomly located over the domain to be sampled, and second, a random point is selected within each random tessellation cell. Let  $C$  be a polygon congruent to the tessellation cells, let  $C(0)$  be the cell enclosing the (non-random) origin, and  $C(s)$  be  $C(0)$  translated to the point  $s$ . Formally,  $C(s) = \{t / t - s \in C(0)\}$ . Following Stevens (1997), the inclusion functions for the RTS design are

$$\mathbf{p}(s) = \frac{I}{|C(s)|} = \frac{I}{|C|}$$

and

$$\mathbf{p}(s, t) = \mathbf{p}(s)\mathbf{p}(t) \left\{ 1 - \frac{|C(s) \cap C(t)|}{|C|} \right\},$$

where  $|C|$  denotes the area of  $C$ .

The RTS design is a variation on a systematic design that avoids the alignment problems that can occur with a completely regular systematic design. Like a systematic design, an RTS design does not allow variable probability spatial sampling. Stevens (1997) introduced the Multiple-Density, Nested, Random-Tessellation Stratified (MD-NRTS) design to provide for variable spatial sampling intensity. The geometric concept underlying the MD-NRTS was the notion of coherent intensification of a grid: adding points to a regular grid in such a way as to result in a denser regular grid with similarly-shaped but smaller tessellation cells.

We have since extended the same notion by generalizing to a process that creates a potentially infinite series of nested, coherent grids. In the limit, the process results in a function that maps 2-dimensional space into 1-dimensional space. We show how to use this to generate a sample of a spatial population so that (1) the sample has a specified first order inclusion function; and (2) subject to (1), the sample is evenly spread over the extent of the population. We will show that the technique can be applied to point-like, line-like, and area-like populations, that is, to discrete, linear, and extensive populations.

## 2.1. Random quadrant-recursive maps from $\mathbb{I}^2$ to $\mathbb{I}$

To be useful in achieving a spatially-balanced sample, the function  $f$  that maps  $\mathbb{I}^2 \rightarrow \mathbb{I}$  must preserve some proximity relationships, and so we need to impose some restrictions on the class of functions to be considered. Mark (1990), in studying discrete 2- to 1-dimensional maps, defined a property called quadrant-recursive, which required that sub-quadrants be mapped onto sets of adjacent points. To define

the continuous analogue, let  $Q_{jk}^n = \left[ \frac{j}{2^n}, \frac{j+1}{2^n} \right] \times \left[ \frac{k}{2^n}, \frac{k+1}{2^n} \right]$ ,  $j, k = 0, 1, \dots, 2^n - 1$ , and let

$J_m^n = \left[ \frac{m}{4^n}, \frac{m+1}{4^n} \right]$ . A function  $f: \mathbb{I}^2 \rightarrow \mathbb{I}$  is *quadrant-recursive* if for all  $n \geq 0$ , there is some  $m = 0, 1, \dots,$

$4^n - 1$  such that  $f(Q_{jk}^n) = J_m^n$ . Because  $\mathbb{B}(\mathbb{I})$  can be generated by sets of the form  $J_m^n$  and  $\mathbb{B}(\mathbb{I}^2)$  can be generated by sets of the form  $Q_{jk}^n$ , both  $f$  and  $f^{-1}$  are measurable.

We can view a quadrant-recursive function as being defined by the limit of successive intensifications of a grid covering the unit square, where a grid cell is divided into 4 sub-cells, each of which is subsequently divided into 4 sub-sub-cells, and so on. If we were to carry this recursion to the limit, and pair grid points with an address based on the order in which the divisions were carried out, with each digit of the address representing a step in the subdivision, then we obtain a quadrant-recursive function. For example, suppose

we begin with a point at (1, 1), and replace it with 4 points  $p_3 = (1, 1), p_2 = (1/2, 1), p_1 = (1, 1/2)$ , and  $p_0 = (1/2, 1/2)$ . The next step of the recursion replaces each of the first four points  $p_0, \dots, p_3$  with  $p_i - \{(0,0), (0,1), (1,0), (1,1)\}/2^2$ . Thus the point  $p_1 = (1, 1/2)$  is replaced with the 4 points  $p_{13} = (1, 1/2), p_{12} = (1, 1/4), p_{11} = (3/4, 1/2)$ , and  $p_{10} = (3/4, 1/4)$ . The  $n^{th}$  step replaces each of the  $4^n$  points  $p_{i_1 i_2 \dots i_n}$  with  $p_{i_1 i_2 \dots i_n} - \{(0,0), (0,1), (1,0), (1,1)\}/2^{n+1}$ .

A spatially-referenced address can be constructed following the pattern of the partitioning, with each new partition adding a digit position to the address. Thus, in the above example, the first group of four points are assigned the addresses “3”, “2”, “1”, and “0”, with “3” being the original point at (1,1). The successor points to point, “2” get the addresses “23”, “22”, “21”, and “20”, and so forth. The addresses induce a linear ordering of the sub-quadrants. Moreover, if we carry the process to the limit, and treat the resulting address as digits in a base-4 fraction, e.g., “22103...” as the base 4 number  $(0.22103\dots)_4$ , then the correspondence between grid point and address is a quadrant-recursive function.

Recursive partitioning generates a nested hierarchy of grid cells. The derived addressing has the property that all successor cells of a cell have consecutive addresses. Thus, a path from cell to cell, following the recursive partitioning address order, will connect all successor cells of cell “0” before reaching any successor of cell “2”.

A 1-1 continuous mapping of  $\mathbb{I}^2$  onto  $\mathbb{I}$  is not possible, so that quadrant-recursive functions are not continuous. However, they do have the property that all points in a quadrant are mapped onto an interval; all points in any one of the four subquadrants of a quadrant are mapped onto an interval; and so on *ad infinitum*. This property tends to preserve proximity relationships, i.e., if  $s$  is “close to”  $t$ , then  $f(s)$  should “tend to be close to”  $f(t)$ . In the Appendix, we give precision to this statement by showing that if the origin is located at random, and  $s$  is chosen at random from  $\mathbb{I}^2$ , then  $\lim_{|d| \rightarrow 0} E [ |f(s) - f(s + d)| ] = 0$ . Intuitively, two elements that are close together will tend to fall in the same randomly located cell of a size that decreases as the distance between the points decreases. Because the two elements are covered by the same cell, their addresses match to the level of that cell, and thus, in expectation, their address will be close.

A fundamental 1-1 quadrant-recursive map is defined by digit-interweaving. Let  $s = (x, y)$  be a point in  $\mathbb{I}^2$ . Each of the coordinates has an expansion as a binary fraction of the form  $x = 0.x_1x_2x_3\dots, y = 0.y_1y_2y_3\dots$ , where each  $x_i$  and  $y_i$  is either 0 or 1. Define  $f_0(s)$  by alternating successive digits of  $x$  and  $y$ , that is,  $f_0(s) = 0.x_1y_1x_2y_2\dots$ . Clearly,  $f_0$  would be 1-1 except for different expansions of the same number. For example, 0.1 and 0.011111..., where the 1’s continue indefinitely, are two representations of the number 1/2. If we always use the binary representation with an infinite number of 1’s, then  $f_0$  is 1-1. Moreover, every point in  $\mathbb{I}$  is the image of a point in  $\mathbb{I}^2$ , which is obtained by “digit-splitting”. That is, if  $t = 0.t_1t_2t_3\dots$  is in  $\mathbb{I}$ , then  $s = f_0^{-1}(t) = (0.t_1t_3t_5\dots, 0.t_2t_4t_6\dots)$  is the pre-image of  $t$ . Both  $f_0$  and  $f_0^{-1}$  are 1-1 if we always use the representation with an infinite number of 1’s (Hausdorff, 1957, p.45). To show that  $f_0$  is quadrant-

recursive, note that for  $s \in Q_{jk}^n$ , the first  $4^n$  digits of  $f_0(s)$  are fixed, so that  $f_0(s) \in J_m^n$ , where  $m$  is defined by the first  $4^n$  digits. Conversely, the pre-images of every  $t \in J_m^n$  have the same first  $2^n$  digits, and so must be in the same  $Q_{jk}^n$ .

Figure 1 shows the first 4 levels of the recursive-partitioning of the unit square. The address of the cross-hatched subquadrant is, as a base 4 fraction,  $(0.213)_4$ , The associated grid point is at  $(3/4, 1/2)$ , the upper right corner of the subquadrant. Following the convention of having an infinite number of 1's in the expansion, we have  $(3/4, 1/2) = (0.11, 0.1)_2 = (0.1011111\dots, 0.0111111\dots)_2$ . Digit-interweaving gives the image  $(0.1001111\dots)_2 = (0.2133333\dots)_4$ , of which the first 3 digits are the subquadrant address. If we were to carry the recursive-partitioning to the limit, every point in the subquadrant would be assigned an address beginning with  $(0.213)_4$ .

The class of all quadrant-recursive functions can be generated from the function  $f_0$  defined by digit-interweaving by permuting the order in which subquadrants  $Q_{jk}^n$  are paired with the intervals  $J_m^n$ . For example, for  $n = 1$ ,  $f_0(Q_{jk}^1) = J_{2j+k}^1$ . We obtain a different quadrant-recursive function by permuting the subscripts  $\{0, 1, 2, 3\}$  of the image intervals. Thus, under the permutation  $t = \{2, 1, 3, 0\}$ , we get a function such that  $f_t(Q_{jk}^1) = J_{t(2j+k)}^1$ , so that  $f_t(Q_{00}^1) = J_2^1$ ,  $f_t(Q_{01}^1) = J_1^1$ ,  $f_t(Q_{10}^1) = J_3^1$ , and  $f_t(Q_{11}^1) = J_0^1$ . To see that the class of all quadrant-recursive functions is generated by such permutations, express each number in  $I$  as a base 4 number, that is, as  $t = .t_1t_2t_3\dots$ , where each digit  $t_i$  is either a 0, 1, 2, or 3. A function  $h_p: I \rightarrow I$  is a *hierarchical permutation* if  $h_p(t) = 0.p_1(t_1)p_{t_12}(t_2)p_{t_1t_23}(t_3)\dots$ , where  $p_{t_1t_2\dots t_{n-1}n}(\cdot)$  is a permutation of  $\{0, 1, 2, 3\}$  for each unique combination of digits  $t_1, t_2, \dots, t_{n-1}$ . Again, we ensure that  $h_p$  is 1-1 by always using the expansion with an infinite number of non-zero digits. Any quadrant-recursive function can be expressed as the composition of  $f_0$  with some hierarchical permutation  $h_p$ , since the associations  $f(Q_{jk}^n) = J_m^n$  determine the series of permutations, and the permutations define the associations.

If the permutations that define  $h_p(\cdot)$  are chosen at random and independently from the set of all possible permutations, we call  $h_p(\cdot)$  a *hierarchical randomization function*, and the process of applying  $h_p(\cdot)$  *hierarchical randomization*.

## 2.2. Sample selection with probability proportional to arbitrary intensity function

The design specifications must include definition of a desired sample intensity function  $p(s)$ . We refer to  $p(s)$  as an intensity function, since we have not yet introduced a probability measure. We will develop a sample selection method that yields an inclusion probability function equal to  $p(s)$ . For a discrete population,  $p(s)$  has the usual finite-population-sampling interpretation as the target inclusion probability of the population unit located at  $s$ . Of course, we set  $p(s) = 0$  if there is no population element at  $s$ , and require  $0 < p(s) \leq 1$  otherwise. For linear and extensive populations,  $p(s)$  is the target inclusion probability density function. We assume that any linear population consists of a finite number  $m$  of smooth, rectifiable curves:

$$L = \bigcup_{i=1}^m \{ \mathbf{g}_i(t) = (x_i(t), y_i(t)) \mid t \in [a_i, b_i] \}, \text{ with } x_i \text{ and } y_i \text{ continuous and differentiable on } [a_i, b_i]. \text{ We set}$$

$p(s)$  equal to the target number of samples per unit length at  $s$ , for  $s \in L$  and equal to zero elsewhere. For example, if the linear population were a stream network,  $p(s)$  would specify the desired number of samples per km of stream at the point  $s$ . Finally, for an extensive population,  $p(s)$  specifies the target intensity as number of samples per unit area. Note that for 1- and 2-dimensional resources,  $p(s)$  could be a continuous, smoothly-varying function. Formally, we require  $p(s)$  to be bounded and measurable, and strictly positive on  $R$ .

We randomly translate the image of  $R$  in the unit square by adding independent,  $U(0, 1/2)$  offsets to the  $xy$  coordinates. This random translation plays the same role as random grid location does in an RTS design; namely, it guarantees that pairwise inclusion probabilities are non-zero. In particular, in this case it ensures that any pair of points in  $R$  has a non-zero chance of being mapped into different quadrants.

For each of the three types of populations, we define a measure  $f$  of population size. We use the same symbol for all three cases, but the specifics vary from case-to-case. For a finite population, we take  $f$  to be counting measure restricted to  $R$ , so that for any subset  $B \subseteq \mathbb{B}(1^2)$ ,  $f(B)$  is the number of population elements in  $B \cap R$ . For linear populations, we take  $f(B)$  to be the length of the linear population contained within  $B$ . Clearly,  $f$  is non-negative, countably additive, defined for all Borel sets, and  $f(\emptyset) = 0$ , so  $f$  is a measure. Finally, for extensive populations, we take  $f(B)$  to be the Lebesgue measure of  $B \cap R$ . From these definitions of  $p(\bullet)$  and  $f(\bullet)$ , it follows that  $w(B) = \int_B p(s) d\mathbf{f}(s)$  is a measure and that  $w(B)$  is the target number of samples in  $B$ . In particular,  $M = w(1^2)$  is the target sample size, In the following, we assume that  $M$  is an integer. The non-integer case is a simple extension.

Since  $f$  is measurable,  $f^{-1}(B)$  is measurable for  $B \subseteq \mathbb{B}(1^2)$ , so that  $\tilde{F}(x) = \int_{f^{-1}((0,x])} p(s) d\mathbf{f}(s)$  exists. In fact,

$\tilde{F}$  is a distribution function, that is, increasing and right-continuous. For linear and extensive resources,  $\tilde{F}$  is a continuous, strictly-increasing function, but for finite resource populations,  $\tilde{F}$  is a step function with jumps at the images of population elements. We can modify  $\tilde{F}$  to obtain continuity in the finite case via linear interpolation, i.e., let  $x_i, i = 1, \dots, N$  be the ordered jump-points of  $\tilde{F}$ , set  $x_0 = 0, x_{N+1} = 1$ , and, for

$x_i < x \leq x_{i+1}$ , set  $F(x) = \tilde{F}(x) + \frac{\tilde{F}(x_{i+1}) - \tilde{F}(x_i)}{x_{i+1} - x_i}(x - x_i)$ . If we set  $F = \tilde{F}$  for the linear and extensive case, then in every case we have that  $F$  is a continuous distribution function with range  $(0, M]$ .

In the finite case,  $F^{-1}$  is single-valued, so that  $G(x) = \min(x_i / F^{-1}(x) \leq x_i)$  is well-defined. In the linear and extensive cases,  $F^{-1}$  may not be single-valued, but  $F^{-1}(x)$  will always be closed and bounded, so that the  $G(x) = \min\{y / y \in F^{-1}(x)\}$  is well-defined. In all cases, the intensity function  $p$  is positive at  $s = f^{-1}(G(x))$ , that is, there is a population element at  $s$ . Thus,  $f^{-1} \circ G$  maps  $(0, M]$  onto the target population, that is,  $f^{-1} \circ G$  associates every point in  $(0, M]$  with a unique element in the population.

It follows that selecting a sample from  $(0, M]$  also selects population elements via the mapping  $f^{-1} \circ G$ . To get a sample with an inclusion function equal to the target inclusion density, we select a sample from  $(0, M]$  by splitting the range into  $M$  unit-length intervals  $(0, 1], (1, 2], \dots, (M-1, M]$ , and picking one point in each interval, uniformly distributed over the interval. The selection need not be independent, e.g., we may use systematic sampling with a random start and a unit-length selection interval. Because of the hierarchical randomization, we gain no additional “randomness” by picking the points independently. The selection procedure defines an inclusion probability density function on  $(0, M]$  with a corresponding measure  $P_M(\bullet)$ . Note that  $P_M$  coincides with Lebesgue measure on  $(0, M]$ ; in particular, the measure of a sub-interval of  $(0, M]$  is its length.

We induce a measure  $P_1$  on  $I$  via  $P_1(B) = \int_{G^{-1}(B)} dP_M$ , and then in turn a measure  $P_2$  on  $I^2$  via  $P_2(B) = \int_{f^{-1}(B)} dP_1$ .  $P_2$  is an inclusion probability measure on  $I^2$ , and  $P_2(B) = w(B)$ , so that the sample selection method does give an inclusion probability function equal to the target sample intensity function.

The technique of mapping 2-space to a line segment, systematic sampling from the range of the distribution function, and then mapping back to the population elements will always produce a sample with the desired first-order inclusion probability function so long as  $f$  is 1-1 and measurable. The second (and higher) order properties are determined by  $f$  and the specifics of sampling on  $(0, M]$ . We required that  $f$  be quadrant-recursive, and claimed that that was sufficient to give a spatially-balanced sample. This follows from the fact that the map  $f^{-1} \circ (\frac{F}{M}) \circ f$  transforms the unequal intensity surface defined by  $p$  into an equi-probable surface. The quadrant-recursive property of  $f$  guarantees that the sample will be evenly spread over the equi-probable surface, in the sense that each sub-quadrant will receive its expected number of samples, to the resolution determined by the sample size  $M$ .

## 2.4. Reverse hierarchical ordering

The sample points selected by mapping the systematic points along  $(0, M]$  back to the population domain will be ordered in a way that follows the quadrant-recursiveness of  $f$ , tempered by allowance for unequal probability selection. Thus, the first quarter of the points will all come from the same “quadrant” of the equiprobable domain, and will all be approximately neighbors in the original population domain. It follows that four points, one picked from each quarter of the sample points ordered by the systematic selection, will be a spatially balanced sample. Because the random permutations defining the hierarchical randomization are selected independently of one another, it makes no difference, from a distributional standpoint, whether we pick the points systematically from each quarter, or make random selections from each quarter. Therefore, we lose no generality by picking the points that occupy positions corresponding to being at the beginning, one quarter, one half, and three quarters of the way through the ordered list of sample points.

Within each quarter of the list, the points are again quadrant-recursively ordered, so points picked at the beginning, one quarter, one half, and three quarters of the way through each quarter of the list will be spread out over the corresponding quadrant, and so on down through the sequence of subquadrants. We can utilize these properties by re-ordering the systematically selected list so that, at any point in the re-ordered list, the samples up to that point are well-spread out over the population domain.

The order is most conveniently expressed in terms of a base 4 fraction, with the fraction expressing the relative position in the systematically ordered list. Thus, the first four points correspond to the fractions  $(0.0, 0.1, 0.2, 0.3)_4 = (0, 1/4, 1/2, 3/4)_{10}$ . Stepping down a subquadrant level corresponds to adding a digit position to the base 4 fraction, which we fill in in such a way as to spread the sequence of points over the population domain. The pattern for the first 16 points is shown in Table 1. Note that the order corresponds to the ranking obtained by reversing the sequence of base 4 digits, and treating the reversed sequence as a base 4 fraction.

order	base 4	reverse base 4	order	base 4	reverse base 4	order	base 4	reverse base 4	order	base 4	reverse base 4
1	0.00	0.00	5	0.01	0.10	9	0.02	0.20	13	0.03	0.30
2	0.10	0.01	6	0.11	0.11	10	0.12	0.21	14	0.13	0.31
3	0.20	0.02	7	0.21	0.12	11	0.22	0.22	15	0.23	0.32
4	0.30	0.03	8	0.31	0.13	12	0.32	0.23	16	0.33	0.33

Table 1: Generation of reverse hierarchical order.

We can continue this same pattern of adding digit positions through as many positions as necessary to order the entire sample. We call the resulting order *reverse hierarchical order*. It remains to show that reverse

hierarchical order does indeed give a spatially-well-balanced sample for any  $m \in M$ . Clearly this is the case for  $m = 4^k$ , since in that case, the reduced sample can be viewed as a sample selected from a complete GRTS design. Stevens (1997) derived an analytic expression for the pairwise inclusion density for some special intermediate cases. Here, we investigate the spatial balance properties using simulation.

### 3. Spatial properties of GRTS sample points

We can view the sample as a stochastic point process, and use some of the descriptive tools for point processes to investigate the spatial balance, or regularity, of the point process. A variety of statistics have been proposed to assess the regularity of a point process. One class of descriptive statistics is based on counts of event points within cells of a regular grid covering the process domain. The mean count is a measure of the process intensity, and the variance of the counts is a measure of the regularity. Unfortunately, the choice of grid size effects the interpretation of the results. Another class is based on distances between points, e.g., distance to nearest neighbor. Ripley (1976, 1977) used the  $K$  function, first introduced by Bartlett (1964), to summarize the spatial dependence of a point process over a range of scales. The  $K$  function is defined as

$$K(h) = \frac{E \{ \text{number of extra events within a distance } h \text{ of a randomly selected event} \}}{E \{ \text{number of events per unit area} \}}.$$

A common way of characterizing a 1-dimensional point process is via the inter-event distance, e.g., the inter-event time for a time series. An analogous concept is that of Voronoi polygons, For a set of event points  $\{ s_1, s_2, \dots, s_k \}$  in a 2-dimensional domain, the Voronoi polygon for the  $i^{\text{th}}$  point is the collection of domain points that are closer to  $s_i$  than to any other  $s_j$  in the set. The mean area of the Voronoi polygons is the reciprocal of the mean intensity of the process, and the variance of the polygon area is a measure of the regularity of the process.

For the kinds of applications that we have in mind, the domain boundary is an intrinsic aspect of the population. Thus, the interplay of sampling design and boundary on properties of the sample cannot be ignored. Contrary to the usual practice in spatial point process theory, we do not assume that the sample points are a realization of a stationary process. (Obviously, for a non-constant sample intensity function, the point-generation process is not stationary). Furthermore, we make no attempt to remove the influence of the boundary on the various statistics used to describe regularity. For small to moderate sample sizes, and for highly irregular domains, the domain boundary can have substantial impact on the distribution of any statistic used to describe regularity.

The  $K$  function is a good tool for examining spatial dependence of a process over a range of spatial scales. However, it is not particularly suitable for comparing spatial properties of sampling designs with the same number of points. Because the number of points is constant (or nearly so) between the different design options, all of the processes generating the designs have the same intensity. We expect that any difference in spatial properties will show up in a fairly narrow range of scales around the common intensity. A statistic

that focuses on that range should provide more insight into the regularity of the generating process. Thus, we expect that the variance of the size of the Voronoi polygons to be more sensitive than the  $K$  function.

For our simulation study, we selected 1000 samples of size  $M = 256$  from the unit square using the GRTS design and ordered the samples using the reverse hierarchical order. For each  $m$ ,  $10 < m \leq M$ , we calculated the variance of the size of the Voronoi polygons around each point in the  $m$ -point sample. We did the same, except for the reverse hierarchical ordering, for an SRS design. We evaluate the spatial balance by the ratio of the GRTS variance to the SRS variance, so that a ratio less than 1 implies more regularity than SRS. In order to model imperfect frame information, we created domains with a number of randomly-located, square holes. The holes represent non-target or access-denied elements that were *a priori* unknown. Sample points falling in the holes were discarded, resulting in a variable number of sample points in the target domain. As for the complete domain, we order the points using reverse hierarchical ordering, and then calculated the regularity measure (the variance ratio) as the points were added one at a time.

We used three different distributions of hole size: constant, linearly increasing, and exponentially increasing. In each case, the holes comprised 20% of the domain area. Figure 2 shows the placement of the holes for each scenario, and Figure 3 shows the variance ratios for all four scenarios: no voids, exponentially increasing, linearly increasing, and constant size.

In every scenario, the variance ratio is much less than 1. Except for small sample sizes, the ratio stays in the range 0.2 to 0.4. The gradual decrease as the sample size increases is due to the decreasing impact of the boundary: as the sample size increases, the proportion of polygons that intersect the boundary decreases. A similar effect is seen with the different inaccessibility scenarios: even though the inaccessible area is constant, the scenarios with greater perimeter cause more increase in variance.

#### 4. Estimation

The GRTS design produces a sample with specified first order inclusion probabilities, so that the Horvitz-Thompson (Horvitz and Thompson, 1952) estimator or its continuous population analogue (Cordy, 1993 ; Stevens, 1997) can be applied to get estimates of population characteristics. Stevens(1997) provides exact expressions for second order inclusion functions for some special cases of a GRTS. These expressions can also be used to provide accurate approximations for the general case. Unfortunately, the variance estimator based on using these approximations in the usual Horvitz-Thompson or Yates-Grundy-Sen (Yates and Grundy, 1953; Sen, 1953) estimator tends to be unstable. The design achieves spatial balance by forcing the pairwise inclusion probability to approach 0 as the distance between the points in the pair goes to 0. Even though the pairwise inclusion density is non-zero almost everywhere, any moderate-sized sample will nevertheless have one or more pairs of points that are close together, with a correspondingly small pairwise inclusion probability. For both the HT and YG variance estimators, the pairwise inclusion probability appears as a divisor. The corresponding terms in either HT or YG variance estimators will tend to be large, leading to instability of the variance estimator. Stevens and Olsen (in review, 2002) have proposed a

variance estimator that draws on the spatial balance of the GRTS design. A variety of stimulation studies have shown the proposed estimator to be stable and nearly unbiased.

The reverse hierarchical ordering provides the ability to do inverse sampling, i.e., to sample until a given number of samples are obtained in the target population. The true inclusion probability in this case depends on the spatial configuration of the target population, which may be unknown. However, one can compute an inclusion probability that is conditional on the achieved sample size in the target population being fixed.

For example, suppose we want  $M$  sample points in our domain  $R$ . We do not know the exact boundaries of  $R$ , but are able to enclose  $R$  in a larger set  $R^*$ . We select a sample of size  $M^* > M$  from  $R^*$  using an inclusion density  $p^*$  scaled so that  $\int_{R^*} p^*(s) d\mathbf{f}(s) = M^*$ . The inclusion density for the  $k$ -point reverse

hierarchical ordered sample is  $p_k^*(s) = \left(\frac{k}{M^*}\right) p^*(s)$ . Using the inclusion density  $p_k^*$ , the expected number of samples in  $R$  is  $M_k = \int_R p_k^*(s) d\mathbf{f}(s) = \int_{R^*} I_R(s) p_k^*(s) d\mathbf{f}(s)$ . We cannot compute  $M_k$  because the

boundary of  $R$  is unknown, but an estimate is  $\hat{M}_k = \sum_i \frac{I_R(s_i) p_k^*(s_i)}{p_k^*(s_i)} = \sum_i I_R(s_i)$ . We pick  $\tilde{k}$  so that  $\hat{M}_{\tilde{k}} = M$  and base inference on  $p_{\tilde{k}}^*$ . Thus, for example, an estimate of the unknown extent of  $R$  is

$$|\hat{R}| = \sum_i \frac{I_R(s_i)}{p_{\tilde{k}}^*(s_i)},$$

We illustrate this using the same inaccessibility scenarios as for the spatial balance simulation. Results are summarized in Table 2. In each case, the true area of  $R$  is 0.8, so that the estimator using  $p_{\tilde{k}}^*$  is either unbiased or nearly so.

Target Sample Size	Mean Estimated Domain Area		
	Exponential	Constant	Linear
25	0.8000979	0.7969819	0.8010589
50	0.7995775	0.7979406	0.8005739
100	0.7994983	0.7980543	0.8002237
150	0.7994777	0.7997587	0.7995685

Table 2. Domain area estimates using  $p_{\tilde{k}}^*$ .

## 5. Discussion

There are a number of designs that provide good dispersion of sample points over a spatial domain. When we applied these designs to large-scale environmental sampling programs, it very quickly became apparent that we needed a means of (1) accommodating variable inclusion probability, and (2) dynamically adjusting sample sizes. These requirements are rooted in the very fundamentals of environmental management. The first requirement stems from the fact that an environmental resource is rarely uniformly important in the objective of the monitoring. There are always scientific, economic, or political reasons for sampling some portions of a resource more intensively than others. Two features of environmental monitoring programs drive the second requirement. First, these programs tend to long-lived, so that even if the objectives of the program remain unchanged, the “important” subpopulations change, necessitating a corresponding change in sampling intensity. Second, a high-quality sampling frame is often lacking for environmental resource populations. So far as we know, there is no other technique for spatial sampling that “balances” over an intensity metric instead of a Euclidean distance metric or permits dynamic modification of sample intensity.

Adaptive sampling (Thompson, 1992, pp, 261-319) is another way of modifying sample intensity. However, there are some significant differences between GRTS and adaptive sampling in the way the modification is accomplished. Adaptive sampling increases the sampling intensity *locally* depending on the response observed at a sample point. The GRTS intensity change is global.

The GRTS first order inclusion probability (or density) can be made proportional to an arbitrary positive auxiliary variable, e.g., a signal from a remote sensing platform, or a sample intensity that varies by geographical divisions or known physical characteristics of the target population.

The computational burden in the hierarchical randomization can be substantial. However, it need only be carried out to a resolution sufficient to obtain no more than one sample point per subquadrant. The actual point selection can be carried out by treating the subquadrants as if they were elements of a finite population, selecting the  $M$  subquadrants to receive sample points, and then selecting one population element at random from among the elements contained within in the selected subquadrants, according to the probability specified by  $p$ .

The reverse hierarchical ordering adds a feature that is immensely popular with the field practitioners; namely the ability to “replace” samples that are lost do to being non-target or inaccessible. Moreover, we can replace the samples in such a way as to achieve good spatial balance over the population that is actually sampleable, even when that cannot be determined prior to sample selection. Of course, this feature does not eliminate the non-response, nor the bias potentially introduced by no-response. It does, however, allow investigators to obtain the maximum number of samples that their budget will permit them to analyze.

### **Appendix: Proof of Lemma.**

**Lemma:** Let  $f: I^2 \rightarrow I$  be a 1-1 quadrant-recursive function and let  $s \sim U(I^2)$ . Then  $\lim_{|d| \rightarrow 0} E\{|f(s) - f(s+d)|\} = 0$ .

**Proof:** If, for some  $n > 0$ ,  $s$  and  $s + d$  are in the same subquadrant  $Q_{jk}^n$ , then  $f(s)$  and  $f(s + d)$  are in the same interval  $J_m^n$ , so that  $|f(s) - f(s + d)| \leq \frac{1}{4^n}$ . The probability that  $s$  and  $s + d$  are in the same subquadrant is the same as the probability of the origin and  $d = (d_x, d_y)$  being in the same cell of a randomly located grid with cells congruent to  $Q_{jk}^n$ . For  $d_x, d_y \leq \frac{1}{2^n}$ , that probability is equal to  $\frac{|Q^n(0) \cap Q^n(d)|}{|Q^n(0)|} = 1 - 2^n(d_x + d_y) + 4^n d_x d_y$  where  $Q^n(x)$  denotes a polygon congruent to  $Q_{jk}^n$  centered on  $x$ . For  $D(s, d) = |f(s) - f(s + d)|$ , then, we have that  $P\left(D \leq \frac{1}{4^n}\right) \geq 1 - 2^n(d_x + d_y) + 4^n d_x d_y$ . Thus, the distribution function  $F_D$  of  $D$  is bounded below by

$$F_D(u) \geq \begin{cases} 0, & u \leq \frac{1}{4^n} \\ 1 - 2^n(d_x + d_y) + 4^n d_x d_y, & u > \frac{1}{4^n} \end{cases}.$$

Because  $D$  is positive and bounded above by 1,

$$E[D(d)] = 1 - \int_0^1 F_D(u) du \leq 1 - \left\{ \frac{0}{4^n} + \left(1 - \frac{1}{4^n}\right) - 2^n(d_x + d_y) + 4^n d_x d_y \right\}.$$

For fixed  $n$ , we have that

$$\lim_{|d| \rightarrow 0} E[D(d)] \leq \frac{1}{4^n}.$$

But this holds for all  $n$ , so that

$$\lim_{|d| \rightarrow 0} E[D(d)] = 0.$$

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Figure 1. First four levels of a quadrant recursive partitioning of the unit square. The address associated with the cross-hatched cell is “213”.

Figure 2. Void patterns used to simulate inaccessible population elements.

Figure 3. Ratio of GRTS Voronoi polygon size variance to SRS Voronoi polygon size variance as a function of point density based on 1000 replication of a sample of size 256.

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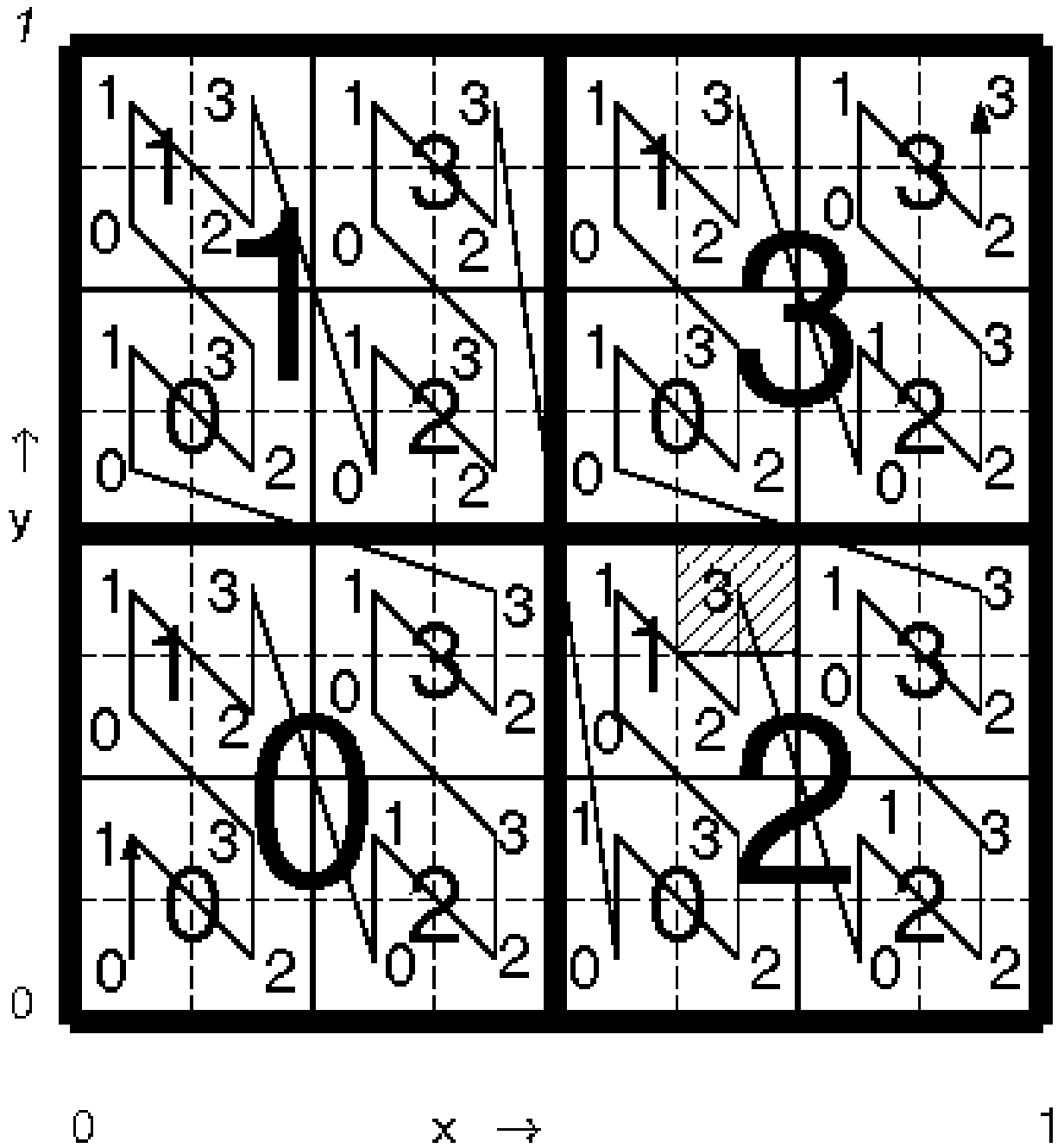


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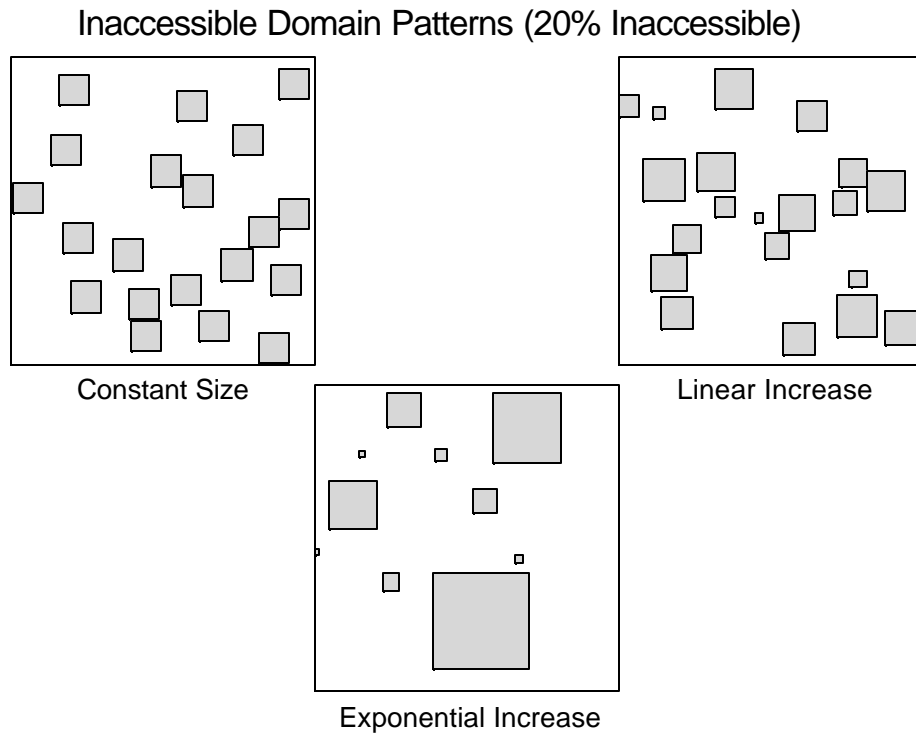


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