2 Sampling Techniques for Plants and Soil

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2.1 Introduction

The practical implementation of precision farming requires that the spatial and temporal variability of soils and crops be measured and understood. It is usually insurmountable and expensive to measure everything, but it is also almost always unnecessary to do so. Survey sampling and stereology provide mathematically valid techniques to make reliable inferences about spatial populations based on small samples. Stereology provides a stochastic approach to measurement of geometrical parameters of a given structure such as volume, surface area, curve length, or 'particle'[1] number (Baddeley and Jensen, 2004).

Soil surveys in many countries have traditionally been based on 'purposive sampling' at points or along transects, in which the surveyor chooses sample locations based on knowledge of the survey area with some restriction to ensure a balanced sample. Another approach that has been used in surveys of small, heterogeneous populations has been for the surveyor to inspect the population and select a small sample of 'typical' units that appear to be 'close to the average'. Many soil surveys deliberately exclude areas of a field that are known to be considerably different from the rest of the field and which could produce inaccurate treatment maps such as for variable rate fertilization (Francis and Schepers, 1997). Although under the right conditions such non-probability sampling methods can give useful results, there is no guarantee that a method that works well under one set of circumstances (which can only be determined for a situation in which the results are known) will do so under another (Cochran, 1977). The need for random sampling procedures for soil surveys has been recognized (Roels and Jonker, 1983; Abbitt, 2002).

When strong correlations exist between population parameters of interest and ancillary variables that are more readily measured, then ancillary data can be used to design efficient unbiased protocols for estimation and for prediction by interpolation (Sections 2.3.1.1, 2.3.2, 2.3.5, 2.4). The increasing resolution, availability and affordability of remote sensing images has made it feasible to collect timely information on soil and crop variability by examining multispectral, near infrared or thermal infrared images (Basso et al., 2001; Best and Zamora, 2008). The normalized difference vegetation index (NDVI) (Tucker, 1979) is correlated with canopy vigor, density, and size and with fruit quality (Price, 1992; Carlson and Ripley, 1997; Zaman et al., 2004; Fletcher et al., 2004; Best et al., 2008; Best and Zamora, 2008; Bramley et al., 2003; Lamb et al., 2004). NDVI may indirectly indicate variability of soil parameters causing variability in tree growth (Taylor, 2004; Zaman and Schuman, 2006). Soil color obtained from aerial images can be an indication of organic matter content and other soil properties (Francis and Schepers, 1997; Kerry and Oliver, 2003). Apparent soil electrical conductivity (EC)

[1] Any discrete physical object contained in a 3-D object, e.g. grains or aggregates of soil, cells, fruit, leaves

measured intensely using electromagnetic induction sensors and elevations measured using GPS may be correlated with a number of other soil parameters (Taylor, 2004; Friedman, 2005; Johnson et al., 2005).

Both survey sampling and stereology have many potential errors of methodology into which researchers may easily fall (Baddeley and Jensen, 2004). Statistically valid inferences about the population can be made if: 1) samples are selected randomly[2] with positive (non-zero) probability, and 2) the sample size is sufficiently large to reflect the variability of soil or crop characteristics. Limiting sampling to regions that are readily accessible (e.g. lower branches of a tree to estimate nutrient content for the entire tree) violates the requirement for a non-zero probability and may introduce bias in the estimator unless the variation across the tree branches is spatially homogeneous, see Section 2.2.

2.2 Design-based and model-based approaches

Two approaches to statistical inference from a sample have developed: design-based and model-based (Thompson, 1992).

Design-based approaches provide unbiased estimators of the parameters of interest by using a well defined random selection procedure, and require no statistical model of the structure such as object shape, stationarity or isotropy. Design-based methods are valuable for the study of highly organized, heterogeneous structures.

In model-based approaches the random variation is assumed to arise from intrinsic randomness in the population. The population is regarded as a single realization of a stationary and/or isotropic stochastic process and the estimated mean value of a variable does not depend on the location and shape of the sample windows or probes[3]. It is therefore not necessary to randomize sample locations. Researchers in precision agriculture and soils have mostly relied upon model-based sampling methods. This has sometimes been under the misconception that design-based sampling requires independence of samples (see Bruis and de Gruijter, 1997, and the discussion subsequent to it). A model-based approach is often preferred when our aim is to formulate models describing the spatial arrangement of a population. Models of the population can be of considerable practical advantage when based on knowledge of the natural phenomena (e.g. climate, dynamics of weed populations, predators or disease) influencing the distribution of the population or when models (e.g. regression relations, process based crop models, soil property functions) are available describing a relationship between the variable of interest with an auxiliary variable. Geostatistical interpolation methods (Section 2.4) are model-based. When a statistical model can be assumed for the population, an adaptive sampling strategy is often optimal (Thompson and Seber, 1996) (Section 2.5). Model based approaches are the basis of several variance prediction models used in stereology (Section 2.6).

Model-based designs can be very sensitive to departures from the assumed model and lead to biased estimators (Baddeley and Jensen, 2004). A less precise, yet robust, design-based estimator may then

[2] The term random is used to mean non-deterministic. It does not mean that events must be independently distributed.
[3] The term probes in stereology is defined in Section 2.2.

be preferred. When the assumptions underlying an assumed model are valid, model-based inference can be more precise than design-based inference (e.g. Särndal, 1978).

2.3 Sampling concepts

The concepts reviewed here are taken from survey theory (Cochran, 1977; Thompson, 1992) and from design-based stereology (Baddeley and Jensen, 2004). Consider the study of a finite 'population' of discrete 'units' arbitrarily numbered 1, 2, …, *N*, where the population size *N* may be unknown (depending on the sampling design). Although usually described with respect to discrete elements (e.g. plants, insects), the theories are equally applicable to continuous media (e.g. soil) that are divided up into non-overlapping discrete sub-units. Suppose the population is the collection of all fruit on a group of trees, then the sampling units may be plots, trees, branches, fruit clusters or any other division that is practically convenient. Our aim is to investigate the population by taking a 'random sample' – a randomly selected part of the population – with the goal of drawing conclusions about the population from information observed from the sample. Of particular interest are population totals (e.g. total number of fruit, total canopy surface area), population means (e.g. mean soil nitrogen content, mean weed density, mean fruit size) and the spatial-temporal variation of such quantities (e.g. distribution of fruit size classes, spatial variation of water content).

A uniform random (UR) 'sampling design' is any well defined procedure for selecting a sample in which all elements of the population are given an equal probability of being selected. UR sampling (together with isotropically random direction, i.e. IUR sampling, for length and surface area estimation) guarantees unbiasedness at the level of geometric sampling, but does not guarantee adequate precision. There are many ways to implement UR sampling, including simple random sampling (SR) and systematic random sampling (SUR, Section 2.3.1). Non-uniform designs are also possible, e.g. probability proportional to size (PPS) sampling, and can be very efficient for sampling inhomogeneous or rare populations (Section 2.3.2).

In simple random sampling without replacement (SR-wor), we use a random digit generator or a table of random digits to select a fixed number, *n*, of distinct units with label numbers between 1 and (known) *N*. The sampling probability for each unit is *n*/*N*. Simple random sampling with replacement (SR-wr), which generates independent samples, is generally the most inefficient of sampling designs (followed by SR-wor) but serves as a reference procedure because it is the only design for which the mathematical properties are completely known. Three UR sampling designs for selecting plots from a 'field' are illustrated in Figure 2.1(b)-(d). The Smooth fractionator design (d) is described in Section 2.3.1.1.

A general estimator of the population total, *Q*, may be written (Horvitz and Thompson, 1952) as

$$\hat{Q} = \sum_{i=1}^{n} \frac{q_i}{\pi_i} \tag{2.1}$$

where q_i is the content (the amount of the parameter under study) of unit *i* in the sample, π_i is the positive sampling probability of unit *i*, and *n* is the sample size (number of units). The sampling probabilities need only be known for the sampled units, but they must be known exactly to provide unbiased estimates of the population total. A UR design is a special case of the Horvitz-Thompson

(HT) estimator (2.1) in which the sampling probability is a constant. SR and PPS sampling provide unbiased estimators of the population mean. Multiplying by the sample size provides an unbiased estimator of the population total, $\hat{Q} = n\hat{\bar{q}}$. Systematic sampling and the HT estimator provide unbiased estimators of the population total. The corresponding estimator of the population mean, $\hat{\bar{q}} = \hat{Q}/n$, is generally biased for SUR sampling because the denominator n is a random variable. The bias decreases as n^{-1} (e.g. Cochran, 1977). If the denominator varies little, the bias is negligible.

In stereology several other concepts are introduced: A 'probe' is a geometric entity (3D slice, 2D plane, 1D line, 0D point) used to penetrate and sample an object. A 'test system' is a set of probes used to obtain stereological estimates, e.g. a regular grid of points for estimating 2D area (Figure 2.2). (The classic work of Warren Wilson (1960) and Warren Wilson and Reeve (1959) to estimate LAI and related parameters using linear probes, and the recent studies by Radtke and Bolstad (2001) and Wulfsohn et al. (2010) provide examples of this stereological principle.) The 'containing space' is the space in which the features of interest are entirely contained (the size and extent of the containing space need not be known exactly). A 'reference space', is a well defined object of known or measurable size, compared to which the size of the feature of interest can be expressed (Weibel, 1980). An example is provided by Wulfsohn and Nyengaard (1999). They estimated the total number of root hairs N (the population total) on a plant root system with a total length L (the reference space, estimated using an unbiased procedure as in Wulfsohn et al., 1999) by the product of the mean density of root hairs per unit root length (N_L) and L.

2.3.1 Systematic random sampling

Systematic uniform random sampling often offers an appropriate balance between the estimator precision and the time spent to obtain samples. It is easy to execute without mistakes, and in many situations is more precise than SR for a given sample size. SUR sampling has been shown to be superior to SR sampling for autocorrelated, stationary populations when the spatial correlation function decreases with distance between units (see Cochran, 1977; Cressie, 1993).

In SUR sampling, every m-th unit in the population is chosen where m is the 'sampling period' and the first unit is selected with 'random start'. The random start is obtained by randomly selecting an integer between 1 and m. Each unit of the population appears in the sample with probability ('sampling fraction') $1/m$. A SUR sample of plots in a field and a procedure for evenly spacing the plots is presented in Figure 2.1(c). Sampling on the corners of a regular square grid ('grid sampling' or 'lattice design') or, equivalently at fixed intervals along equally spaced parallel transects (e.g. Flatman and Yfantis, 1984; Mulla and Bhatti, 1997), is probably the most commonly used SUR design used in soil and crop surveys. Triangular or hexagonal tessellations of plots have also been advocated for purposes of semivariogram estimation and spatial interpolation. A SUR procedure for sampling of branches on a stem is illustrated in Figure 2.3(a).

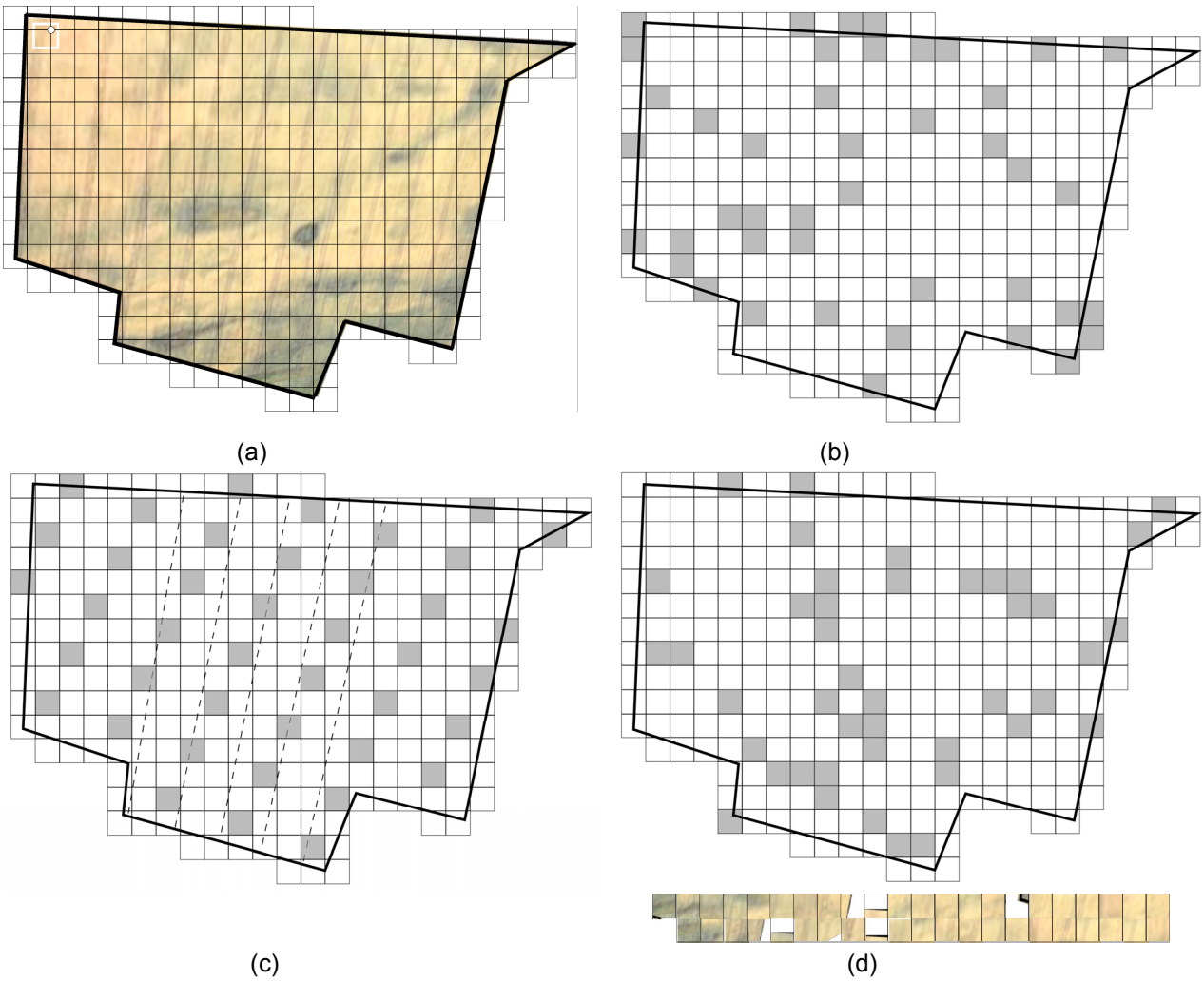


Figure 2.1: Three examples of uniform random (UR) sampling designs for selecting plots in an arbitrarily shaped field, all with the same sampling fraction: (a) A random point is placed within the unit tile (white square), which then defines the UR placement of a tessellation of N = 301 sampling units. The tessellation is of extent to completely contain the field (it defines the containing space). Providing that the tessellation of plots is positioned randomly, then all the following designs provide units (and thereby elements of the population of interest contained within the units) – including edge plots and empty plots – with equal probability. (b) A simple random sample (without replacement) of 43 units. (c) A systematic uniformly random (SUR) sample with sampling fraction $1/m$ = 1/7 and random start 3 (where the top left quadrat has been designated as unit 1, the quadrat to its right as unit 2, etc.). To avoid aligning samples the position of the selected units is shifted $k = \text{round}(\sqrt{m}) = 3$ units on consecutive rows. When m is exactly divisible by k then the position of the selected unit is shifted k + 1 units on the first consecutive row and by k units on the remaining rows. The combination of sampling unit size and sampling period avoids alignment with tramlines (indicated by dashed lines), a potential cause of periodicity in the soil or crop. (d) SUR sample with $1/m$ = 1/7 sampling fraction taken from the Smooth arrangement of the units based on mean plot intensity ('smooth fractionator' design). The sampled units are shown in their smooth order (from top left to right, and then bottom right to left) in the strip below the map.

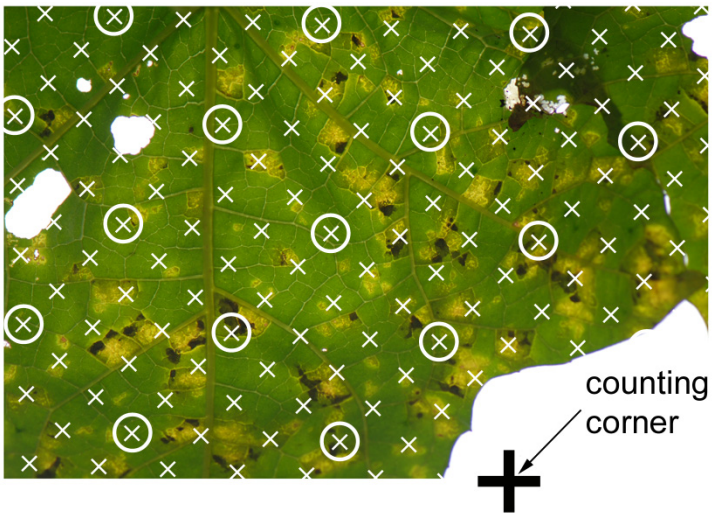


Figure 2.2: Point counting. A (0-dimensional) point is defined as the upper right corner of a cross. The number of intersections, *P*, between the UR positioned square point grid and the feature of interest is counted. An unbiased estimator of the feature area is given by $\hat{A} = a_p P$, where the grid constant, a_p, is the area associated with a single point. A double grid is illustrated. The fine grid (all points, grid constant a_p cm^2/point) is used to estimate the area of infected (yellow, 9 intersections) and diseased (black, 3 intersections) leaf surface while the coarse grid (circled points, grid constant equal to $9 \cdot a_p$) is used to estimate total surface area (15 intersections). The area fraction of infected+diseased leaf is 12/(15×9) = 0.089 (Photograph of banana leaf courtesy of David Collinge, University of Copenhagen).

Systematic sampling behaves very poorly when a sampling period is chosen that is close to any periodicity in the population variable under study. Management and cultivation effects such as evenly spaced and aligned wheel tracks, trees, irrigation furrows, fertilizing bands, or tillage rows can cause soil or crop conditions to vary systematically (Wollenhaupt et al., 1997; Mulla and McBratney, 2002). The arrangement of branching and axillary flowering structures on parent units of a plant is periodic (phyllotaxy, length of internode). Sequences of patterns may not be clearly evident at some stages of development and scales (Guédon et al., 2001). When visible or known, sampling periods and plot spacing and orientation can be selected so as to not coincide with these periodicities (e.g. Figure 2.1(c)). To avoid sampling units from only one side of a plant stem, leaf sampling periods that are multiples of the phyllotaxic period should be avoided in a systematic design such as shown in Figure 2.3. An approach that has been recommended to reduce errors due to periodicity in the landscape is to take simple randomly positioned samples within systematic random plots, using ‘unaligned sampling’ (Cochran, 1977; Mulla and McBratney, 2002; Webster and Oliver, 2007; Wollenhaupt et al., 1994, 1997) or ‘one-per-stratum’ stratified sampling (Breidt, 1995). Breidt (1995) showed that systematic sampling and one-per-stratum stratified sampling designs are special cases of ‘Markov chain designs’ in which the *x* and *y* coordinates of sample points evolve according to Markov chains.

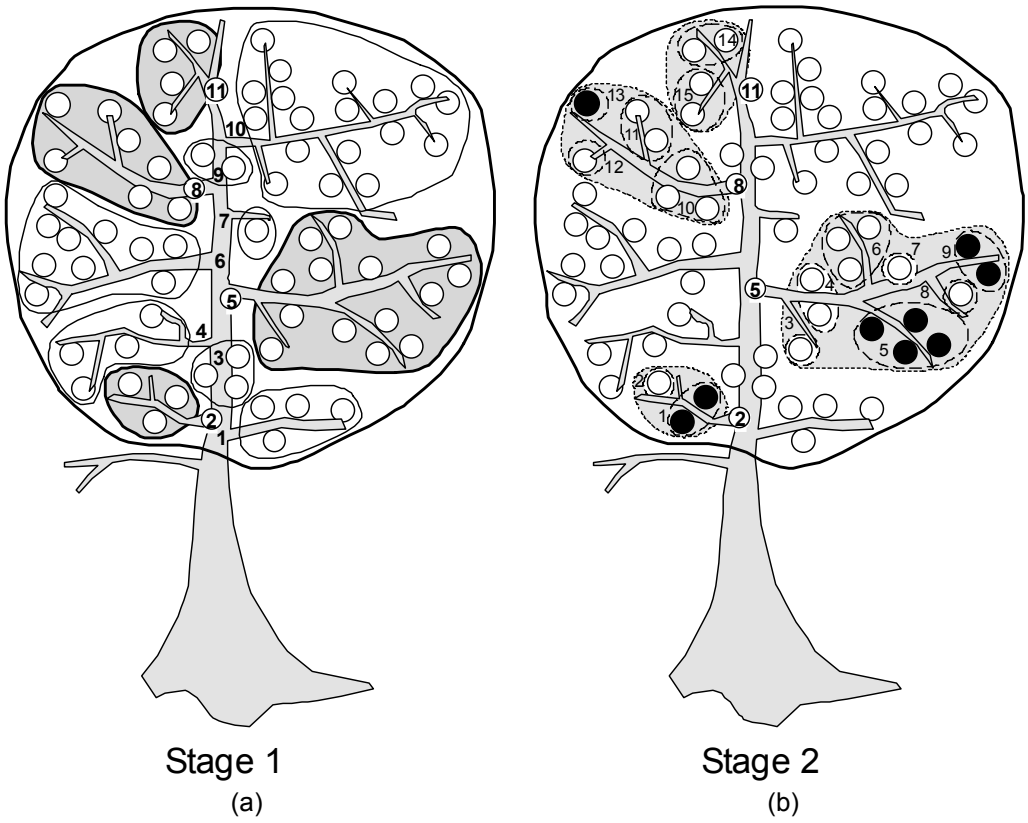


Figure 2.3: A two-stage fractionator sampling design applied to a tree: (a) Primary branches and stem (—) serve as primary sampling units in the first sampling stage, and (b) higher order branches (----) are the sampling units in the second stage. Consider sampling the structure with stage 1 sampling fraction $1/m_1$ = 1/3 and stage 2 fraction $1/m_2$ = 1/4, and uniform random starts equal to 2 and 1, respectively. (Stage 1): The first stage sample contains all particles (e.g. fruit) on branches 2, 5, 8 and 11 (circled numbers). (Stage 2): The final sample (filled circles) contains all fruit on branch segments 1, 5, 9 and 13 within the sampled branches. In practice, data is collected as the surveyor steps systematically through the structure: Starting at primary branch 2 we select 2 fruit on branch segment 1. Then step m_2 = 4 branch segments as follows: one remaining segment on branch 2, then jump to branch 5 (2 + m_1 = 5) to segment number 5 where we sample 4 fruit, and so on. Empty units (branches with no fruit) have been ignored. An unbiased estimate of the total number of fruit on the tree is given by the product of the aggregate sampling period m = 12 and the total content of the sample (9 fruit). Figure modified from Maletti and Wulfsohn (2006).

2.3.1.1 Smooth fractionator

The 'smooth fractionator' provides a general, straightforward technique to reduce the estimator variance for SUR sampling of heterogeneous populations (Gundersen, 2002; Gardi et al., 2006). It aims to increase estimator precision by increasing within-sample variability and reducing the variability between samples (Gundersen et al., 1999). The procedure is as follows: (1) Conceptually or physically divide up the population into distinct units. (2) Order the units of the population in increasing size. The size here is that of the parameter of interest or that of any quantifiable associated variable (e.g. shape,

texture, spectral intensity, slope, etc.) that is positively correlated with this parameter. (3) Push out every second unit to produce an ordering of the units in a monotonically increasing and then decreasing size. (4) Take a SUR sample of the smooth arrangement. Figure 2.4 shows examples of smooth arrangements of plants and sub-regions of images.

Figure 2.1(d) shows a sample of plots selected using a smooth fractionator with the plot mean red-band intensity (between-plot coefficient of variance, CV = standard deviation/mean = 11%) as the associated variable. (In this example, assume that the parameter of interest is perfectly positively correlated with the intensity.) The coefficient of error (CE = SEM/mean, where SEM = standard error of the mean) due to taking a sample of plots, CE_{plots}, is 1.8% for SR-wr, 1.6% for SR-wor, 3.6% for SURS, and a negligible 0.038% for the Smooth design. Clearly, when surveying sampling locations at the field scale, the ease associated with systematic sampling is lost, an increase in cost which may not justify the gain in precision. The use of GIS and GPS makes smooth fractionator designs more practical.

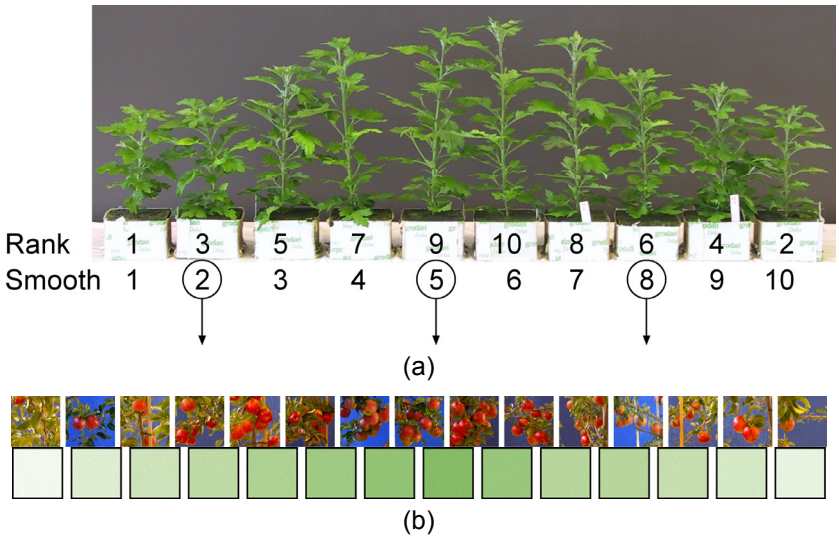


Figure 2.4: The smooth fractionator. (a) A smooth arrangement of plants, using plant height as an indicator of plant surface area for estimating total canopy surface area. 'Rank' indexes plants by increasing height, while 'Smooth' is the labeling of plants according to the smooth height arrangement. In this example a sample of plants is selected with fraction 1/3 with random start 2 from the smooth arrangement. Figure modified from Wulfsohn et al. (2010). (b) A smooth ordering can be implemented based on an auxiliary or associated variable continuously sampled using non-invasive sensors, e.g. the proportion of red pixels in an image window as an associated variable for (red) apple number, or the NDVI value at a location in the field as an indicator of varying crop and soil conditions.

Wulfsohn et al. (2010) examined the efficiency of the smooth fractionator for estimating the total surface area, A_t, of a canopy made up of 50 chrysanthemum plants (between-plant CV(A) = 65%). For a sample size of 10 plants and a precise estimator of leaf area, $CE_{plants}(\hat{A}_t)$ for the Smooth design was 2% when ordering by plant area (Figure 2.4(a)), 10% when using Smooth with three plant height

classes as the associated variable and with plants randomly arranged within height classes before smoothing (introducing a random noise component), and 21% using SR-wor.

2.3.2 Probability Proportional to Size (PPS) sampling

Gardi et al. (2007a) presented a probability proportional to size (PPS) design called the 'proportionator'. Image analysis is used to automatically assign weights to the sampling units, the units are put in a smooth order based on their weights (an optional step), and then a sample of specified size *n* is sampled systematically on the ordinate of the cumulative weight using a sampling period of *Z/n* with random start (Figure 2.5). The probability of sampling a unit is strictly proportional to the recorded weight of the unit and therefore known exactly. An unbiased estimator of the population total is obtained by applying the HT equation (2.1) with $\pi_i = z_i / (Z/n)$, where z_i is the weight of unit *i* and $Z = \sum_{i=1}^{N} z_i$.

Gardi et al. (2007a) compared the performance of SR-wr (i.e., independent sampling), SUR, Smooth fractionator and PPS sampling for estimating the total number of 2500 rectangular 'particles' (of one color intensity but of varying area) and the total and average particle area (using point counting), from a 2D irregularly shaped region divided UR into roughly 400 sampling units. The total intensity of a sampling unit was used as the ancillary variable and weight for Smooth and PPS sampling, respectively. Simulations were carried out for moderately inhomogeneous (between-unit *CV* = 67%), intermediary (*CV* = 155%), clustered (*CV* = 188%) and sparse (*CV* = 293%) particle spatial distributions. Qualitatively and quantitatively the precision of point counting for area estimation was almost identical to that for number estimation. In all cases, SR-wr was the least precise estimator, SURS a few times more precise than SR, Smooth always more precise than SURS, and PPS the most precise except for the homogeneous distribution where Smooth has a slightly smaller *CE*. Increased clustering reduced the precision, with the effect considerably more pronounced for SR and SURS than for Smooth and PPS.

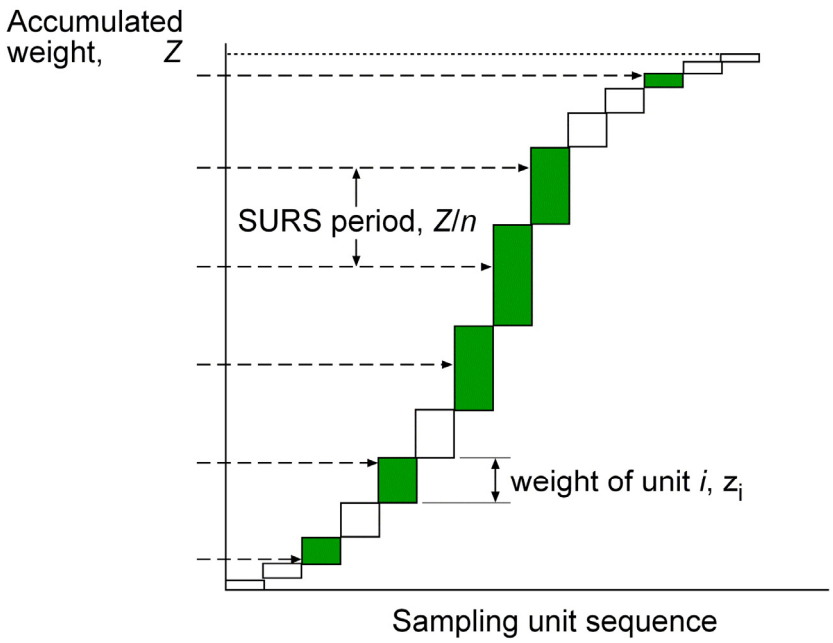


Figure 2.5: Proportionator (PPS) sampling. The complete set of *N* sampling units is listed in arbitrary order or, as illustrated here, arranged in a sequence based on the weights as for the smooth fractionator before SUR sampling. The ordinate shows the accumulated weight. Sampling on the ordinate is systematic with sampling period *Z*/*n* and UR start. The probability of sampling a unit is proportional to the recorded weight of the unit. Sampled units are highlighted (*n* = 6 in this example). Figure based on Gardi et al. (2007a).

Like for the smooth fractionator, the precision of the proportionator is dependent on having a strong positive correlation between weights and counts. Any noise in the relationship between weight and count such as outliers, particles that intersect a sampling unit but are not sampled by the same unit (see Section 2.7), reduces precision.

2.3.4 Multistage designs

A ‘‘level’ is a sampling design in which the measurements are made at a constant scale. There are several reasons for using multilevel (multistage, nested) designs. To obtain a sample of seeds from a vegetable crop, it may be convenient to first take a sample of rows from a field, then a sample of fruit from plots located along the sampled rows, and finally take a sample of seeds from the sampled fruit. One may observe ancillary variables at one scale and make final measurements much more efficiently at a finer resolution. Indices obtained from remote sensing images or soil maps might be used to design stratified (Section 2.3.5), Smooth or PPS designs for field and orchard crops. Basso et al. (2001) used remote sensing to target sampling of soil and crop for input to a crop model and combined remote sensing with model output to identify management zones and to interpret yield maps.

In some cases the variable under study may only be observable at the object scale or under higher magnification. The physical characteristics of weeds are similar to those of crops, complicating the detection of weeds and weed patches in a growing crop (Stafford et al., 1996; Christensen and Heisel, 1998). Thus, weed maps for patch spraying may need to be developed by combining manual and automatic measurements at different scales, such as using aerial imaging (Stafford and Miller, 1993) and vehicle-mounted cameras (Brivot and Marchant, 1995; Christensen et al., 1997) supplemented by georeferenced observations or measurements of attributes (e.g. patch shape and size). Handheld data-logging sampling software can be used to facilitate selection and recording of samples (Stafford et al., 1996; Gardi et al., 2007b).

Multistage SURS designs are called 'fractionator' designs in stereology. Figure 2.3 illustrates a two-stage fractionator for UR sampling of particles (fruit, buds, leaves, spurs, etc.) on a tree. This design is easily applied in practice for a group of trees by treating the union of branches as a single continuous sequence of sampling units (Wulfsohn et al., 2006a). Aggelopoulou et al. (2010) used a two-stage (trees, branches) design to map flowering in an orchard. Data from a SUR sample of 162 apple trees were collected in one day – a sample size adequate for semivariogram estimation and for interpolation. Aravena et al. (2010) used a three-stage design (tree, branch, segment) with systematic sampling of trees and the design illustrated in Figure 2.3 within trees, to estimate total yield in several rows of 14 commercial fruit orchards. Yields at harvest ranged from several thousand bunches for table grapes to over 40,000 fruit for kiwis and apples. Accuracies of better than 5% were obtained in six orchards and between 5-10% in five orchards for workloads of 30-150 minutes, typically less than 90 minutes. Two yield estimates had absolute errors of about 20%. A variance analysis indicated that in one of these orchards a precision of 10% could be obtained for a similar workload by changing the sampling periods for the three stages.

The smooth fractionator is usually applied in a multistage context. Steps 1–4 (Section 2.3.1.1) are repeated as many times as desired to the sampled units obtained in the preceding stage (nesting). Data are collected only at the last stage. The aggregate sampling fraction is given by the product of individual sampling fractions, $1/m = 1/(m_1 \cdot m_2 \cdot \ldots \cdot m_k)$. A nested design leads to dependent observations, which means that inferences can also be made about macro-micro relations if data are recorded at relevant stages.

2.3.5 Cluster sampling

Cluster sampling is particularly convenient for sampling large or complex populations. To conduct cluster sampling, divide the population into a finite number of separate subsets ('clusters') in any fashion that is practically convenient. These clusters are treated as 'primary sampling units'. Then select a random sample (e.g. SR, SUR) of clusters. To uniformly and randomly sample fruit on a tree, take a UR sample of branches. If all clusters have an equal probability of being selected, then each unit in the population has equal probability of appearing in the cluster sample. The fractionator design presented in Figure 2.3 is a two-stage nested systematic cluster sampling design. The primary sampling units are primary branches, while the higher order branches serve as the second stage clusters.

2.3.6 Stratified sampling

Stratified sampling provides a technique for variance reduction. The population is partitioned into non-overlapping subsets ('strata') and each stratum is treated as a separate population for sampling purposes; samples are selected independently from each stratum (e.g. requiring a new random start for each stratum for stratified SURS). Strata can be physical or conceptual. It may be possible to divide an inhomogeneous population into subpopulations (which need not be spatially contiguous), each of which is internally homogeneous. Examples of possible strata are soil horizons, biogeographical areas, morphological zones within plants and management zones based on easily measured ancillary variables such as vegetation indices, yield productivity, soil properties and/or past field history (Basso et al., 2001; Bramley and Hamilton, 2004; Bramley, 2005; Taylor, 2004; Wulfsohn et al., 2006a; Zaman and Schuman, 2006; Sciortino et al., 2008; Best and Zamora, 2008). The benefit of stratification is gained by using different sampling fractions in the different strata (Figure 2.6). Higher sampling fractions could be used in strata which have a comparatively high contribution to the population total to ensure their contributions are estimated more accurately. Very small (but non-zero probability) sampling fractions could be used in areas of a field (delineated as strata) known to be odd and likely to introduce biases when producing management maps for variable rate application. More intensive sampling could be used in strata where variation is large, and sparse sampling applied in strata where properties are more spatially uniform. Seber (2002) reported that large gains in precision can be obtained if the sampling fraction allocated to each stratum is proportional to the square root of the population density in the stratum. Sampling densities for say soil nutrient testing are selected based on prior knowledge of the spatial scale of variability of that nutrient or its mobility through the soil profile (e.g. Francis and Schepers, 1997). McBratney et al. (1999) proposed an iterative procedure for partitioning a field into strata with approximately equal variances based upon intensively sampled correlated ancillary data such as from crop or soil monitors or aerial images. Gallego (2005) described a method to combine stratified, systematic and PPS sampling of satellite images.

Figure 2.6 shows a sampling design in which stratified and cluster sampling have been combined to optimize sampling of fruit from an orchard, the five trees in a cluster would be treated as a continuous sequence of branches for further subsampling as in Wulfsohn et al. (2006a). The purpose of sampling across spatial clusters (blocks) of trees at each sampling location is to reduce the contribution of local variability to the total estimator variance, similar to compositing soil samples obtained from small regions.

2.3.7 Directed or targeted sampling

In sampling programs undertaken for precision farming, an important objective may be to identify areas of a field that are distinctly different from the rest of the field to create variable rate application maps (Mulla, 1993; Francis and Schepers, 1997). A number of studies have used 'directed' or 'targeted' sampling designs, in which sampling is carried out in regions of the field or crop that appear to be visually different from the rest of the field. A frequent motivation is to make accurate prescriptions on the basis of relatively few samples. Christensen et al. (2005) were able to discriminate between N, P and NPK stress in maize plants using visual-NIR reflectance by sampling specific leaf growth stages within a plant, but were not successful when reflectance data for the entire plant were used. Pocknee (2000) showed that directed soil sampling was more effective for characterizing vineyard management

zones. For economic constraints much of the crop and soil property sampling for precision agriculture has been conducted manually on grids with 100 m spacing or more (McBratney et al., 1999; Griffin, 1999). A 100 m regular grid is sometimes excessively coarse to produce accurate prescriptions for site specific soil management (e.g. Brooker et al., 1995, Brooker and Warren, 1997) while in other cases it may be unnecessarily intensive. Griffin (1999) and Mulla and McBratney (2002) advocate targeted sampling as a supplement for a rigorous sampling design, e.g. supplementing samples taken on a regular systematic grid with a few samples taken at locations where there is visible evidence of large changes in the measured property e.g. from aerial photos, electromagnetic induction maps or from patterns in yield maps observed over several years. Bramley (2003) demonstrated that vineyard soil surveys could be improved by using high resolution soil sensing and elevation modeling supplemented by targeted ground-truthing.

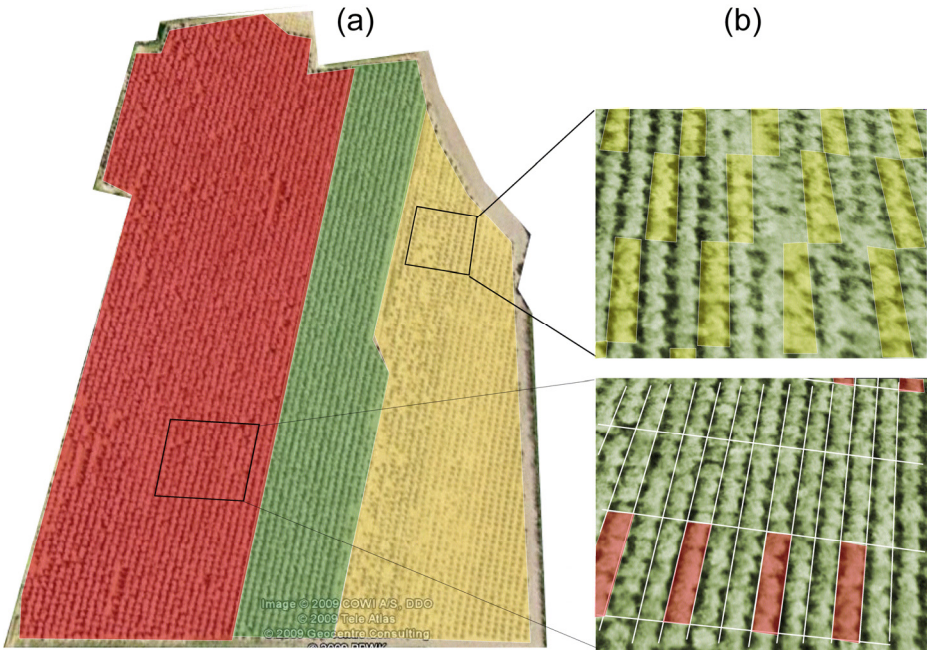


Figure 2.6: A stratified cluster sampling design. (a) Three management zones (the strata) have been identified in an orchard, e.g. based on low, medium and high yielding zones from remote sensing images (highlighted using different colors/tones). (b) In each of the strata, a nested cluster sampling design is applied, with different sampling fractions. The first stage sampling units are blocks of five adjacent trees in a row. In the low yielding (right) zone, a systematic sampling fraction of 1 in 3 sampling units is used with uniform random start. In the high yielding (left) stratum a systematic sample of 1 in 9 sampling units is selected with random start. An intermediate sampling fraction is used in the medium yielding (middle) stratum. Within each of the selected sampling units, a systematic sample of fruit might be obtained using a multistage design such as that shown in Figure 2.3 (perhaps with different sampling fractions in each zone to obtain a desired total sample size in each stratum). The estimator of the population total is the sum of the estimates from the three strata, with proper accounting for the different sampling fractions.

2.4 Geostatistical sampling

The sampling designs presented in the above sections are design-based. The population was considered to be fixed while the sampling design introduced randomness in the sample. When observations are made at sample locations and the objective is to predict values at non-sampled locations (spatial prediction) or to determine parameters of a spatial regression, it is useful to take a model-based approach. The value of the population parameter at location $\boldsymbol{x}$ is now considered to be a random variable z. Given sampled values observed at locations $\mathbf{X} = \{\mathbf{x}_1,...,\mathbf{x}_n\}$, the aim may be to predict the value z_0 at a new location $\boldsymbol{x}_0$. Typically, the values of the variable of interest at nearby nonsampled locations are not independent of each other.

Given accurate measurements at sample locations, kriging provides the interpolation with least bias, and is known as a best linear unbiased predictor (BLUP). Kriging is an exact interpolator, i.e. it reinstates the measurement values at the observation locations. Different types of kriging and geostatistical simulation for interpolation of stationary and non-stationary data have been described in several textbooks [e.g. Matheron, 1963; Journel and Huijbregts, 1978; Isaaks and Srivistava, 1989; Cressie, 1993; Goovaerts, 1997; Lantuéjoul, 2002; Wackernagel, 2003]. A number of studies have compared kriging and non-parameteric interpolaton methods such as inverse distance methods, nearest neighbor, Delauney triangulation and cubic splines (Laslett et al., 1987; Isaaks and Srivistava, 1989; Wollenhaupt et al., 1994; Gotway et al., 1996). When intensive sampling is carried out on a regular grid, kriging, inverse distance, and cubic splines give similar predictions. Kriging is generally superior when the data to be interpolated have a well-developed spatial structure, and are sampled at more than 70-80 points with spacings less than the range of the semivariogram in clusters or at irregular spacings (Laslett et al., 1987; Gotway et al., 1996; Mulla and McBratney, 2002).

There are two primary concerns when sampling for spatial prediction using kriging. One is sampling for parameter estimation. Kriging requires knowledge about the variances of differences between sample locations (the variogram) or the covariances. The second consideration is the placement of samples to minimize variances associated with interpolation. A common dilemma is that geostatistically designed sampling schemes rely upon knowledge of the semivariogram, yet the semivariogram is often unknown until the site is sampled. The sampling needed to determine the semivariogram is often the largest part of the task (Webster and Burgess, 1984) but sampling designs that are efficient for parameter estimation are not necessarily efficient for spatial prediction. A typical compromise is to supplement a systematic grid with some closely related sample locations (Figure 2.7). Diggle and Lophaven (2006) found that supplementing a regular grid with a fixed number k of additional points located uniformly randomly within a small radius of a grid point as in Figure 2.7 yielded more accurate predictions than a regular grid supplemented by more finely filled grids within k randomly chosen cells of the primary grid. Another approach is to use transect designs with points separated by decreasing distances along the transect (Pettitt and McBratney, 1993). Systematically rotated transects positioned on a systematic grid can be used to investigate anisotropy. It may be necessary to conduct a preliminary pilot study to establish the spatial scale. Pettitt and McBratney (1993) reviewed approaches to design and analysis of soil surveys to investigate the spatial variation of an attribute where little of no prior knowledge of the scale of the variation is known. They proposed an approach that was a hybrid of design- and model-based approaches.

Both the total number of samples and the spacing between samples affect the accuracy of an experimental semivariogram (Goovaerts, 1997; Webster and Oliver, 2007). The distance between sample points needs to be just small enough to resolve the scale of variation at the field level. The sampling interval for regular grid sampling programs should be from ¼ to ½ the average semivariogram range of the property of interest to preserve the main patterns of variation (Flatman and Yfantis, 1984).

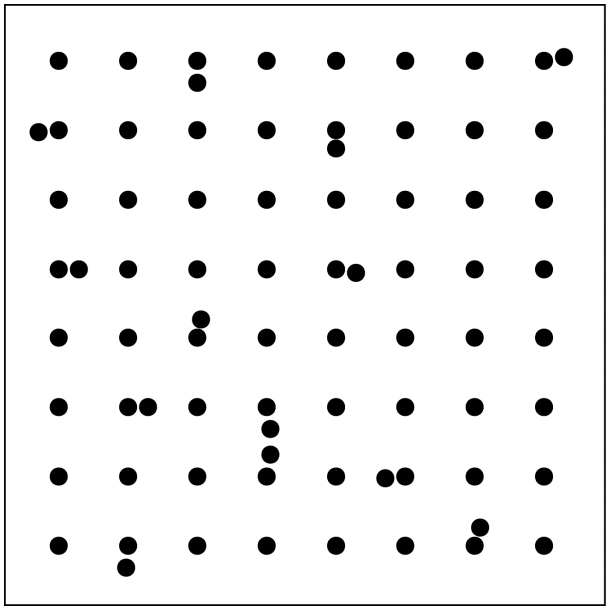


Figure 2.7: Example of a 'lattice plus close pairs' sampling design (Diggle and Lophaven, 2006), aimed at efficient spatial prediction when the variogram is also unknown.

Webster and Oliver (1992) recommend 100 to 150 data locations to obtain a reliable experimental semivariogram for soil attributes using grid sampling and Matheron's method of moments. Where variation is anisotropic even more data may be needed. Kerry and Oliver (2007) found that an adequate model semivariogram for soil properties in four fields in the UK could be obtained using 50 locations at an appropriate distance apart when the residual maximum likelihood (REML) method for semivariogram estimation was used. The REML approach is parametric and the data is assumed to follow a multivariate Gaussian distribution (Patterson and Thompson, 1971; Cressie, 1993; Pardo-Igúzquiza, 1997). The REML method does not yield an experimental semivariogram. Linear combinations of the data celled 'generalized increments' are used to simultaneously filter out the trend and estimate the parameters of the variance-covariance matrix.

When the semivariogram is known, it can be used to evaluate different sampling designs even before samples are collected. One type of analysis is to determine optimal spacing and spatial arrangement of grids for kriging by comparing mean square prediction errors (also called kriging variances). The kriging variance depends only on the semivariogram (or covariance function) and the distances between sampled and unsampled locations, which means it can be computed even when no

measurements have been made at the potential sampling locations. McBratney et al. (1981), McBratney and Webster (1981) and Yfantis et al. (1987) considered the problem of spacing *n* systematic sampling sites on square, triangular and hexagonal grids to achieve an acceptable value of the kriging variance over the region of interest. For a given number of locations per unit area, making observations at the vertices of equilateral triangles minimizes kriging variance. The gain in precision is usually so small that square grids are more commonly used (Webster and Oliver, 2007). Semivariograms of ancillary data can be also used to guide spacing of sampling grids for correlated properties (Kerry and Oliver, 2003). The most efficient placement of grid sampling locations is in the center of each grid cell (Webster and Burgess, 1984).

Kriging variance increases as nugget variance. i.e., the variance due to sampling and measurement noise, increases. Compositing or bulking of soil or biomass samples in small regions or accumulating a sample over a group of plants (treated as a block average) may be used to reduce short-range fluctuations that add to the noise. The aim is to reduce the workload of sampling while retaining some of the precision that comes from having a larger sample size. A model of the semivariogram combined with the kriging equations can be used to determine the optimum number of composite samples to collect at sampling locations (Webster and Burgess, 1984; Oliver et al., 1997). Kriging variances are computed for different combinations of support (size and shape or area) and configurations of sampling locations within the blocks. From these, a combination that meets the tolerance for a given parameter can be selected. In the absence of tolerance limits, Oliver et al. (1997) recommended that for soil nutrient mapping 16 cores be bulked from within a few meters of the sampling location.

Rich data sets may be aggregated into grids of larger cells, where each cell value represents the average of all points contained within the cell, to remove unnecessary small-scale detail. Perez-Quezada et al. (2003) aggregated yield data into 20-m by 20-m cells, using the same mask coverage from year to year, to compare yields for different years in the same locations. Bulking and aggregation of samples involves a ‘change of support’ and values are smoothed. Even where average values are not greatly affected by the smoothing, the observed variability (e.g. as expressed by the *CV*) can be substantially reduced, especially where small-scale variability exists.

2.5 Adaptive sampling

Surveys and mapping of rare, spatially clustered populations such as some weed species and insects or early-onset plant diseases or pests may motivate the use of adaptive sampling designs (Thompson, 1992; Fleischer et al., 1999). Rather than selecting the sample of units prior to the survey, the procedure for selecting sites or units may depend on observed values of the variable of interest during the survey (Thompson, 1992). The goal is to achieve gains in precision or efficiency, compared to conventional designs with similar sample sizes, or to increase the number of elements observed for a given sampling effort. A number of different adaptive sampling strategies exist including ‘sequential sampling’ (Ghosh et al., 1997) and ‘adaptive cluster sampling’ (Thompson and Seber, 1996). Chao and Thompson (2001) considered the problem of optimal selection of new sampling sites to augment a systematic arrangement of sites.

With ‘sequential estimation’ a fixed number of sampling units are collected and the population mean or total is estimated along with a measure of the uncertainty, e.g. confidence interval bounds or the *CE,* under some assumed spatial pattern of the disease or pest. If the predicted uncertainty is within a

desired value sampling ceases, otherwise additional units are added sequentially until the desired uncertainty is obtained. With sequential sampling for classification, sampling ends when sufficient numbers of individuals are collected so that conclusions regarding the population can be drawn with a desired degree of certainty. Sequential sampling designs have been used in a number of studies for pest and disease monitoring in specialty crops (e.g. Allsopp, 1990; Hamilton and Hepworth, 2004; Turechek and Madden, 1999; Gent et al., 2007). Sequential sampling can behave very poorly if the sequential sampling scheme is stopped before the variation in the population is captured because of having sampled similar units or when the population is auto-correlated (Robinson and Hamann, 2008).

In ‘adaptive cluster sampling’ the set of primary sampling units is selected using a probability method, and whenever the observed property of interest in a primary sampling unit meets a given criterion (e.g. weeds are detected in a plot) neighboring sampling units are added to the sample (Figure 2.8). Adaptive cluster sampling will usually provide an improved indication of the spatial extent of the population of interest than non-adaptive designs. The selected sample will generally not provide a design-unbiased estimator of the population mean or total because inclusion probabilities may not be completely known. Thompson (1992) describes design-unbiased estimators of the population mean and total for several adaptive cluster and stratified adaptive cluster designs.

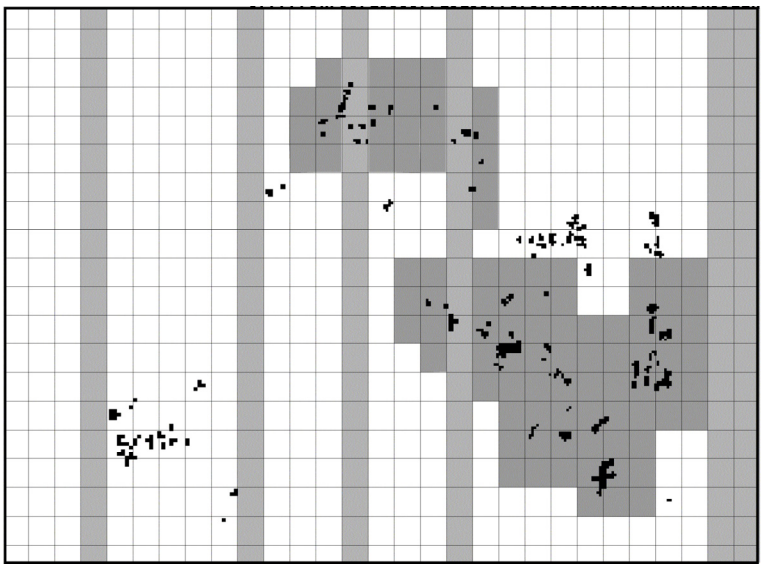


Figure 2.8: An adaptive cluster sampling design with initial SR selection of six strip plots. The final sample is highlighted.

2.6 The accuracy of an estimator

The accuracy of an estimator can be considered the accumulation of two important properties: bias (systematic error, the difference between the expected value of an estimator and the true parameter value) and precision (random error or noise). We can decompose the mean squared error (MSE) into a sum of the bias and variance of the estimator:

$$\mathrm{MSE} = \mathrm{var}(\hat{Q}) + \mathrm{bias}^2(\hat{Q}) \tag{2.2}$$

Both quantities are important and need to be sufficiently small to achieve good estimations. Bias cannot be detected from the data (Mandel, 1964). The much desired property of unbiasedness is a consequence of UR (or IUR) sampling. An important principle in sampling is that variances are governed largely by sample size rather than by the proportion of the population included in the sample, except when sampling small populations (Stuart, 1984; Thompson, 1992). Designing systems to meet requirements for unbiased sampling makes it possible then to achieve a desired precision by controlling sample size.

The total variance (MSE) of an unbiased estimator can be written

$$\mathrm{MSE}(\hat{Q}) = \mathrm{var}(\hat{Q}) = \mathrm{var}(Q) + \mathrm{var}_e(\hat{Q}) \tag{2.3}$$

where $\mathrm{var}(\hat{Q})$ is the total (observed) variance, $\mathrm{var}(Q)$ is the biological (or natural, intrinsic) variance (i.e. the true variability between individuals in the population), and $\mathrm{var}_e(\hat{Q})$ is the sampling error variance. The biological variance is the only meaningful variance for management purposes. Equation 2.3 can also be expressed in terms of the dimensionless squared coefficient of variance (CV = SD/mean, where SD is the standard deviation) and the squared coefficient of error (CE = SEM/mean, where SEM is the standard error of the mean) as

$$\mathrm{CV}^2(\hat{Q}) = \mathrm{CV}^2(Q) + \mathrm{CE}^2(\hat{Q}) \tag{2.4}$$

For a multistage nested design, the total estimator variance can be decomposed into components due to each stage of sampling (Cochran, 1977; Baddeley and Jensen, 2004). Examples are provided by Wulfsohn et al. (2010) and Aravena et al. (2010), respectively, for optimizing estimators of canopy surface area and fruit yield. In many cases it is sufficient to devise sampling schemes so that the contribution of sampling error variance to the total observed variance is small compared to the biological variance. The convention is to aim for $\frac{1}{5}\mathrm{CV}^2 \le \mathrm{CE}^2 \le \frac{1}{2}\mathrm{CV}^2$ to achieve a balance between precision and cost. Gardi et al. (2007b) describe handheld software that can be used to assist in collecting data using multistage stereological designs and obtain estimates of the variance contributions due to each stage of sampling.

The coefficient of error of any estimator $\hat{Q}$ can be calculated based on k independent realizations of the estimator $\{\hat{Q}_1, \hat{Q}_2, \ldots, \hat{Q}_k\}$ by applying:

$$\mathrm{CE}^2(\hat{Q}) \approx \left(1 - \frac{1}{K}\right) \frac{1}{(k-1)} \frac{\sum_{i=1}^{k} (\hat{Q}_i - \bar{\hat{Q}})^2}{\left(\bar{\hat{Q}}\right)^2} \tag{2.5}$$

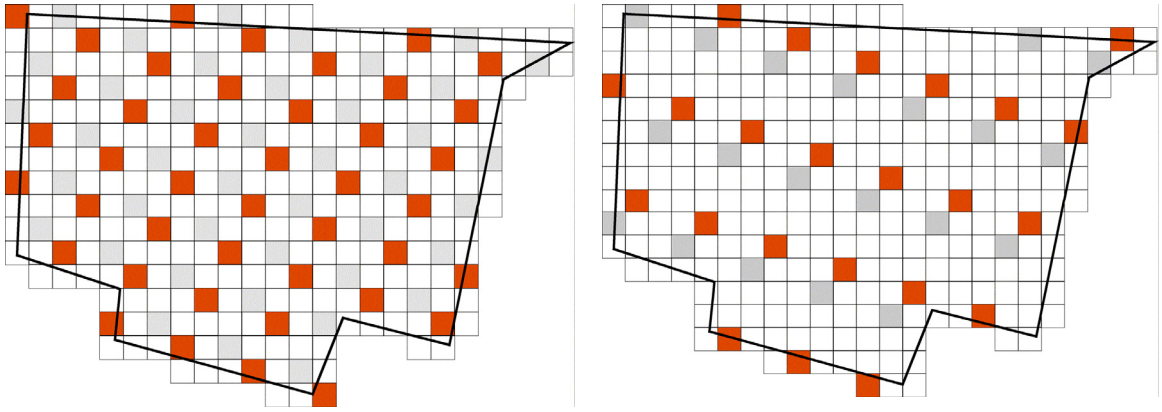
where $\bar{\hat{Q}} = \frac{1}{k}\sum_{i=1}^{k} \hat{Q}_i$ and K is the number of all possible realizations of $\hat{Q}$. The variance components of a nested design may be estimated by including independent replication at each level of the sampling

design, e.g. to determine optimal allocation of effort across sampling stages from a pilot study (Baddeley and Jensen, 2004).

A variation of independent repeated sampling to estimate the total variance of any complex, multistage design, is provided by the “random groups” (RG) method (Wolter, 1985). We use *k* repeated samples according to the design (e.g. *k* systematic samples for a SUR design) with repetition applied at the primary sampling stage and the sampling fraction scaled proportionally so as to yield the same final sample size. Figure 2.9 illustrates the difference between repeated sampling with independent replication and the RG method for the design shown in Figure 2.1(c). For the design in Figure 2.3, we may use k = 2 replications at the tree level, repeated for say n = 8 randomly selected trees in an orchard, and compute an average *CE*,

$$CE \approx \left[\frac{1}{n} \sum_{i=1}^{n} \frac{\hat{\mathrm{var}}_e(\hat{Q}_i)}{\hat{Q}_i} \right]^{0.5} \tag{2.6}$$

We distribute the work across trees (which have high biological variability) rather than attempt to obtain precise estimates for individual trees. The RG method is generally biased for SUR for which there is generally dependency between samples. In contrast, an unbiased (but still imprecise) estimate of the CE of the proportionator (Section 2.2.2) can be obtained at no extra cost by taking k = 2 independent samples each of size $n/2$ and applying Eq. 2.5. The estimator of the total now used is the average of the two independent estimates, with only a small loss in precision compared to using a single sample of size n (Gardi et al., 2007a). Aravena et al. (2010) used repeated sub-sampling of *sample data* at each sampling stage and variance decomposition to construct a semi-empirical model for the estimator CE.



(a) (b)

Figure 2.9: Repeated-sampling variance estimation procedures for an SUR design with sample size n and period m = 7, cf. Fig. 2.1(c). An estimate of the population total is obtained by computing the mean of the estimates obtained from the two samples. (a) Resampling with SUR period m = 7 and two independent replicates (random-wr starts 1 and 3). The average total sample size is 2n. An estimate of the CE is given by Eq. 2.5 with $\hat{Q}_i = \hat{Q}_{m,i} = m\sum_{j=1}^{[n]} q_j$, k = 2 and K = 7. (b) "Random Groups" procedure with k = 2 replicates each with period $k \cdot m$ = 14 (aggregate period m = 7) and random-wor starts 2 and 6, respectively. The average total sample size is n. An estimate of the CE is given by Eq. 2.5 with $\hat{Q}_i = \hat{Q}_{2m,i} = 2m\sum_{j=1}^{[n/2]} q_j$, k = 2 and K = 7.

2.6.1 Predicting the variance of an estimator from a single sample

In practice, resampling procedures can be prohibitively time consuming and methods to estimate variances from single sample are desirable. Devising suitable variance predictors for SUR designs is generally very difficult because the observations of the sample are not independent. Single-sample variance predictors are generally biased, with the degree of bias depending on the extent to which model assumptions are violated for the population under study. Wolter (1985) discusses the performance of large number of variance predictors. The Poisson distribution, according to which CE = $1/\sqrt{n}$ (n is the sample size), provides a model for counting noise and is often assumed as a starting point for a pilot study. Matherons' transitive approach to modeling the covariogram is the basis of several single-sample variance predictors developed for systematic sampling designs in stereology (Matheron, 1971; Cruz-Orive, 1989). Cruz-Orive (1990, 2004) proposed semi-empirical models for predicting the sampling error variance of a fractionator sample. Maletti and Wulfsohn (2006) evaluated the performance of several models and resampling applied to fractionator sampling of trees. Several estimators have been proposed motivated by the problem of estimating the volume of a structure from a systematic sample of area sections (e.g. Matheron, 1971; Gundersen and Jensen, 1987; Cruz-Orive, 1989; Kiêu, 1997, Gundersen et al., 1999; García-Fiñana and Cruz-Orive, 2004). Wulfsohn et al. (2010) showed that similar models could be used to accurately predict variance components of a canopy surface area estimator that combined fractionator sampling of leaves and point counting of leaf area. Point counting (Figure 2.2) using grids of 1.8 and 4.3 cm^2 were found to perform as well as image analysis and a commercial area meter, respectively, for estimating the surface area of a chrysanthemum canopy.

2.7 Sources of bias and unbiased counting rules

The act of sampling a spatial structure by observing it in a bounded window or plot complicates the estimation of geometric characteristics by loss of information due to edge effects. Baddeley (1999) identified two main types of edge effects: 'sampling bias' where the probability of observing an object depends on its size and 'censoring effects' where the full extent of the object to be measured cannot be observed within the window. Sources of non-sampling biases include projection artifacts, operator effects, and biases arising due to difficulties in defining the features of interest.

There are two general approaches to dealing with sampling bias:

(1) The use of unbiased sampling rules, e.g. the 'disector' (Sterio, 1984, Figure 2.10(a)-(b)), the tiling rule (Gundersen, 1978, Fig. 2.10(c)), and the 'associated point rule' (Miles, 1978) (Figure 2.10(d)). These generally require some information from outside the sampling window. We have used the disector counting/sampling rule (a) within a SUR design to estimate the total yield of seed cucumber grown as a row crop in farmer fields, achieving precisions of 10% or better (unpublished report).

(2) The use of weighted sampling methods. Usually these are of the spatial Horvitz-Thomson type, where spatial sampling bias is corrected by weighting each sampled object by the reciprocal of the sampling probability, e.g. the domain can be tessellated with copies of the sampling window and then each sampled object is weighted by the reciprocal of the number of windows that intersect it.

Observation bias due to occlusions of features observed under projection, such as in a 2D image, can be substantial. Wulfsohn et al. (2006b) found occlusion biases in counting of flowers and fruit on small trees of –18% to –31%. In combination with occlusion errors, biases (both positive and negative) can arise because of errors in thresholding and feature recognition. Several studies reporting on algorithms for automatic recognition of apples using 2D images of trees have achieved successful recognition rates from 56% to 100% (typically 85-97%). Rates of false positives were usually less than 5% (Bulanon et al., 2002; Stajnko et al., 2004; Tabb et al., 2006) but could be as high as +15–83% (Stajnko et al., 2004). Bulanon et al. (2002) reported biases of –18% (average of 10 images) under poor lighting conditions. The data of Stajnko et al. (2004) indicate biases of –13% to +21% for averages from thermal images of 20 trees obtained at four development stages.

In some situations there can also be considerable error in recording samples. In surveys of insects in a field it is highly unlikely that every individual will be captured or detected. When carrying out observations of hard-to-detect or rare events such as some weed species or diseases along transects or in plots, the probability of detecting an object depends in some way on its distance from the observer as well as on its size. Thompson (1992) presents methods for estimating and modeling detectability, i.e., the probability that an object in a selected sampling unit is observed.

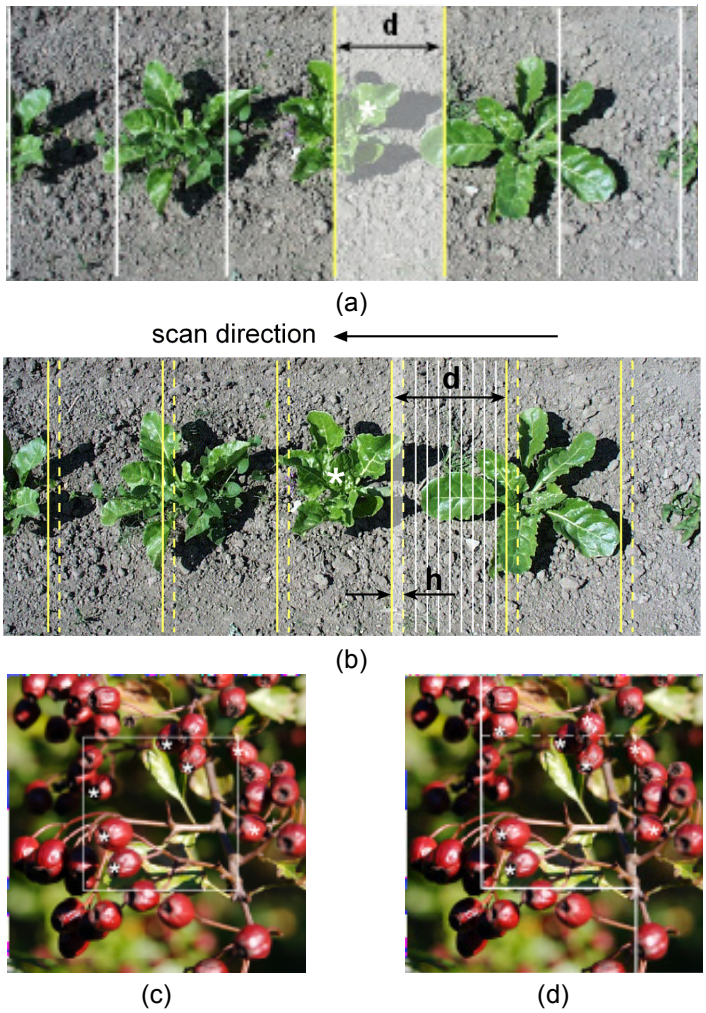


Figure 2.10: Unbiased counting rules used to select objects with equal probability in UR positioned finite windows. (a) 'Disector' or 'first-time' rule (Sterio, 1984). An object is sampled if it overlaps the strip in question but does not cross the right border of the strip (i.e. an object is selected by the first strip which intersects it, when the strips are ordered from right to left). The plant marked (*) is sampled by the highlighted strip. (b) Illustration of 'physical disector' sampling rule (Sterio, 1984). Strips narrower than the horizontal width of any object are used in this example to develop a fractionator with h/d = 1/10 sampling fraction for a 'double systematic subsampling' design. The dashed line is called a counting line while the fulldrawn line is called a lookup line. An object is sampled by a strip of width h if it intersects the counting line but does not intersect the lookup line. The plant marked with an asterisk is sampled by the highlighted strip. (c) Associated point rule (Miles, 1978) samples the 7 fruit indicated with asterisks, which all have their (dimensionless) left tangent point located in the sampling window. (d) Tiling rule (Gundersen, 1978) applied to sample the 8 fruit indicated with asterisks, all of which overlap the window and do not cross the infinite boundary with fulldrawn lines. (Photograph of plants in (a) and (b) by Hans-Werner Griepentrog, University of Copenhagen).

2.8 Remarks

The proper application of sampling principles is necessary to obtain design- or model-unbiased estimators of population attributes and their variability and this is equally true whether variables are measured manually or automated using non-destructive sensors – a machine moving through a field or orchard, equipped with sensors to measure crop yield or structure is performing 'spatial sampling' (Wulfsohn et al., 2004). Equipped with the basic sampling and variance reduction techniques reviewed in this section there is considerable flexibility to design practical sampling protocols for precision farming of soils and specialty crops. Prior knowledge and ancillary information obtained by remote sensing and non-destructive soil and plant sensors can be used within a random sampling framework to design protocols that provide an appropriate balance between statistical precision and cost (time and technology investment).

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