CHAPTER 8

SAMPLING RARE POPULATIONS

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8.1 METHODS FOR SAMPLING RARE POPULATIONS

8.1.1 Principles

Rare populations, such as downed trees or single valuable living trees, are often important with respect to biodiversity, for example. The problem is that such populations are difficult to cope with in a normal forest inventory. In the sample plot inventory method designed for surveying the mean volume of living trees, the area of a sample plot is typically very small relative to the total area. In such a case, only a few observations from rare populations (or perhaps none at all) will be obtained. The standard errors may therefore be very large. For these reasons, specific methods have been developed for sampling rare populations. A typical case is that of estimating the volume of downed woody debris in area level (see Ringvall 2000, Ståhl et al. 2001). A few recently developed methods are included in this chapter, but there are numerous others for those interested, see Bebber et al. (2003) and Williams and Gove (2003), for example.

The estimating of wildlife populations constitutes a field of application which is in many respects different from tree surveys. Animals can move and hide, and the sampling process itself may cause them to move. Thus a true sampling frame may not exist and the probability of any one animal being sampled has in many cases been calculated after the sample has been drawn (Schreuder et al. 1993). Hence the probability of errors is also greater in animal surveys. The primary parameters of interest in wildlife surveys are usually population size or density, birth and mortality rates and immigration and emigration rates.

A. Kangas and M. Maltamo (eds.), Forest Inventory – Methodology and Applications, 119–139.

8.1.2 Strip sampling

Strip sampling is often used for rare population inventories. Since this method typically covers a large area compared with plot sampling, it means a lot of work when applied to living trees. Since the autocorrelation between two subsequently located parts of the strip is high, this method is also inefficient for use with living trees. Observations on rare populations are typically located so far apart, however, that autocorrelation is not a problem. The workload in strip inventory is not prohibitive when rare populations are involved.

Strip sampling can be regarded as a sample plot inventory in which the plots are very large. Computationally, the easiest case is when the area is divided into N non-overlapping strips and n strips are selected from these by simple random sampling. The strips may also be selected using a certain spacing, however, in which case they may be (at least partially) overlapping. In sampling downed trees, the case may be either that 1) whole logs are measured if the butt is located on the strip, or that 2) only the parts of the logs that are located on the strip are measured. The former assumption is used in this chapter. Sometimes the same formulae may apply to both cases. For volume estimation, for instance, both definitions can be employed in the same formulae. For estimating the number of downed logs, however, the first case is more straightforward.

One problem with this approach is that the strips are usually of different lengths and areas, so that their mean is an inefficient estimator for population mean (Shiver and Borders 1996). This problem can be overcome by using the strip area as an auxiliary variable x. The estimator for the total volume (or other variable of interest) will then be (see Stehman and Salzer 2000)

$$\hat{T}_R = \hat{R}A_T = \frac{\sum_{i=1}^{n} V_i}{\sum_{i=1}^{n} A_i} A_T , \tag{8.1}$$

where V_i is the total volume of strip i , A_i is the area of strip i and A_T is the total area.

If the mean volume per hectare is of interest, it is enough to estimate the ratio $\hat{R} = \sum_{i=1}^{n} V_i \Big/ \sum_{i=1}^{n} A_i$. The estimator of variance for the estimator (8.1) is obtained with (Cochran 1977)

$$Var(\hat{R}) = \frac{1}{\mu_x^2} \frac{\hat{s}_u^2}{n} \left(\frac{N-n}{N} \right), \tag{8.2}$$

where

$$\hat{s}_u^2 = \frac{\sum_{i=1}^{n} V_i^2 + \hat{R}^2 \sum_{i=1}^{n} A_i^2 - 2\hat{R} \sum_{i=1}^{n} A_i V_i}{n-1} \quad \text{and}$$

$\mu_x = \frac{A_T}{N}$ is the mean area of strips, N is the total number of strips in the area and n is the number of sampled strips.

The variance estimator for total volume is obtained by multiplying the variance of the ratio (8.2) by A_T^2. The true mean area of the strips is often unknown and can be replaced with the mean area in the sample (Thompson 1992, p. 62).

8.1.3 Line intersect sampling

Line intersect sampling (LIS) was first presented by Canfield (1941) and was developed in the 1960s to sample the amount of slash and fuel wood remaining after logging and for estimating road lengths, for example (Warren and Olsen 1964, Matérn 1964, van Wagner 1968). Nowadays, it is often used for estimating the number of downed trees in biodiversity contexts.

Assume a line located in an area in a direction θ. This method implies that all the objects intersected by the line are included in the sample. The probability of a tree being selected is dependent on the length of the sampling line L and the effective length of the tree l', i.e. its (maximum) length perpendicular to the sampling line. If the tree is assumed to be a line (i.e. it has no width) this can be calculated directly from its angle γ with the sampling line, $l' = l \sin(\gamma)$.

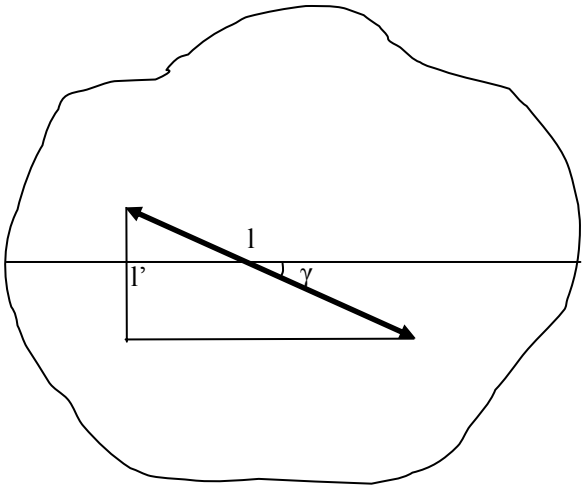


Figure 8.1 Scheme of line intersect sampling.

The total value of a variable of interest, y, per area A, according to the Horwitz-

Thompson estimator (see sections 2.1 and 2.8), is then (Kaiser 1983 p. 969)

$$\hat{T} = \frac{1}{L}\sum_{i=1}^{n}\frac{y_i}{l'(\theta)}, \tag{8.3}$$

where the effective length is given as a function of the sampling line angle θ. If the tree is not horizontal but tilted at an angle δ_i, the effective length will also depend on $cos(\delta_i)$. If the angles are measured, there is no need to make any assumptions concerning their distribution. This is quite tedious, however. If it is assumed that the sampling line angle θ varies uniformly between 0 and π, the expected value of the effective length of tree i is $E(l_i'(\theta)) = 2l_i/\pi$ (Kaiser 1983). From these results an estimator for the total value of y per square metre can be obtained with (De Vries 1973)

$$\hat{T} = \frac{\pi}{2L}\sum_{i=1}^{m}\frac{y_i}{l_i}, \tag{8.4}$$

where L is the the total length of the lines (m), l_i is the lengtht of the tree i (m), y_i is the variable of interest for unit i (e.g. volume, weight, length) and m is the number of units observed.

If the volume of the trees is defined using Huber's formula as

$$v_i = \pi\left(\frac{d_i}{2}\right)^2 l_i, \tag{8.5}$$

where d_i is the (intersectional) diameter of tree i (cm), the equation (8.4) can be transformed to (De Vries 1973 p. 8)

$$\hat{T} = \frac{\pi^2}{8L}\sum_{i=1}^{m} d_i^2 . \tag{8.6}$$

This formula gives the volume directly in cubic metres per hectare. If the interest lies in estimating the length of downed trees, a count of the trees intercepting the line is sufficient, since the length is then reduced from (8.4). If the interest lies in the volume, is will suffice to measure the diameters of the trees. If other characteristics such as the number of downed trees per hectare are desired, the lengths of the trees need to be measured as well.

The diameter of an intercepting tree can be measured either in the middle of the log, at both ends (using Smalian's volume formula) or at the point where the tree intersects with the line. The main issue is to obtain an unbiased estimate of the mean diameter of the trees. The sampling line chooses one diameter from each tree, and the mean of these gives an unbiased estimate for the mean in the population (Van

Wagner and Wilson 1976). Therefore all these methods given fairly similar results, at least in large samples.

The variance of the LIS estimator can be calculated from the variation between the lines (De Vries 1974 p. 133):

$$Var(\hat{T}) = \frac{\sum_{j=1}^{n} L_j (\hat{T}_j - \hat{T})^2}{(n-1)\sum_{j=1}^{n} L_j}, \tag{8.7}$$

where n is the number of lines, $\hat{T}_j$ is the total volume per hectare estimated from line j, $\hat{T}$ is the total volume per hectare in the area and L_j = length of line j.

The formulae presented above assume that the lines are measured in random directions, or that the trees have fallen in random directions. If these assumptions are not correct, the formulae may give inefficient estimates. In many cases, however, the downed trees may tend to fall in a certain direction, with exactly the same orientation in the extreme case. Bell et al. (1996) noted in a simulation study that one single sampling line gave large errors for certain mean angles. This probably holds true for several parallel lines, but lines in the shape of a square or L gave practically as good estimates with all mean angles.

There is no need as such to make any assumptions concerning the orientation of fallen trees in random sampling, however, as the inference is based on the design and the population of fallen trees is assumed to be fixed. If the sampling lines are located systematically, the situation is similar to ordinary systematic sampling: the inferences are based on the assumption of random orientation of the trees if formulae for random sampling are to be used.

Example 8.1

Antti Mäkinen

The inventory was carried out over an area of about 150 hectares at Tytinmäki, employing 6 east-west lines located at 100 metre intervals. The lines were directed from. The diameters of all downed trees intersecting the lines were measured at the intersection point (Table 8.1) and the volume per hectare for each line was calculated with $\hat{T}_i = \frac{\pi^2}{8L_i}\sum_{j=1}^{m_i} d_j^2$. The results for each line i are presented in the Table 8.2.

Table 8.1 Measured data.

Tree	Line	d	Tree	Line	d	Tree	Line	d	Tree	Line	d
1	1	4.6	53	2	28.7	115	3	5.8	167	5	9.1
2	1	17.8	54	2	11.1	116	3	13.7	168	5	5.7
3	1	5	55	2	8.9	117	3	14.8	169	5	11
4	1	8	56	2	6.1	118	3	5.9	170	5	7.2
5	1	5.5	57	2	8.8	119	4	26.9	171	5	9.6
6	1	9	58	2	10.4	120	4	12.4	172	5	28.4
7	1	19.3	59	2	5.5	121	4	9	173	5	7.7
8	1	7.6	60	2	16.9	122	4	11.5	174	5	14.9
9	1	10.8	61	2	15.8	123	4	5.7	175	5	7.4
10	1	7.9	62	2	14.7	124	4	8	176	5	12.2
11	1	21	63	2	6.1	125	4	9.3	177	5	8.1
12	1	8.2	64	2	6.2	126	4	12.4	178	5	10.1
13	1	13.5	65	2	13.6	127	4	7.5	179	5	13.8
14	1	16.5	66	2	5.8	128	4	8.9	180	5	7.7
15	1	10	67	2	7.8	129	4	10.3	181	5	11.5
16	1	7	68	2	5.7	130	4	7	182	5	15.9
17	1	5.5	69	3	7.4	131	4	9.5	183	5	5.2
18	1	31	70	3	5.8	132	4	16.1	184	5	7
19	1	24.7	74	3	5.8	133	4	6.2	185	5	25.1
20	1	7.5	75	3	5.5	134	4	8.7	186	5	12.5
21	1	8.4	77	3	6.1	135	4	16	187	5	24.6
22	1	13.5	80	3	7.7	136	4	11.8	188	5	13.2
23	1	16.5	81	3	5.4	137	4	31.5	189	5	8.1
24	1	9	83	3	7.4	138	4	9.2	190	5	15.8
25	1	12	84	3	5.2	139	4	6.9	191	5	5.3
26	1	8.5	87	3	7.3	140	4	22.6	192	5	5.9
27	1	5.4	89	3	11.3	141	4	12.2	193	6	6.4
28	1	5.6	90	3	6.8	142	4	8.2	194	6	10.7
29	1	5.8	91	3	10.4	143	4	17.7	195	6	13.3
30	1	18	92	3	29.3	144	4	5	196	6	5.2
31	1	9	93	3	5.1	145	4	8.6	197	6	28.5
32	2	9	94	3	9.9	146	4	13.8	198	6	12.5
33	2	22.4	95	3	25.7	147	4	29.2	199	6	15.8
34	2	11.8	96	3	17.9	148	4	7.5	200	6	14.8
35	2	7.4	97	3	18.9	149	4	12.5	201	6	5.4
36	2	7	98	3	9.7	150	4	16	202	6	9.9
37	2	13.4	99	3	6.7	151	4	12	203	6	5
38	2	12	100	3	7.5	152	4	10.9	204	6	14.6
39	2	33.4	101	3	14.7	153	4	14.1	205	6	7
40	2	14.5	102	3	13.6	154	4	11.2	206	6	19.8
41	2	7.2	103	3	7.3	155	4	6	207	6	7.3
42	2	6.5	104	3	5.9	156	4	5.8	208	6	12.4
43	2	18.3	105	3	14	157	4	5.4	209	6	11.6
44	2	26.2	106	3	11.3	158	4	6	210	6	23.2
45	2	11.2	107	3	5.4	159	4	9.7	211	6	16.8
46	2	7.8	108	3	11.2	160	4	6.3	212	6	6.7
47	2	11.4	109	3	5.8	161	4	14.6	213	6	14.9
48	2	27.7	110	3	7.7	162	5	6.9	214	6	8.5
49	2	10.8	111	3	13.7	163	5	5.2			
50	2	6.2	112	3	9.8	164	5	11.5			
51	2	8.5	113	3	11.2	165	5	9			
52	2	24.3	114	3	28.6	166	5	8.2			

Table 8.2 The line results.

i	$D_i = \sum_{j=1}^{m_i} d_j^2$	L_i	$\hat{T}_i = \frac{\pi^2}{8L_i} D_i$	$L_i(\hat{T}_i - \hat{T})^2$
1	5238.35	1900	3.401345	3003.639
2	7909.99	1700	5.740329	1988.981
3	5973.66	1800	4.094282	573.3578
4	7420.71	1300	7.042257	7385.942
5	4849.16	1400	4.273151	208.0733
6	4104.17	1300	3.894859	758.4263

The volume per hectare is then the (weighted) mean of T_i or

$$\hat{T} = \frac{\pi^2}{8L}\sum_{i=1}^{6} D_i = \frac{\pi^2}{8 \cdot 9400} \cdot 35496.04 = 4.659$$

and the estimated standard deviation is

$$S_e(\hat{T}) = \sqrt{\frac{\sum_{i=1}^{6} L_i (T_i - T)^2}{(6-1)9400}} = \sqrt{\frac{13918.42}{(6-1)9400}} = 0.544 .$$

8.1.4 Adaptive cluster sampling

Adaptive cluster designs have been discussed at least since the work of Wald in 1947. In an adaptive design the probability of selecting a new unit depends on the value of the variable of interest y in the previous unit. This kind of design is necessarily sequential (Thompson 1990, Thompson and Seber 1996). Adaptive designs have been regarded as useful in cases where some rare characteristic is clustered in the population. For instance, it could be assumed that given one individual of a rare species, other individuals are also likely to exist nearby. Thus concentrating the sample in the neighbourhood of the one known individual is likely to produce others. The neighbourhood may be defined using spatial proximity, or other proximity measures.

The basic design for adaptive cluster sampling includes an initial sample of size n_1, selected using simple random sampling. The selection could be made either with or without replacement (see Chapter 2), but a design without replacement is assumed in this chapter. The mean for this sample is an unbiased estimator of the population mean.

It is assumed that for each sampling unit i there is a neighbourhood A_i, which also includes the unit i itself. If the initial sample is based on a grid of square units, (Figure 8.2), the neighbourhood can be defined, for instance, in terms of

adjacent squares to the left, right, top and bottom of unit *i*. The neighbourhood does not depend on the values of *y* in the units. The neighbourhood is also symmetric, i.e. if *i* is a neighbour to *j*, then *j* is also a neighbour to *i*.

The selection of additional units from the neighbourhood depends on the condition *C*, which can, for example, be defined so that it is satisfied by every value of *y* larger than or equal to a predefined value *c*. If a sample unit *i* satisfies the condition *C*, all the units in its neighbourhood will be included in the sample. If any of those units satisfies the condition, then its will also be included, and so on.

All the units selected as a result of first selecting unit *i* for the initial sample belong to the same cluster, and all the units in one cluster that satisfy condition *C* belong to a same network. Consequently, selecting any of the units in the network results in selecting all the other units as well. The units in the cluster that do not satisfy the condition, i.e., do not belong to the network, are called edge units. Selection of an edge unit does not result in the selection of any other units. These edge units are regarded as networks of size one.

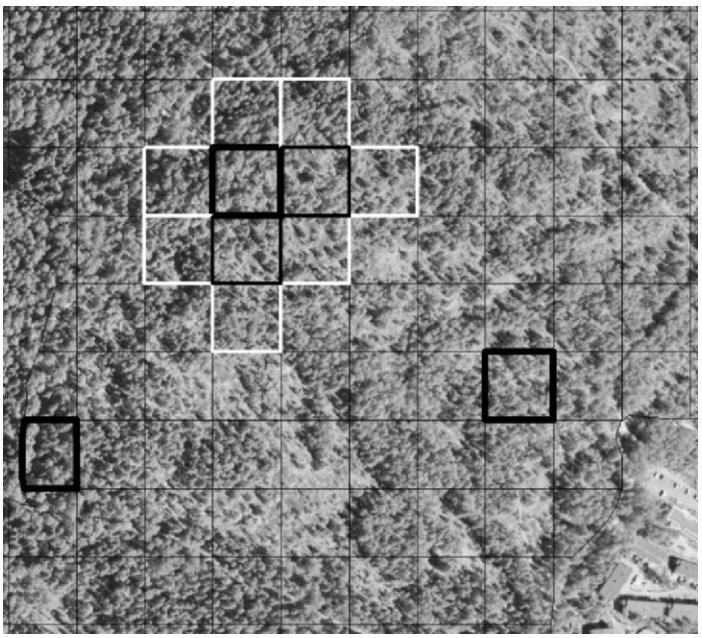


Figure 8.2 Adjusted cluster sampling based on squares. The first-order sample squares are delimited with thick black lines and the additional units with thinner lines. The additional units satisfying condition C are delimited with black lines and those not satisfying the condition with white lines.

Thus each unit will be included in the sample if a) any unit of the network it belongs to is selected, or b) any unit of the network of which unit i is an edge unit is selected (Thompson 1990). Assume m_i to be the number of units in the network to which unit i belongs and a_i to be the number of units in networks of which unit i is an edge unit. Then a_i will be zero if unit i belongs to a network and m_i will be one if unit i is an edge unit. The probability p_i of selecting unit i in any one of n_1 draws will then be

$$p_i = \frac{m_i + a_i}{N} \tag{8.8}$$

and the probability of unit i being included in all the draws will be (Thompson 1990)

$$\alpha_i = 1 - \binom{N - m_i - a_i}{n_1} \Big/ \binom{N}{n_1}. \tag{8.9}$$

In this kind of sample, the classical sample mean is a biased estimator. In principle, a Horwitz-Thompson estimator (see Chapter 2.1) could be used with the inclusion probabilities, but some of the a_i:s, i.e., sizes of networks for which a_i is an edge unit, may be unknown. Therefore the estimator is modified so that only the initial sample of n_1 units and the units belonging to the networks (and satisfying the condition) are used. The modified Horwitz-Thompson estimator is then calculated using the inclusion probabilities for those units, to yield

$$\alpha_i^* = 1 - \binom{N - m_i}{n_1} \Big/ \binom{N}{n_1}. \tag{8.10}$$

If an indicator variable J_i is defined as having the value 0 if the unit i does not satisfy the condition or does not belong to the initial sample and the value 1 otherwise, an unbiased estimator for the mean is obtained using (Thompson 1990)

$$\hat{\bar{y}}_{HT*} = \frac{1}{N} \sum_{i=1}^{v} \frac{y_i J_i}{\alpha_i^*}, \tag{8.11}$$

where v is the number of distinct units in the sample.

To obtain a variance estimator for this, the notation is changed to include distinct networks k instead of units i. The sum of the values of y in network k is denoted as $y_{k.}$. The inclusion probability α_i^* is the same for all units in network k and is denoted with π_k. The probability of one unit belonging to networks j and k is defined as

$$\pi_{jk} = 1 - \frac{\binom{N - m_j}{n_1} + \binom{N - m_k}{n_1} + \binom{N - m_j - m_k}{n_1}}{\binom{N}{n_1}}, \quad (8.12)$$

and an unbiased estimator for the variance of $\hat{\bar{y}}_{HT*}$ would be

$$\mathrm{var}(\hat{\bar{y}}_{HT*}) = \frac{1}{N^2} \sum_{k=1}^{\kappa} \sum_{j=1}^{\kappa} y_k . y_j . (\pi_{kj} - \pi_k \pi_j) / (\pi_k \pi_j \pi_{kj}), \quad (8.13)$$

where κ is the number of distinct networks. Estimates for the mean and its variance can also be calculated with a modified Hansen-Hurwitz type estimator (Thompson 1990).

Adaptive schemes have been used in forestry by Roech (1993, 1994) and Acharya et al. (2000), for instance. Roech (1993) used a probability proportional to size (i.e. point sampling-type estimator) instead of simple random sampling in the initial sample. This type of sampling is potentially very efficient, but may be inconvenient in the field as the final sample size cannot be determined beforehand.

8.1.5 Transect and point relascope sampling

In transect relascope sampling (TRS), logs on the forest floor are viewed using a wide-angle relascope. All trees of a length great enough to fill the angle-gauge at any point on the survey line are included in the sample (Ståhl 1998). In point relascope sampling (PRS), on the other hand, trees are included in the sample only if they fill the angle-gauge when viewed from certain sampling points (Gove et al. 1999).

Estimation in transect relascope sampling (Fig 8.2) is based on the Horvitz-Thompson estimator. The estimator for the total value T of any variable of interest is obtained as (Ståhl 1998)

$$\hat{T} = D \sum \frac{y_i}{l_i (1/\sin v + \cot v \cos w_i)}, \quad (8.14)$$

where D is the distance between the lines (= A/L , i.e. the total area divided by the length of the line), v is the angle of the relascope , l_i = the length of tree i and w_i the angle between tree i and the line.

The probability of a log being included in the sample is calculated as the width h of its inclusion area perpendicular to the survey line divided by the distance D between the lines (Figure 8.3).

However, if it can be assumed that the direction of the transects is random, or that the logs have fallen in random directions, the angle w does not have to be

measured. Then the formula can be simplified (as in the LIS case) to

$$\hat{T} = D\sum \frac{y_i}{l_i(1/\sin v + 2/\pi \cot v)}. \tag{8.15}$$

If the variable of interest is the total length of the fallen trees, the formula can be further simplified, as y_i and l_i cancel each other out. Assuming that the true area A is known, that n transects of fixed length L are laid out in random directions, and that y_{ki} is the volume of log i on transect k and l is its length, the estimator for the total volume can be presented as (Ringvall et al. 2001)

$$\hat{T} = \frac{A}{nL}\left(\frac{1}{\sin v} + \frac{2}{\pi}\cot v\right)^{-1} \sum_{k=1}^{n}\sum_{i=1}^{m_k} \frac{y_{ki}}{l_{ki}}. \tag{8.16}$$

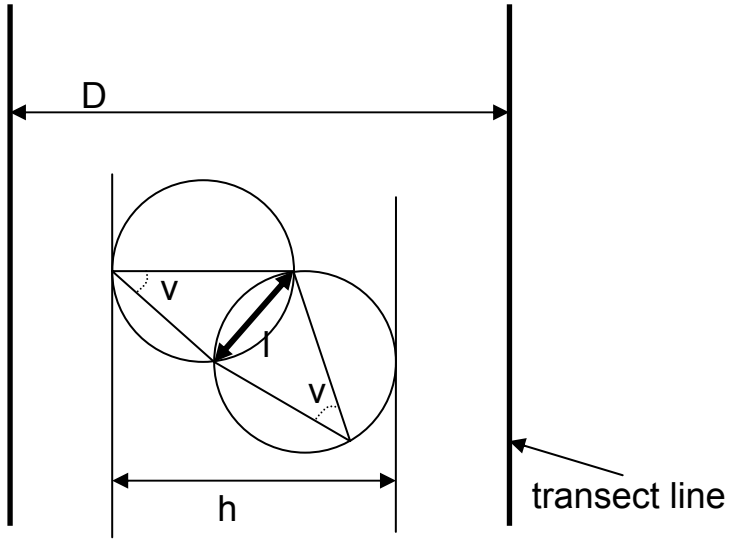


Figure 8.3 The scheme for transect relascope sampling. The tree is represented by the thick arrow. It can be seen with the angle v from any point in the two circles. The measurer cruises the transect line and measures the tree if the transect goes through either of these circles (i.e. the transect goes between the thin lines which define the width of the inclusion area h). The tree in the figure is not included in the sample, since the transect line does not intercept h.

As in angle-count sampling, the first term (excluding area A) can be interpreted here as a relascope factor λ, while l_{ki}/λ is the inclusion probability of the trees. This differs from normal angle-count sampling, however, in that the angles v are much larger. The estimator is comparable to LIS, but it is possible to draw more sample trees with the same sampling line length L. The estimator of variance can be calculated as for LIS, namely by calculating the variation between the transects.

In the case of point relascope sampling, an estimate for a variable y interest for the entire tract, based on a single sampling point k, is estimated as follows (Gove et al. 1999, 2002):

$$\hat{T}_k = A\left(\frac{\pi - v + \sin v \cos v}{2\sin^2 v}\right)\sum_{k=1}^{m_k}\frac{y_{ki}}{l_{ki}^2} = A\lambda\sum_{k=1}^{m_k}\frac{y_{ki}}{l_{ki}^2}, \quad (8.17)$$

where A is the tract area, λ is the relascope factor, which is dependent on the relascope angle v, m_k is the number of observations made from point k and l_{ki} is the length of log i as observed at point k.

As the sampling probability in point relascope sampling is proportional to the squared length of downed trees (length in transect relascope sampling), an estimate for the squared length of downed trees can be obtained simply by counting the trees filling the angle-gauge.

If the points are selected at random, the estimate for the tract total will be the average of the point estimates, and the variance can be obtained from the variation between the points, as in SRS (Gove et al. 2002):

$$\mathrm{var}(\hat{T}) = \frac{1}{n(n-1)}\sum_{k=1}^{n}\left(\hat{T}_k - \hat{T}\right)^2. \quad (8.18)$$

The transect and point relascope sampling methods require slope corrections (section 4.4) as well as normal plot-based methods (Ståhl et al. 2002).

8.1.6 Guided transect sampling

Variables such as downed tree volume might be very difficult to see from remote sensing material, but it is often possible to observe other variables that are correlated with them and in this way to distinguish those parts of the area that are of greatest interest. In guided transect sampling, remote sensing material is used as auxiliary information in order to increase the probability of a transect passing through an area of interest.

Guided transect sampling is a two-stage sampling method. In the first stage, strips of large width are systematically located in the area to be sampled and divided into a grid of cells (Figure 8.4). The objects to be sampled are then selected from among the grid cells in the strips to form a route or strip within them (Figure 8.5). The idea is to select the grid cells forming the route with probabilities proportional to covariate values. The selected route is measured on strip survey principles, for example.

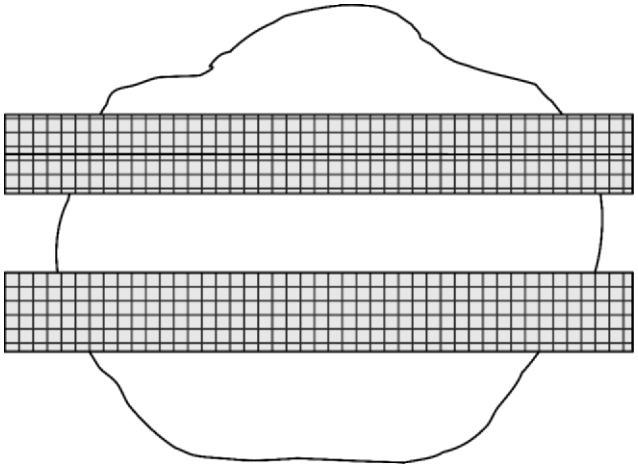
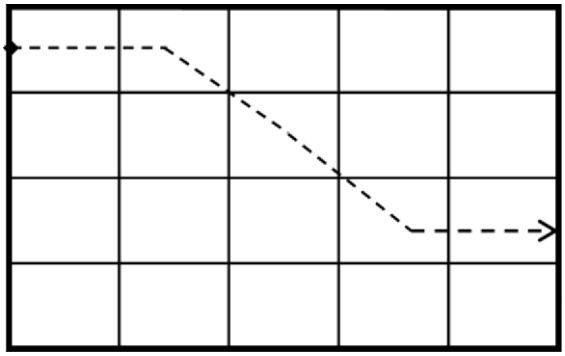


Figure 8.4 Two transects selected from an area.



Figuer 8.5 A route within one transect. .

The route, i.e. the grid cells to be measured, can be selected in several ways, e.g. by allowing only transitions from one cell to a neighbouring cell in an onward grid cell column (Figure 8.4), or else transitions to any cell in an onward column (within the first-phase strip). Furthermore, a probability can be calculated for each transition, so that the route is formed step by step. Another possibility is to calculate the probability for the whole route at one time. In this case, a large number of possible routes are first generated without considering the covariate data and the final route is selected from among these, based on PPS sampling using the sum of the covariate values of the grid cells through which the route passes (scaled to the sum of that for all routes) as the probability value (Ståhl et al. 2000); viz,

$$q = \frac{Q_i}{\sum_{k=1}^{K} Q_k}, \tag{8.19}$$

where

$$Q_k = \sum_{j=1}^{m_k} x_{kj},$$

given that x_{ki} is the covariate value for route k at cell j, m_k is the number of cells on route k, and the covariate value is the pixel value for a satellite channel or numerical aerial photo channel, for example.

Selection is based on arbitrary probabilities, and the results of the inventory are calculated using the Horwitz-Thompson estimator. The estimate for the total value is (Ståhl et al. 2000)

$$\hat{T}_i = \sum_{j=1}^{m_i} \frac{y_{ij}}{\pi_{ij}}, \tag{8.20}$$

where y_{ij} is the variable of interest in strip i and grid cell j and π_{ij} is the inclusion probability of grid cell j in strip i

In the case presented here, the inclusion probability can be calculated as the sum of the covariate values for all the routes including cell j divided by the sum of all covariate values:

$$\pi_{ij} = \frac{\sum_{s \in S} Q_s}{\sum_{l \in L} Q_l}. \tag{8.21}$$

The variance of this estimator could in principle be calculated using the Horwitz-Thompson variance estimator (2.2), but unfortunately not all the joint inclusion probabilities π_{ij} are larger than zero, as is required (i.e. only one cell is selected from each column). The variance could nevertheless be estimated from the variation between the first-stage strips.

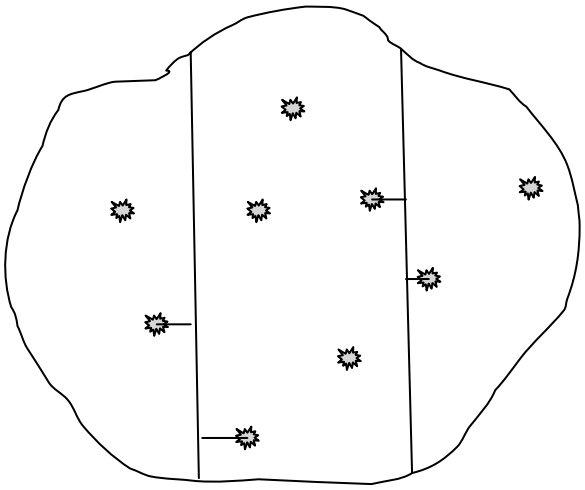


Figure 8.6 The scheme for line transect sampling.

8.2 WILDLIFE POPULATIONS

8.2.1 Line transect sampling

Line transect sampling (LTS), which has been used for estimating the density of wildlife populations (see Buckland et al. 1993), is based on (randomly located) lines on which the objects of interest (e.g. game animals) are observed. The objects themselves are assumed to be randomly distributed in the area (Burnham et al. 1980 p. 14). It is assumed that the probability of observing object i depends on the distance from the line, i.e., the longer the distance the smaller the probability of observation. There are four assumptions on the reliability of the estimates depends (Burnham et al. 1980 p. 14):

1. The probability directly on the line is one, i.e. objects on the line are never missed.
2. The objects do not move before or after being sighted, i.e. each animal is counted, and is counted only once.
3. Distances and angles are measured exactly, and
4. Sightings do not depend on each other but are independent events.

The distance is measured as a perpendicular (or right-angle) distance from the line (Figure 8.6). If it cannot be measured directly, it can be calculated from the sighting distance and the sighting angle (the angle between the transect and the line of sight) .

Given the function $g(x)$ describing the probability of observation as a function of distance x, an unbiased estimate of the density D is obtained as (e.g. Burnham et al. 1980)

$$\hat{D} = \frac{n}{2L\hat{a}}, \tag{8.22}$$

where

$$\hat{a} = \int_0^w g(x)dx, \tag{8.23}$$

w is the maximum distance at which observations are made, and $\hat{a}$ can be interpreted as half of the effective strip width.

This formula can be rewritten in the form (Schreuder et al. 1993, p. 329)

$$\hat{D} = \frac{n\hat{f}(0)}{2L}, \tag{8.24}$$

where n is the number of observations along the line, *f(0)* is the detectability curve, i.e. the probability of detection evaluated at distance 0, assuming $f(x) = g(x)/a$, i.e. *f(x)* is similar to *g(x)* except that it is scaled to integrate to one, and L is the length of the line.

The function g can be estimated using the exponential probability distribution, for example, as

$$g(x) = e^{-\lambda x}. \tag{8.25}$$

Although estimating the detectability curve is not easy, once achieved, it can be used to determine the density, as (Gates et al. 1968 p. 138)

$$\hat{D} = \frac{n}{2L\hat{C}}, \tag{8.26}$$

where

$$\hat{C} = \frac{\sum_{i=1}^{n} x_i}{n-1}.$$

In this and all other formulae based on (8.22), $\hat{a}$ can be interpreted in the manner of a mean sighting distance. The variance of this estimator can be calculated from the variability between the independent lines. The overall density is (Schreuder et al. 1993 p. 329)

$$\hat{D}_{LTS} = \frac{\sum_{i=1}^{R} l_i \hat{D}_i}{L}, \tag{8.27}$$

where l_i is the length of transect i, R is the number of transects and L is the total length of the transects. The variance is then

$$S^2_{D_{LTS}} = \frac{\sum_{i=1}^{R} l_i (\hat{D}_i - \hat{D}_{LTS})^2}{L(R-1)}. \tag{8.28}$$

8.2.2 Capture-recapture methods

There are many variations on capture-recapture methods for estimating the sizes of animal populations (Krebs 1998). The simplest one was developed for closed populations (i.e. it is assumed that no immigration or emigration takes place). In this approach a sample of n_1 individuals is first captured, marked and released. Then, at a later time (after the animals have been re-distributed over the area), a new sample of n_2 animals is captured and the number m of marked animals among them is calculated.

The traditional estimator for the capture-recapture scheme is the Petersen estimate, or Lincoln index (Seber 1982, 1986, Shiver and Borders 1996, p. 329)

$$\hat{N} = \frac{n_1 n_2}{m}, \tag{8.29}$$

where n_1 and n_2 are the animals sampled on the first and second occasions, respectively, and m is the number of marked animals among those captured on the second occasion. This estimate is biased, however, and another, less biased, formulation has been proposed (Pollock et al. 1990, p. 10):

$$\hat{N} = \frac{(n_1+1)(n_2+1)}{(m+1)} - 1. \tag{8.30}$$

This modified version was originally given by Chapman (1951). The first model is based on the assumption of a binomial distribution, or sampling with replacement, and the latter on a hypergeometric distribution, or sampling without replacement (Seber 1986, p. 274). Even this estimate may be highly erroneous with values of m under 10, however. The variance of this estimator can be approximated as (Seber 1982)

$$Var(\hat{N}) = \frac{(n_1+1)(n_2+1)(n_1-m)(n_2-m)}{(m+1)^2(m+2)}. \tag{8.31}$$

Many other, more complex capture-recapture methods for open populations and multiple captures have been based on this same idea (e.g. Seber 1982, 1986, Otis et al. 1978, Pollock et al. 1990).

One can also decide before the second occasion to continue until a fixed number m of marked animals are captured. In such a case the estimation is indirect, and the estimator (without replacement) is (Shiver and Borders 1996, p. 333)

$$\hat{N} = \frac{(n_1 + 1)n_2}{m} - 1 , \tag{8.32}$$

with the (approximate) variance estimator

$$Var(\hat{N}) = \frac{(n_1 - m + 1)(\hat{N} + 1)(\hat{N} - n_1)}{m(n_1 + 2)} . \tag{8.33}$$

Besides the requirement for a closed population, the basic assumptions behind the capture-recapture model are (Otis et al. 1978, Pollock et al. 1990, Schreuder et al. 1993)

1. All animals have a similar probability of capture.
2. The marked individuals are randomly distributed among the population after the initial capture.
3. The marks do not get lost or overlooked.
4. Marking does not affect the probability of recapture.

The first of these assumptions is likely to be violated, as the probability of capturing males, for instance, may be greater than that of capturing females. Likewise the fourth one may be violated, as the animals captured on the first occasion may be more wary the next time, so that the probability decreases, or in some cases they may become "trap happy", i.e. the probability of capture may increase.

8.2.3 The wildlife triangle scheme

Wildlife populations in Finland are monitored using a triangle census programme that began in the late 1980's (Lindén et al. 1996). The base unit is a permanent route of length 12 km that forms an equilateral triangle (each side is 4 km). These wildlife triangles are traced out by local hunteing clubs and censused twice a year by volunteers. Tetraonids (capercaillie *Tetrao urogallus*, black grouse *Tetrao tetrix* L, hazel grouse *Bonasia bonasia* L. and willow grouse *Lagopus lagopus* L.) are censused in a belt of width 60 m by a chain of three people in mid-August, the total census area covered by one triangle thus being 0.72 km^2. The whole monitoring programme, comprising some 1500 triangles at present, is coordinated by the Finnish Game and Fisheries Research Institute (Lindén et al. 1996). The triangles are not randomly located, however.

In the wildlife triangle scheme all birds are assumed to be detected in the

above-mentioned 60m belt. Thus the method is essentially a strip census, a special case of line transect sampling with a probability of 1 for detecting birds over the whole strip. The density can then be estimated simply by

$$D = \frac{n}{A} = \frac{n}{2l\mu}, \tag{8.34}$$

where A is the area of the strip, l is its length and 2μ is its total width (Högmander 1995).

In winter counts, when animal tracks in the snow are counted, the situation is more complicated. The counting is done either after a snowfall or by checking the triangle twice and either marking or covering the tracks on the first occasion, so that the counting proper is done the next morning (Lindén et al. 1996). All tracks intercepting the triangle are counted. Counts of this kind are used for calculating the relative densities of 34 mammal species, including mountain and brown hares, red and flying squirrels, red and arctic foxes, pine marten and so on. These relative densities could also be transformed to absolute densities, but such calculations are not usually made.

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