

Quantitative Analysis by the Point-Centered Quarter Method

Kevin Mitchell

Department of Mathematics and Computer Science
Hobart and William Smith Colleges
Geneva, NY 14456
mitchell@hws.edu

2007.06.25; Revised 2015.07.15

Abstract

This document is an introduction to the use of the point-centered quarter method. It briefly outlines its history, its methodology, and some of the practical issues (and modifications) that inevitably arise with its use in the field. Additionally this paper shows how data collected using point-centered quarter method sampling may be used to determine importance values of different species of trees and describes and derives several methods of estimating plant density and corresponding confidence intervals. New to this revision is an appendix of R functions to carry out these calculations.

1 Introduction and History

A wide variety of methods have been used to study forest structure parameters such as population density, basal area, and biomass. While these are sometimes estimated using aerial surveys or photographs, most studies involve measurement of these characteristics for individual trees using a number of different sampling methods. These methods fall into two broad categories: plot-based and plotless. Plot-based methods begin with one or more plots (quadrats, belts) of known area in which the characteristics of interest are measured for each plant. In contrast, plotless methods involve measuring distances for a random sample of trees, typically along a transect, and recording the characteristics of interest for this sample. The point-centered quarter method is one such plotless method.

The advantage to using plotless methods rather than standard plot-based techniques is that they tend to be more efficient. Plotless methods are faster, require less equipment, and may require fewer workers. However, the main advantage is speed. The question, then, is whether accuracy is sacrificed in the process.

Stearns (1949) indicated that the point-centered quarter method dates back at least 150 years and was used by surveyors in the mid-nineteenth century making the first surveys of government land. In the late 1940s and early 1950s, several articles appeared that described a variety of plotless methods and compared them to sampling by quadrats. In particular, Cottam et al. (1953) compared the point-centered quarter method to quadrat sampling and derived empirically a formula that could be used to estimate population density from the distance data collected. Since the current paper is intended as an introduction to these methods, it is worth reminding ourselves what the goal of these methods is by recalling part of the introduction to their paper:

As our knowledge of plant communities increases, greater emphasis is being placed on the methods used to measure the characteristics of these communities. Succeeding decades have shown a trend toward the use of quantitative methods, with purely descriptive methods becoming less common. One reason for the use of quantitative techniques is that the resulting data are not tinged by the subjective bias of the investigator. The results are presumed to represent the vegetation as it actually exists; any other investigator should be able to employ the same methods in the same communities and secure approximately the same data.

Under the assumption that trees are distributed randomly throughout the survey site, Morisita (1954) provided a mathematical proof for the formula that Cottam et al. (1953) had derived empirically for the estimation of population density using the point-centered quarter method. In other words, the point-centered quarter method could, in fact, be used to obtain accurate estimates of population densities with the advantage that the point-centered quarter method data could be collected more quickly than quadrat data. Subsequently, Cottam and Curtis (1956) provided a more detailed comparison of the point-centered quarter method and three other plotless methods (the closest individual, the nearest neighbor, and the random pairs methods). Their conclusion was:

The quarter method gives the least variable results for distance determinations, provides more data per sampling point, and is the least susceptible to subjective bias. . .

It is the opinion of the authors that the quarter method is, in most respects, superior to the other distance methods studied, and its use is recommended.

Beasom and Hauke (1975) compared the same four plotless methods and also concluded that point-centered quarter method provides the most accurate estimate of density. In a comparison of a more diverse set of methods (Engeman et al., 1994) have a more nuanced opinion of whether the point-centered quarter method is more efficient in the field and more accurate in its density estimates, especially in situations where individuals are not distributed randomly.

In recent years, as the point-centered quarter method has been used more widely, variations have been proposed by Dahdouh-Guebas and Koedam (2006) to address a number of practical problems that arise in the field (multi-stem trees, quarters where no trees are immediately present).

One use of the point-centered quarter method is to determine the **relative importance** of the various tree species in a community. The term “importance” can mean many things depending on the context. An obvious factor influencing the importance of a species to a community is the number of trees present of that species. However, the importance of some number of small trees is not the same as the importance of the same number of large trees. So the size of the trees also plays a role. Further, how the trees are distributed throughout the community also has an effect. A number of trees of the same species clumped together should have a different importance value than the same number of trees distributed more evenly throughout the community.

Measuring importance can aid understanding the successional stages of a forest habitat. At different stages, different species of trees will dominate. Importance values are one objective way of measuring this dominance.

The three factors that we will use to determine the importance value of a species are the density, the size, and the frequency (distribution). Ideally, to estimate these factors, one would take a large sample, measuring, say, all the trees in a 100×100 meter square (a hectare). This can be extraordinarily time consuming if the trees are very dense. The point-centered quarter method provides a quick way to make such estimates by using a series of measurements along a transect.

2 Materials and Methods

The procedure outlined below describes how to carry out point-centered quarter method data collection along a 100 m transect. It can be scaled up or down, as appropriate, for longer or shorter transects. While this analysis can be carried out alone, groups of two or three can make for very efficient data collection. Material requirements include a 50 or 100 meter tape, a shorter 5 or 10 meter tape, a notebook, a calculator or tablet, and a table of random numbers (Table 16) if the calculator cannot generate them.

1. Generate a list of 15 to 20 random two-digit numbers. If the difference of any two is 4 or less, cross out the second listed number. There should be 10 or more two-digit numbers remaining; if not, generate additional ones. List the first 10 remaining numbers in increasing order. It is important to generate this list before doing any measurements.
2. Lay out a 100 m transect (or longer or shorter as required). Multiple transects may be required to survey large areas.

3. The random numbers represent the distances along the transect at which data will be collected. Random numbers are used to eliminate bias. Everyone always wants to measure that BIG tree along the transect, but such trees may not be representative of the community.¹ The reason for making sure that points are at least 5 meters apart is so that the same trees will not be measured repeatedly. Caution: If trees are particularly sparse, both the length of the transect and the minimum distance between points may need to be increased.
4. The smallest random number determines the first sampling point along the transect. At this and every sampling point, run an imaginary line perpendicular to the transect. This line and the transect divide the world into four quarters, hence the name, point-centered quarter method.

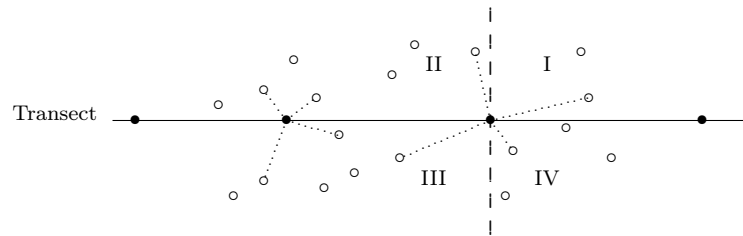


FIGURE 1. Sample points along a transect with the nearest trees in each quarter indicated by ·····.

5. Select one of the quarters. In that quarter, locate the tree nearest to the sampling point. For the purposes of this exercise, to be counted as a “tree” it should have a minimum diameter of 4 cm or, equivalently, a minimum circumference of 12.5 cm. Caution: In other situations, different minimum values may be appropriate.

For each sampling point, record:

- (a) the quarter number (I, II, III, or IV) or other designation (e.g., NE, NW, SE, SW);
- (b) the distance from the sampling point to the center of the trunk of the tree, measured to the nearest 0.1 m (Caution: Review Appendix A on the 30–300 Rule.);
- (c) the species of the tree;
- (d) and the diameter at breast height (DBH) or circumference at chest height (CCH) to the nearest cm, but again observe the 30–300 Rule.

Note: Brokaw and Thompson (2000) have shown that it is important to use the same height to measure the diameter or circumference. They suggest using a standard height of 130 cm and employing the notation D_{130} rather than DBH to indicate this. Whatever height is used should be explicitly noted in the results.

Note: Tree calipers are an easy way to measure diameters, but are often unavailable. It may be more convenient to measure the girth (circumference) of each tree instead of the diameter.

Cautions: If a tape is used to measure DBH, avoid protrusions on the trunk. If calipers are used, an average from three caliper readings is recorded. If girths are recorded, rather than convert each girth to a diameter, change the column heading from DBH to CCH. Make the appropriate scaling adjustment in later calculations, whenever diameters are involved.

See Table 1 for how this data should be organized. Repeat this for the other three quarters at this sampling point. If a tree species cannot be identified, simply record it as A, B, C, etc., and collect and label a sample leaf that for comparison purposes at other quarters and later taxonomic identification.

6. Repeat this process for the entire set of sampling points.

¹Even Cottam and Curtis (1956) warn us about this tendency: “Repeated sampling of the same stand with different investigators indicates that some individuals have a tendency to place the sampling points so that large or unusual trees occur more commonly than they occur in the stand.”

7. Carry out the data analysis as described below.

For trees with multiple trunks at breast height, record the diameter (circumference) of each trunk separately. What is the minimum allowed diameter of each trunk in a such multi-trunk tree? Such decisions should be spelled out in the methods section of the resulting report. At a minimum, one should ensure that the combined cross-sectional areas of all trunks meet the previously established minimum cross-sectional area for a single trunk tree. For example, with a 4 cm minimum diameter for a single trunk, the minimum cross-sectional area is

$$\pi r^2 = \pi(2)^2 = 4\pi \approx 12.6 \text{ cm}^2.$$

3 Data Organization and Notation

The Data Layout

Table 1 illustrates how the data should be organized for the point-centered quarter method analysis. Note the multi-trunk Acacia (8 cm, 6 cm; D_{130}) in the third quarter at the second sampling point. The only calculation required at this stage is to sum the distances from the sample points to each of the trees that was measured. **Note:** A sample of only five points as in Table 1 is too few for most studies. These data are presented only to illustrate the method of analysis in a concise way.

TABLE 1. Field data organized for point-centered quarter method analysis.

Sampling Point	Quarter No.	Species	Distance (m)	D_{130} (cm)
1	1	Acacia	1.1	6
	2	Eucalyptus	1.6	48
	3	Casuarina	2.3	15
	4	Callitris	3.0	11
2	1	Eucalyptus	2.8	65
	2	Casuarina	3.7	16
	3	Acacia	0.9	8, 6
	4	Casuarina	2.2	9
3	1	Acacia	2.8	4
	2	Acacia	1.1	6
	3	Acacia	3.2	6
	4	Acacia	1.4	5
4	1	Callitris	1.3	19
	2	Casuarina	0.8	22
	3	Casuarina	0.7	12
	4	Callitris	3.1	7
5	1	Acacia	1.5	7
	2	Acacia	2.4	5
	3	Eucalyptus	3.3	27
	4	Eucalyptus	1.7	36
Total			40.9	

Notation

We will use the following notation throughout this paper.

n	the number of sample points along the transect
$4n$	the number of samples or observations one for each quarter at each point
i	a particular transect point, where $i = 1, \dots, n$
j	a quarter at a transect point, where $j = 1, \dots, 4$
R_{ij}	the point-to-tree distance at point i in quarter j

For example, the sum of the distances in the Table 1 is

$$\sum_{i=1}^5 \sum_{j=1}^4 R_{ij} = 40.9.$$

4 Basic Analysis

The next three subsections outline the estimation of density, frequency, and cover. The most widely studied of the three is density. In Section 5 we present a more robust way to determine both a point estimate and a confidence interval for population density. For those familiar with R, Appendix D provides scripts to quickly carry out all these calculations. In this section density, frequency, and cover are defined both in absolute and relative terms. The relative measures are then combined to create a measure of importance.

Density

Absolute Density

The **absolute density** λ of trees is defined as the number of trees per unit area. Since λ is most easily estimated per square meter and since a hectare is 10,000 m², λ is often multiplied by 10,000 to express the number of tree per hectare. The distances measured using the point-centered quarter method may be used to estimate λ to avoid having to count every tree within such a large area.

Note that if λ is given as trees/m², then its reciprocal $1/\lambda$ is the mean area occupied by a single tree. This observation is the basis for the following estimate of λ . (Also see Section 5.)

From the transect information, determine the **mean distance** \bar{r} , which is the sum of the nearest point-to-tree distances in the quarters surveyed divided by the number of quarters,

$$\bar{r} = \frac{\sum_{i=1}^n \sum_{j=1}^4 R_{ij}}{4n}.$$

For the data in Table 1,

$$\bar{r} = \frac{40.9}{20} = 2.05 \text{ m.}$$

Cottam et al. (1953) showed empirically and Morisita (1954) demonstrated mathematically that \bar{r} is actually an estimate of $\sqrt{1/\lambda}$, the square root of the mean area occupied by a single tree. Consequently, an estimate of the density is given by

$$\text{Absolute density} = \hat{\lambda} = \frac{1}{\bar{r}^2} = \frac{16n^2}{\left(\sum_{i=1}^n \sum_{j=1}^4 R_{ij}\right)^2}. \quad (1)$$

For the data in Table 1,

$$\hat{\lambda} = \frac{1}{\bar{r}^2} = \frac{1}{2.05^2} = 0.2380 \text{ trees/m}^2,$$

or, equivalently, 2380 trees/ha.

One way to “see this” is to imagine a forest where the trees are uniformly distributed on a square grid whose sides are $\bar{r} = 2.05$ m long. If a tree is located at the center of each square in this “forest,” then the mean distance \bar{r} between trees is 2.05 m. Such a forest is illustrated in Figure 2. Each tree occupies a square of side 2.05 m, and so the density is $1/2.05^2 = 0.2380$ trees/m². Though such a uniform arrangement of trees violates the assumption of randomness, the figure does illustrate what is happening “on average” or in the mean. (See Appendix B for a careful derivation of this estimate.)

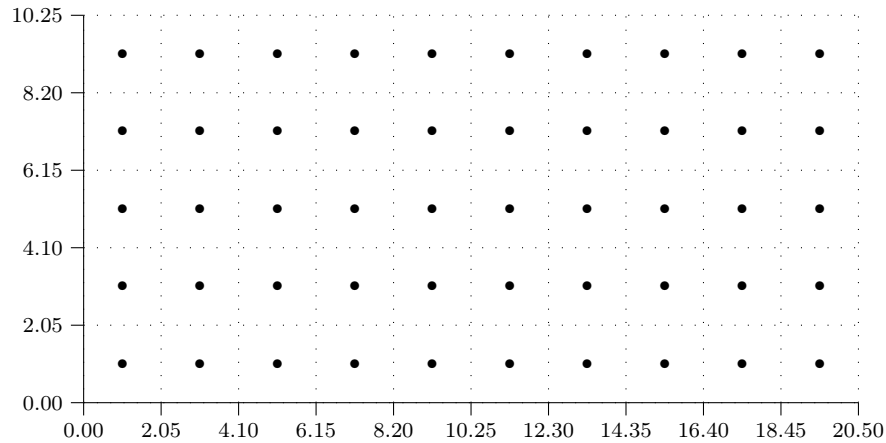


FIGURE 2. A grid-like forest with trees uniformly dispersed so that the nearest neighbor is 2.05 m.

Absolute Density of Each Species

The absolute density of an individual species is the expected number of trees of that species per square meter (or hectare). The **absolute density λ_k of species k** is estimated as the proportion of quarters in which the species is found times the estimated absolute density of all trees.

$$\hat{\lambda}_k = \frac{\text{Quarters with species } k}{4n} \times \hat{\lambda}. \quad (2)$$

Table 2 gives the absolute density for each species in Table 1.

TABLE 2. The absolute density of each species.

Species	Frequency/Quarter	Trees/ha
Acacia	$8/20 = 0.40$	$0.40 \times 2380 = 952$
Eucalyptus	$4/20 = 0.20$	$0.20 \times 2380 = 476$
Casuarina	$5/20 = 0.25$	$0.25 \times 2380 = 595$
Callitris	$3/20 = 0.15$	$0.15 \times 2380 = 357$
Total		2380

Relative Density of a Species

The **relative density** of each species is the percentage of the total number observations of that species,

$$\text{Relative density (Species } k) = \frac{\hat{\lambda}_k}{\hat{\lambda}} \times 100.$$

Equivalently by making use of (2), we may define

$$\text{Relative density (Species } k) = \frac{\text{Quarters with species } k}{4n} \times 100. \quad (3)$$

In the current example, using the first definition, the relative density of a species can be found by making use of the data in column 3 of Table 2. For example,

$$\text{Relative density of Eucalyptus} = \frac{476}{2380} \times 100 = 20.0.$$

Using the alternative method in (3) as a check on earlier calculations we see that the relative density is just the proportion in column 2 of Table 2 times 100. For example,

$$\text{Relative density of Eucalyptus} = \frac{4}{20} \times 100 = 20.0.$$

The relative densities should sum to 100 plus or minus a tiny round-off error.

TABLE 3. The relative density of each species.

Species	Relative Density
Acacia	40.0
Eucalyptus	20.0
Casuarina	25.0
Callitris	15.0

Based on simulations, Cottam et al. (1953) suggest that about 30 individuals of a particular species must be present in the total sample before confidence can be placed in any statements about relative frequency.

Cover or Dominance of a Species

Absolute Cover

The cover or dominance of an individual tree is measured by its **basal area** or cross-sectional area. Let d , r , c , and A denote the diameter, radius, circumference, and basal area of a tree, respectively. Since the area of a circle is $A = \pi r^2$, it is also $A = \pi(d/2)^2 = \pi d^2/4$. Since the circumference is $c = 2\pi r$, then the area is also $A = c^2/4\pi$. Either $A = \pi d^2/4$ or $A = c^2/4\pi$ can be used to determine basal area, depending on whether DBH or CCH was recorded in Table 1.

The first step is to compute the basal area for each tree sampled, organizing the data by species. This is the most tedious part of the analysis. A calculator that can handle lists of data or a spreadsheet with its sort function can be very handy at this stages (see Appendix D). For the data in Table 1, the basal area for each tree was obtained using the formula $A = \pi d^2/4$. For trees with multiple trunks, the basal area for each trunk was computed separately and the results summed (see Acacia in Table 4).

TABLE 4. The basal area of each tree.

Acacia		Eucalyptus		Casuarina		Callitris		Total
D ₁₃₀ (cm)	Area (cm ²)	D ₁₃₀ (cm)	Area (cm ²)	D ₁₃₀ (cm)	Area (cm ²)	D ₁₃₀ (cm)	Area (cm ²)	
6	28.3	48	1809.6	15	176.7	11	95.0	
8, 6	78.5	65	3318.3	16	201.1	19	283.5	
4	12.6	27	572.6	9	63.6	7	38.5	
6	28.3	36	1017.9	22	380.1			
6	28.3			12	113.1			
5	19.6							
7	38.5							
5	19.6							
Total BA	253.7		6718.4		934.6		417.0	8323.7
Mean BA	31.71		1679.60		186.92		139.00	416.19

Next, determine the total cover or basal area of the trees in the sample by species, and then calculate the mean basal area for each species.² Be careful when computing the means as the number of trees for

²Note: Mean basal area **cannot** be calculated by finding the mean diameter for each species and then using the formula $A = \pi d^2/4$.

each species will differ. Remember that each multi-trunk tree counts as a single tree.

The **absolute cover** or **dominance** of each species is expressed as its basal area per hectare. This is obtained by taking the number of trees per species from Table 2 and multiplying by the corresponding mean basal area in Table 4. The units for cover are m²/ha (not cm²/ha), so a conversion factor is required. For Acacia,

$$\text{Absolute Cover (Acacia)} = 31.71 \text{ cm}^2 \times \frac{952}{\text{ha}} \times \frac{1 \text{ m}^2}{10,000 \text{ cm}^2} = 3.0 \frac{\text{m}^2}{\text{ha}}.$$

TABLE 5. The total basal area of each species.

Species	Mean BA (cm ²)	Number/ha	Total BA/ha (m ² /ha)
Acacia	31.71	952	3.0
Eucalyptus	1679.60	476	79.9
Casuarina	186.92	595	11.1
Callitris	139.00	357	5.0
Total Cover/ha			99.0

Finally, calculate the total cover per hectare by summing the per species covers.

Relative Cover (Relative Dominance) of a Species

The **relative cover** or **relative dominance** (see Cottam and Curtis, 1956) for a particular species is defined to be the absolute cover for that species divided by the total cover times 100 to express the result as a percentage. For example, for Eucalyptus,

$$\text{Relative cover (Eucalyptus)} = \frac{79.9 \text{ m}^2/\text{ha}}{99.0 \text{ m}^2/\text{ha}} \times 100 = 80.7.$$

The relative covers should sum to 100 plus or minus a tiny round-off error. Note that the relative cover can also be calculated directly from the transect information in Table 4.

$$\text{Relative cover (Species } k) = \frac{\text{Total BA of species } k \text{ along transect}}{\text{Total BA of all species along transect}} \times 100. \quad (4)$$

For example,

$$\text{Relative cover (Eucalyptus)} = \frac{6718.4 \text{ cm}^2}{8323.7 \text{ cm}^2} \times 100 = 80.7.$$

TABLE 6. The relative cover of each species.

Species	Relative Cover
Acacia	3.0
Eucalyptus	80.7
Casuarina	11.2
Callitris	5.1

The Frequency of a Species

Absolute Frequency of a Species

The **absolute frequency** of a species is the percentage of sample points at which a species occurs. Higher absolute frequencies indicate a more uniform distribution of a species while lower values may indicate clustering or clumping. It is defined as

$$\text{Absolute frequency} = \frac{\text{No. of sample points with a species}}{\text{Total number of sample points}} \times 100. \quad (5)$$

For example,

$$\text{Absolute frequency (Acacia)} = \frac{4}{5} \times 100 = 80\%.$$

Note that absolute frequency is based on the number of sample points, not the number of quarters!

TABLE 7. The absolute cover of each species.

Species	Absolute Frequency
Acacia	$(4/5) \times 100 = 80$
Eucalyptus	$(3/5) \times 100 = 60$
Casuarina	$(3/5) \times 100 = 60$
Callitris	$(2/5) \times 100 = 40$
Total	240

Note that the total will sum to more than 100%.

Relative Frequency of a Species

To normalize for the fact that the absolute frequencies sum to more than 100%, the **relative frequency** is computed. It is defined as

$$\text{Relative frequency} = \frac{\text{Absolute frequency of a species}}{\text{Total frequency of all species}} \times 100. \quad (6)$$

For example,

$$\text{Relative frequency (Acacia)} = \frac{80}{240} \times 100 = 33.3.$$

The relative frequencies should sum to 100 plus or minus a tiny round-off error.

TABLE 8. The relative frequency of each species.

Species	Relative Frequency
Acacia	33.3
Eucalyptus	25.0
Casuarina	25.0
Callitris	16.7

What is the difference between relative frequency and relative density? A high relative frequency indicates that the species occurs near relatively many different sampling points, in other words, the species is well-distributed along the transect. A high relative density indicates that the species appears in a relatively large number of quarters. Consequently, if the relative density is high and the relative frequency is low, then the species must appear in lots of quarters but only at a few points, that is, the species appears in clumps. If both are high, the distribution is relatively even and relatively common along the transect. If the relative density is low (appears in few quarters) and the relative frequency is high(er), then the species must be sparsely distributed (few plants, no clumping).

The Importance Value of a Species

The **importance value** of a species is defined as the sum of the three relative measures:

$$\text{Importance value} = \text{Relative density} + \text{Relative cover} + \text{Relative frequency.} \quad (7)$$

The importance value gives equal weight to the three factors of relative density, cover, and frequency. This means that small trees (that is, with small basal area) can be dominant only if there are enough of them widely distributed across the transect. The importance value can range from 0 to 300.

For the data in Table 1, even though eucalypti are not very common, because of their size they turn out to be the most important species within the community. Because the importance values sum to 300, to make comparisons easier, many researchers choose to report the relative importance, which is just the importance value divided by 3.

TABLE 9. The importance value of each species.

Species	Relative Density	Relative Cover	Relative Frequency	Importance	Relative Importance
Acacia	40.0	3.0	33.3	76.3	25.4
Eucalyptus	20.0	80.7	25.0	125.7	41.9
Casuarina	25.0	11.2	25.0	61.2	20.4
Callitris	15.0	5.1	16.7	36.8	12.3

EXERCISE 4.1. Look ahead to the data from Mueller-Dombois and Ellenberg (1974) in Example D.1. Calculate the importance value of each species by hand and verify that the results given there are correct.

Comment. Each of the measures that make up relative importance may be calculated without knowing the absolute density of the trees at the site [review (3), (4), and (6)]. In fact, any estimate for the absolute density of all species leads to the same relative densities for each species. Consequently, the actual value of density of the plot is not needed to determine relative importance. However, in most studies, absolute density is one of the parameters of greatest interest. Because of this, there have been a number of different methods to estimate absolute density from point-centered quarter method data proposed in the literature. In the next section we explore one of these and others are discussed in Appendix B. Whichever method is used, relative importance is unaffected.

Pollard (1971) showed that the estimate of Cottam and Curtis (1956) of λ in (1) is biased.³ Nonetheless, this estimate appears widely in the literature and, so, has been used here. Another drawback of the estimate in (1) is that no confidence limits are available for it. We now address both of these issues.

5 Population Density Reconsidered

Pollard (1971) and Seber (1982) derived an unbiased estimate of the absolute population density using point-centered quarter method data that we now present. It also has the advantage that it can be used to determine confidence intervals for the density.

Intuition

The discussion that follows is meant to inform our intuition and by no means constitutes a proof of any of the results. That would require a substantially more sophisticated argument (see Appendix B).

Assume that trees are randomly distributed in the survey area. Think of the random points along the transect as representing “virtual trees.” The measured distance R_{ij} is a nearest-neighbor distance from a virtual to a real tree and is an estimate of the actual mean nearest-neighbor tree-to-tree distance.

³Pollard (1971) states that the reason for this is Cottam and Curtis (1956) chose to estimate the mean area A occupied by a tree as the reciprocal of λ . Rather than estimate A directly, as we saw in (1) they estimated \bar{r} , which is the reciprocal of the square root of A . Squaring and inverting leads to a biased estimate of A .

If an actual tree-to-tree distance were r meters, we could draw circles of radius $r/2$ centered at each tree. See Figure 3. Notice that the circles would not overlap and that only one tree would lie in each circle.

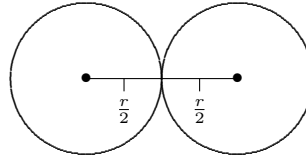


FIGURE 3. When trees are r units apart, circles of radius $r/2$ centered at each tree do not overlap and only one tree would lie within each circle.

The area of each circle is $\pi(r/2)^2 = \pi r^2/4$ m². Since there is exactly 1 tree per circle and since the circles don't overlap, the density is 1 tree per $\pi r^2/4$ m², or equivalently,

$$\frac{4}{\pi r^2} \text{ trees/m}^2.$$

The observed point-to-tree distances R_{ij} are the estimates of the actual distances. So $\pi(R_{ij}/2)^2 = \pi R_{ij}^2/4$ m² is an estimate of the sample mean area of a circle occupied by an individual. Using the $4n$ area estimates along the transect, an unbiased estimate of the mean area occupied by an individual is

$$\frac{\sum_{i=1}^n \sum_{j=1}^4 \frac{\pi R_{ij}^2}{4}}{4n - 1} = \frac{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2}{4(4n - 1)}.$$

Note: For this estimate to be unbiased, the denominator is one less than the actual number of observations, that is, $4n - 1$. The density is the reciprocal of the mean circular area.

FORMULA 5.1. An unbiased estimate of the **population density** λ is given by

$$\hat{\lambda} = \frac{4(4n - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2},$$

where the units are typically items/m². Multiplying by 10,000 yields trees/ha. The variance is given by

$$\text{Var}(\hat{\lambda}) = \frac{\hat{\lambda}^2}{4n - 2}.$$

EXAMPLE 5.1. Reanalyze the data in Table 1 by calculating $\hat{\lambda}$ using Formula 5.1.

SOLUTION. First we determine

$$\sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2 = (1.1)^2 + (1.6)^2 + \cdots + (1.7)^2 = 100.71.$$

Unlike in (1), remember to square the distances first, then sum. The density estimate is

$$10,000\hat{\lambda} = 10,000 \cdot \frac{4(4n - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{10,000(4(20 - 1))}{100.71\pi} = 2402 \text{ trees/ha.}$$

This estimate is about 1% higher than the earlier biased estimate of 2380.

Confidence Intervals

For larger samples, approximate confidence interval estimates for λ may be calculated in the following way. For details and for an exact confidence interval, see Appendix B. For an R script to compute an exact confidence interval see Appendix D.

FORMULA 5.2. For $n > 7$, the endpoints of a confidence interval at the $(1 - \alpha)100\%$ level are determined by

$$\text{lower endpoint: } C_1 = \frac{\left(z_{\frac{\alpha}{2}} + \sqrt{16n - 1}\right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2}$$

and

$$\text{upper endpoint: } C_2 = \frac{\left(z_{1-\frac{\alpha}{2}} + \sqrt{16n - 1}\right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2},$$

where z_β is the standard normal z -score corresponding to probability β .

EXAMPLE 5.2. The following data were collected at Lamington National Park in 1994. The data are the nearest point-to-tree distances for each of four quarters at 15 points along a 200 meter transect. The measurements are in meters. Estimate the tree density and find a 95% confidence interval for the density.

Point	I	II	III	IV
1	1.5	1.2	2.3	1.9
2	3.3	0.7	2.5	2.0
3	3.3	2.3	2.3	2.4
4	1.8	3.4	1.0	4.3
5	0.9	0.9	2.9	1.4
6	2.0	1.3	1.0	0.7
7	0.7	2.0	2.7	2.5
8	2.6	4.8	1.1	1.2
9	1.0	2.5	1.9	1.1
10	1.6	0.7	3.4	3.2
11	1.8	1.0	1.4	3.6
12	4.2	0.6	3.2	2.6
13	4.1	3.9	0.2	2.0
14	1.7	4.2	4.0	1.1
15	1.8	2.2	1.2	2.8

SOLUTION. In this example, the number of points is $n = 15$ and the number of samples is $4n = 60$. Using Formula 5.1, the point estimate for the density is

$$\hat{\lambda} = \frac{4(4n - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{4(59)}{347.63\pi} = 0.2161 \text{ trees/m}^2.$$

Since the number of points is greater than 7, confidence intervals may be calculated using Formula 5.2. To find a $1 - \alpha = 0.95$ confidence interval, we have $\alpha = 0.05$ and so $z_{1-\frac{\alpha}{2}} = z_{0.975} = 1.96$ and $z_{0.025} = -z_{0.975} = -1.96$. The lower endpoint of the confidence interval is

$$C_1 = \frac{\left(z_{0.025} + \sqrt{16n - 1}\right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{\left(-1.96 + \sqrt{16(15) - 1}\right)^2}{347.63\pi} = 0.1669$$

and the upper endpoint is

$$C_2 = \frac{\left(z_{0.975} + \sqrt{16n - 1}\right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{\left(1.96 + \sqrt{16(15) - 1}\right)^2}{347.63\pi} = 0.2778.$$

Therefore, the confidence interval for the density is

$$(0.1669, 0.2778) \text{ trees/m}^2.$$

The units are changed to hectares by multiplying by 10,000. Thus, $\hat{\lambda} = 2161$ trees/ha while the confidence interval is (1669, 2778) trees/ha.

Cautions

The estimates and confidence intervals for density assume that the points along the transect are spread out sufficiently so that no individual is sampled in more than one quarter. Further, the density estimate assumes that the spatial distribution of the organisms is completely random. For example, it would be inappropriate to use these methods in an orchard or woodlot where the trees had been planted in rows.

EXERCISE 5.1. The following data were collected in interior Alaska by Hollingsworth (2005). The data are the nearest point-to-tree distances in meters for each of four quarters at the first 25 points of 724 sample points. All trees were black spruce, *Picea mariana*. Estimate the tree density and find a 95% confidence interval. [Answer: $\hat{\lambda} = 7037$ trees/ha with a 95% confidence interval of (5768, 8551).]

Point	I	II	III	IV	Point	I	II	III	IV
1	7.7	2.2	1.4	1.6	14	1.2	1.1	1.0	1.4
2	0.97	1.2	1.4	1.5	15	0.5	0.7	0.9	1.1
3	1.4	1.4	1.8	1.6	16	0.52	0.85	0.82	2.1
4	1.7	2.5	2.2	1.8	17	0.51	0.46	1.6	1.1
5	0.77	1.2	1.0	1.2	18	0.46	0.9	1.7	0.65
6	0.38	0.64	1.84	1.7	19	0.35	0.64	0.98	0.53
7	0.45	0.6	0.55	0.62	20	0.98	1.3	2.1	1.6
8	0.15	0.14	0.96	0.9	21	0.35	0.5	0.25	1.0
9	0.39	0.5	0.57	0.88	22	0.4	0.4	0.6	0.8
10	0.72	0.73	0.45	0.75	23	0.6	1.5	1.3	1.1
11	0.35	1.1	0.45	1.1	24	0.4	0.5	0.9	0.8
12	0.55	0.9	0.65	0.9	25	0.5	1.1	2.1	1.1
13	0.8	0.7	0.8	0.9					

EXERCISE 5.2. The following data were collected at Lamington National Park in 1994 by another group of students. The data are the nearest point-to-tree distances (m) for each of four quarters at 14 points along a 200 meter transect. Estimate the tree density and find a 95% confidence interval. [Answer: $\hat{\lambda} = 1382$ trees/ha with a 95% confidence interval of (1057, 1792).]

I	II	III	IV	I	II	III	IV
0.6	1.4	3.6	2.0	3.4	3.4	2.9	2.6
0.6	0.9	3.2	1.8	1.7	3.2	2.7	4.2
2.0	3.9	1.8	2.2	3.8	4.2	3.2	4.4
4.1	7.0	1.6	4.0	1.8	1.1	4.3	3.4
3.2	2.0	1.0	3.8	2.8	0.9	2.7	2.3
2.8	3.3	1.3	0.8	1.4	5.0	4.5	2.7
3.1	1.9	2.9	3.4	2.0	0.2	3.0	4.0

6 Modifications, Adaptations, and Applications

In Section 1, we indicated that the point-centered quarter method is both efficient and accurate. However, as Díaz et al. (1975) note, in many situations there is

a discrepancy between the behaviour of the real world and the way it is assumed to behave by the model. Thus, reliability and accuracy have not only a statistical component but also a biological one. Most real-life sampling situations violate the assumptions of the underlying models of sampling theory and can render those methods invalid. In such cases, the results may bring about misleading conclusions. In addition, sampling in some environments, such as coastal areas, can be severely constrained by practical considerations.

The material in this section addresses some of these ‘practical considerations’ that occur in the field.

The Problem with ‘Breast Height’ (BH)

Brokaw and Thompson (2000) did an extensive survey of the literature and found that more than half the papers that used BH did not report the actual value used. Of those that did report BH, values ranged from 120 cm to 160 cm. See Table 10.

TABLE 10. The distribution of values stated for ‘breast height’ (BH) in papers published in *Biotropica*, *Ecology*, *Journal of Tropical Ecology*, *Forest Service*, and *Forest Ecology and Management* during the period 1988–1997. Adapted from Brokaw and Thompson (2000), Table 1.

BH (cm)	120	130	135	137	140	150	160	None	Total
Articles	1	113	2	28	27	10	1	258	440

Since the mode of the BH-values listed was 130 cm, Brokaw and Thompson (2000) strongly suggest adopting this as the standard BH-value. They strongly suggest denoting this value by ‘D₁₃₀’ rather than DBH while reserving ‘DBH’ as a generic term. At a minimum, the BH-value used should be explicitly stated. If a value x other than 130 cm is used, it might be denoted as ‘D _{x} ’.

As one would expect, DBH does decrease as height increases. In a field survey of 100 trees, Brokaw and Thompson (2000) found that the mean difference between D₁₃₀ and D₁₄₀ was 3.5 mm ($s = 5.8$, $n = 100$). This difference matters. Brokaw and Thompson (2000) report that this resulted in a 2.6% difference in total basal area. When biomass was calculated using the equation

$$\ln(\text{dry weight}) = -1.966 + 1.242 \ln(\text{DBH}^2)$$

there was a 4.0% difference.

Using different values of BH within a single survey may lead to erroneous results. Additionally, Brokaw and Thompson’s (2000) results show that failing to indicate the value of BH may lead to erroneous comparisons of characteristics such as diameter-class distributions, biomass, total basal area, and importance values between studies.

Vacant Quarters and Truncated Sampling

A question that arises frequently is whether there is a distance limit beyond which one no longer searches for a tree (or other organism of interest) in a particular quarter. The simple answer is, “No.” Whenever possible, it is preferable to make sure that every quadrant contains an individual, even if that requires considerable effort. But as a practical matter, a major reason to use the point-centered quarter method is its efficiency, which is at odds with substantial sampling effort. Additionally, in Section 2 we noted that sample points along the transect should be sufficiently far apart so that the same tree is not sampled at two adjacent transect points. Dahdouh-Guebas and Koedam (2006) suggest that it may be preferable to establish a consistent distance limit for the sampling point to the nearest individual rather than to consider the same individual twice. (Note, however, that Cottam and Curtis (1956) explicitly state that they did not use any method to exclude resampling a tree at adjacent transect points and that resampling did, in fact, occur.)

Whether because a distance limit is established for reasons of efficiency (often called truncated sampling) or to prevent resampling, in practice vacant quarters, that is, quadrants containing no tree, may occur. In such cases the calculation of the absolute density must be corrected, since a density calculated from only those quarters containing observations will overestimate the true density.

Warde and Petranka (1981) give a careful derivation of a correction factor (CF) to be used in such cases. In the language of the current paper, as usual, let n denote the number of sampling points and $4n$ the number of quarters. Let n_0 denote the number of vacant quarters. Begin by computing the density for the $4n - n_0$ non-vacant quarters,

$$\bar{r}' = \frac{\sum_{m=1}^{4n-n_0} R_m}{4n - n_0},$$

where R_m is the distance from tree m to its corresponding transect sample point. This is just the analog to (1). Then

$$\text{Absolute Density (corrected)} = \hat{\lambda}_c = \frac{1}{(\bar{r}')^2} \cdot \text{CF}, \quad (8)$$

where CF is the correction factor from Table 11 corresponding to the proportion of vacant quarters, $\frac{n_0}{4n}$. Note that as the proportion of vacant quarters increases, CF decreases and, consequently, so does the estimate of the density (as it should).

TABLE 11. Values of the correction factor (CF) to the density estimate based on the formula of Warde and Petranka (1981).

$n_0/4n$	CF	$n_0/4n$	CF	$n_0/4n$	CF	$n_0/4n$	CF
0.005	0.9818	0.080	0.8177	0.155	0.7014	0.230	0.6050
0.010	0.9667	0.085	0.8091	0.160	0.6945	0.235	0.5991
0.015	0.9530	0.090	0.8006	0.165	0.6877	0.240	0.5932
0.020	0.9401	0.095	0.7922	0.170	0.6809	0.245	0.5874
0.025	0.9279	0.100	0.7840	0.175	0.6742	0.250	0.5816
0.030	0.9163	0.105	0.7759	0.180	0.6676	0.255	0.5759
0.035	0.9051	0.110	0.7680	0.185	0.6610	0.260	0.5702
0.040	0.8943	0.115	0.7602	0.190	0.6546	0.265	0.5645
0.045	0.8838	0.120	0.7525	0.195	0.6482	0.270	0.5590
0.050	0.8737	0.125	0.7449	0.200	0.6418	0.275	0.5534
0.055	0.8638	0.130	0.7374	0.205	0.6355	0.280	0.5479
0.060	0.8542	0.135	0.7300	0.210	0.6293	0.285	0.5425
0.065	0.8447	0.140	0.7227	0.215	0.6232	0.290	0.5370
0.070	0.8355	0.145	0.7156	0.220	0.6171	0.295	0.5317
0.075	0.8265	0.150	0.7085	0.225	0.6110	0.300	0.5263

Caution: Dahdouh-Guebas and Koedam (2006) propose (without mathematical justification) using a correction factor of $CF' = 1 - \frac{n_0}{4n}$. While this correction factor also lowers the value of the density based on the trees actually measured, this correction differs substantially from that derived by Warde and Petranka (1981). For example, if 5% of the quarters are vacant, then from Table 11 we find $CF = 0.873681$ while $CF' = 0.95$.

The Problem of Unusual Trees or Tree Clusters

Single Trunk Splitting. In Section 2 the problem of trees with multiple trunks was briefly considered. What we had in mind there was a tree whose single trunk split into two or more trunks below breast height (130 cm). See Figure 4. In such a case, there is an unambiguous distance from the point along the transect to the main trunk of the tree. Further, it is natural to obtain the basal area for the tree as the sum of the basal areas for all of the trunks at breast height.



FIGURE 4. A willow tree with a single trunk that splits into multiple trunks below 130 cm.

Tight Clusters. However, other configurations of multi-stem trees are possible. A tree may have tightly-clustered multiple trunks at ground level as in Figure 5. In such a case, the entire complex is a single individual. The distance from the transect reference point may be measured to the center of the cluster or, alternatively, be measured as the average of the distances to each of the trunks. As in the previous case, it is natural to obtain the basal area for the tree as the sum of the basal areas for all of the trunks at breast height. (Note: This differs from the procedure outlined in Dahdouh-Guebas and Koedam (2006) where they suggest using the central stem of the cluster. But they are describing problems with mangroves whose growth architecture is quite different than the trees in the forests of North America. The trees in question here are more similar to those with split trunks.)

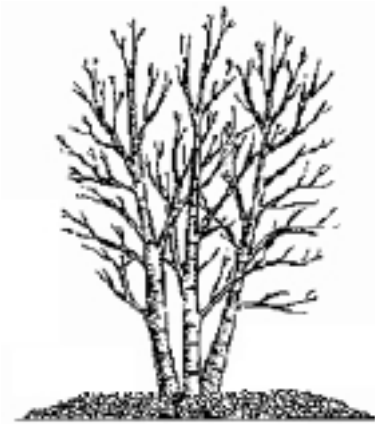


FIGURE 5. A birch tree with tightly clustered multiple trunks at ground level.

Loose Clusters. Tree clusters such as mangroves present significantly more complicated measurement issues for the point-centered quarter method. Even determining the distance from the transect reference point to such a tree is complicated. Individual stems may be interconnected over relatively large distances, so how does one determine which stems are part of the same individual? The researcher facing such issues is directed to a recent paper by Dahdouh-Guebas and Koedam (2006) in which they suggest solutions to these and other related questions.



FIGURE 6. A individual mangrove with its prop roots has a complex array of roots and stems.

Miscellaneous Issues

Crooked Trunks. In Section 2 we indicated that diameters should be measured at a consistent height and suggested that D_{130} be used. However, some trees may be crooked or growing (somewhat) horizon-

tally at 130 cm above the forest floor. Dahdouh-Guebas and Koedam (2006) suggest that the diameter of such a stem or trunk always be measured at 130 cm *along* the stem, whether or not this is actually 130 cm above the ground.

Dead Trees. The implicit but unstated assumption in Section 2 was that we were measuring live trees in the survey. However, depending on the purpose of the survey, dead trees may be important to include. This might be the case if the purpose is to assess exploitable firewood. Such decisions should be explicitly noted in the methods section of the resulting report.

Reversing the roles of live and dead trees, Rheinhardt et al. (1997) used the point-centered quarter method to determine the biomass of standing dead trees in a wetland and also the biomass of coarse woody debris available for nutrient recycling. In the latter case the distance, diameter (minimum 4 inches), and length (minimum 3 feet) of the debris item nearest to the transect sampling point in each quarter was recorded.

Novel Applications

Distance methods have been commonly used for vegetation surveys and are easily adapted to inventories of rare plants or other sessile organisms. The approach may also be useful for population studies of more mobile animal species by obtaining abundance estimates of their nests, dens, roosting sites, or scat piles.

Grasslands. The point-centered quarter method has been adapted to measure density and importance values when sampling grassland vegetation. Dix (1961) used the distance, measured at ground level, from the sampling point to the emergence from the soil of the nearest living herbaceous shoot in each quarter. Since this was the only measurement recorded, importance values were determined using only relative densities and relative frequencies.

Penfound (1963) modified Dix's method to include a relative cover or weight component to better match importance values of trees. In particular, once the distance to a culm or plant was measured, the plant was cut off at soil level and later its oven-dry weight was determined. The relative weight for each species was determined as the total weight for the species divided by the total weight for all species times 100 to express the result as a percentage. The importance of each species was then defined as the sum of the relative frequency, relative density, and relative weight.

On the surface of it, the aggregation often exhibited grassland populations violates the assumption of the random distribution assumption of the point-centered quarter method. Indeed, empirical studies by Risser and Zedler (1968) and Good and Good (1971) indicate that the point-centered quarter method appears to underestimate species density in such cases. In particular, Risser and Zedler (1968) suggest that when using the point-centered quarter method on grasslands, one should check against counts made using quadrat samples.

Animal Surveys. The point-centered quarter method was adapted in a series of projects of students of mine to determine the densities and importance values of certain sessile or relatively slow moving marine organisms.

One group carried out a project surveying holothurians (sea cucumbers) in the reef flat of a coral cay. Transects were laid out in the usual way and the distance and species of the nearest holothurian to each sampling point were recorded for each quarter. These data allowed computation of the relative density and relative frequency for each species. To take the place of relative cover, the volume of each holothurian was recorded. Volume was estimated by placing each individual in a bucket full of sea water and then removing it. The bucket was then topped off with water from a graduated cylinder and the volume of this water recorded. Since volume and mass are proportional, the relative volume is an approximation of the relative biomass. The sum of the relative density, relative frequency, and relative volume for each species gave its importance value.

A similar survey was conducted both in a reef flat and in an intertidal zone of a sand island for asteroidea (sea stars) using radial "arm length" instead of DBH. Another survey, this time of anemones in the intertidal zone of a sand island was conducted. Since these organisms are more elliptical than circular, major and minor axes were measured from which area occupied could be estimated.

While no extensive testing of the accuracy of these methods was conducted, say against values derived from using quadrats, the use of the point-centered quarter method in each case provided at least a reasonable preliminary snapshot of the relative importance and densities of the organisms surveyed.

A Final Caution. Whenever encountering a non-typical situation, it is important to note the situation and its resolution in the resulting report. Be consistent about all such choices. Additional problem issues with possible resolutions are described in Dahdouh-Guebas and Koedam (2006, Appendix B).

A Accuracy, Precision, and the 30–300 Rule

All biologists are aware of the importance of accuracy and precision in data collection and recording. While these two terms are used synonymously in everyday speech, they have different meanings in statistics. **Accuracy** is the closeness of a measured or computed value to its true value, while **precision** is the closeness of repeated measurements of the same quantity to each other. A biased but sensitive instrument may yield inaccurate but precise readings. On the other hand, an insensitive instrument might result in an accurate reading, but the reading would be imprecise, since another reading of the same object would be unlikely to yield an equally accurate value. Unless there is bias in a measuring instrument, precision will lead to accuracy.

Some measurements are by their nature precise. When we count eggs in a monitor lizard's nest and record the number as 9 or 13, these are exact numbers and, therefore, precise variates. Most continuous variables, however, are approximate with the exact value unknown and unknowable. Recordings of continuous variable data imply a level of precision by the number of digits used. For example, if the length of an adult female monitor lizard is recorded as 97.2 cm, the implied true value of the length is between 97.15 and 97.25 cm. In other words, the last digit recorded defines an interval in which the exact value of the variable resides. A measurement of 97 cm implies a length between 96.5 and 97.5 cm.

In most studies too much precision can slow down data collection while not contributing significantly to the resolution of scientific questions. While it doesn't make sense to measure large eucalyptus trees to the nearest millimeter or to weigh sperm whales to the nearest gram, what level of precision should be recorded? To how many significant figures should we record measurements? Many biologists use the **thirty-three hundred rule (30–300)** to determine precision for data sets. This rule is easy to apply and will save a great deal of time and effort. Array the sample by order of magnitude from largest to smallest measurement. The number of unit steps between the largest and smallest value should be between 30 and 300. For example, if you were collecting small shells in the intertidal zone of a beach and the largest was 9 mm and the smallest was 5 mm, the number of units steps would be 4 (a unit step is a millimeter in this example). If you recorded the lengths to the nearest tenth of a millimeter with the largest being 9.2 mm and the smallest 5.1 mm in length, the unit step is now 0.1 mm and there are 41 unit steps ($9.2 - 5.1 = 4.1$ mm or 41 tenths of mm) in the data array. The data set will now give you enough precision for most statistical analyses and allow for a reasonable error in recording, that is, a mistake of 1 in the last digit recorded is now less than 2.5% as opposed to 25% when the data were recorded to the nearest millimeter.

If sedge plant heights were measured to the nearest tenth of centimeter with the tallest being 194.3 cm and the shortest being 27.1 cm, the unit step would be tenths of centimeters and the data array would have 1672 unit steps ($194.3 - 27.1 = 167.2$ or 1672 tenths of cm). Clearly there is more precision in this data set than is needed. Recording these plant heights to the nearest centimeter would yield 167 unit steps ($194 - 27 = 167$ cm) and would give enough precision for analysis while saving time and effort in data collection.

B Technical Details

This section outlines the derivation of the density estimate in Section 4 and the estimate and corresponding confidence interval endpoints in Section 5. It also discusses other similar methods of estimating density using plotless methods.

Derivation of Equation (1)

Assume that a set of points (plants) is distributed randomly over a two-dimensional region where λ is the mean number of points per unit area (density). The probability that a randomly chosen region of unit area will contain x points is given by the Poisson distribution

$$\frac{\lambda^x e^{-\lambda}}{x!}.$$

More generally, start with a circle of radius r that is centered at a point chosen at random along a transect. Assume that the circle has been divided into q equiangular sectors and let the region in question be one of these sectors. Then its area is $\pi r^2/q$. If $q = 1$, the region is the entire circle; if $q = 4$ this is the point-centered quarter method. Morisita (1954) used the term ‘‘angle methods’’ to describe density estimates based on this process. The expected number of points in one such sector of the circle is $\lambda \pi r^2/q$ and the so the probability of finding x points in a sector is

$$\frac{(\lambda \pi r^2 q^{-1})^x e^{-\lambda \pi r^2 q^{-1}}}{x!}. \quad (9)$$

Setting $x = 0$, we obtain the probability that a sector of the circle of radius r will contain no points.

$$P(\text{no individuals in a sector circle of radius } r) = e^{-\lambda \pi r^2 q^{-1}}. \quad (10)$$

Equation (10) is a function of r that represents the probability that the distance from the sample point to the nearest individual within the sector is at least r . Consequently,

$$P(\text{at least 1 individual in the circle of radius } r) = 1 - e^{-\lambda \pi r^2 q^{-1}}. \quad (11)$$

Differentiating (11) gives the probability density function for r

$$f(r) = 2\lambda \pi r q^{-1} e^{-\lambda \pi r^2 q^{-1}}. \quad (12)$$

Therefore, the probability that there is at least one individual in the sector between distances a and b from the center of the circle is

$$\int_a^b 2\lambda \pi r q^{-1} e^{-\lambda \pi r^2 q^{-1}} dr. \quad (13)$$

The expected (mean) value of r is obtained by integrating $rf(r)$ over $(0, \infty)$. Using integration by parts and then the substitution $u = \frac{\sqrt{\lambda \pi}}{\sqrt{q}} r$,

$$\begin{aligned} E(r) &= \int_0^\infty 2\lambda \pi r^2 q^{-1} e^{-\lambda \pi r^2 q^{-1}} dr \\ &= -r e^{-\lambda \pi r^2 q^{-1}} \Big|_0^\infty + \int_0^\infty e^{-\lambda \pi r^2 q^{-1}} dr \\ &= 0 + \frac{\sqrt{q}}{\sqrt{\lambda \pi}} \int_0^\infty e^{-u^2} du \\ &= \frac{\sqrt{q}}{\sqrt{\lambda \pi}} \cdot \frac{\sqrt{\pi}}{2} \\ &= \frac{\sqrt{q}}{2\sqrt{\lambda}}, \end{aligned} \quad (14)$$

Solving for the density λ in (14) we obtain

$$\lambda = \frac{q}{4[E(r)]^2}. \quad (15)$$

Using the sample mean \bar{r} to estimate $E(r)$ and the point-centered quarter method with $q = 4$, we obtain the estimate of the density in (1),

$$\hat{\lambda} = \frac{1}{\bar{r}^2}$$

As Pollard (1971) and others point out, this estimate is biased.

Derivation of Formula 5.1

The intuition used in Sections 4 and 5 was that the density and the mean area occupied by a tree are reciprocals of each other. Assume that n random sampling points have been selected along a transect and that there are q equiangular sectors centered at each such point. For $i = 1, \dots, n$ and $j = 1, \dots, q$ let R_{ij} denote the distance from the i th sample point to the nearest individual in the j sector. Since these distances are independent, using (12) the likelihood of their joint occurrence is the product

$$\begin{aligned} & \left(2\lambda\pi R_{11}q^{-1}e^{-\lambda\pi R_{11}^2}\right) \left(2\lambda\pi R_{12}q^{-1}e^{-\lambda\pi R_{12}^2}\right) \cdots \left(2\lambda\pi R_{nq}q^{-1}e^{-\lambda\pi R_{nq}^2}\right) \\ & = (2\lambda\pi q^{-1})^{nq} (R_{11}R_{12} \cdots R_{nq}) e^{-\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}. \end{aligned} \quad (16)$$

To simplify notation, denote the nq distances R_{ij} by R_m for $m = 1, \dots, nq$ using the one-to-one correspondence $R_{ij} \longleftrightarrow R_{(i-1)q+j}$. For example, $R_{11} \longleftrightarrow R_1, R_{1q} \longleftrightarrow R_q, R_{21} \longleftrightarrow R_{q+1}$, and $R_{nq} \longleftrightarrow R_{nq}$. Then (16) becomes

$$(2\lambda\pi q^{-1})^{nq} (R_1 R_2 \cdots R_{nq}) e^{-\lambda\pi q^{-1} \sum_{m=1}^{nq} R_m^2}. \quad (17)$$

Using the nq sample distances, an estimate of the mean area occupied by a tree is given by

$$\frac{\pi q^{-1} \sum_{m=1}^{nq} R_m^2}{nq}.$$

If our intuition is correct, the expected value of the reciprocal of this mean area

$$\begin{aligned} E \left[\frac{nq}{\pi q^{-1} \sum_{m=1}^{nq} R_m^2} \right] \\ = \int_0^\infty \cdots \int_0^\infty \int_0^\infty \frac{nq}{\pi q^{-1} \sum_{m=1}^{nq} R_m^2} (2\lambda\pi q^{-1})^{nq} (R_1 R_2 \cdots R_{nq}) e^{-\lambda\pi q^{-1} \sum_{m=1}^{nq} R_m^2} dR_1 dR_2 \cdots dR_{nq} \end{aligned} \quad (18)$$

should be λ . To carry out this calculation, use the substitution (see Pollard, 1971)

$$u_j = \lambda\pi q^{-1} \sum_{m=1}^j R_m^2 \quad j = 1, \dots, nq$$

with Jacobian

$$J(u_1, u_2, \dots, u_{nq}) = \begin{vmatrix} 2\lambda\pi q^{-1} R_1 & 0 & \cdots & 0 \\ 2\lambda\pi q^{-1} R_1 & 2\lambda\pi q^{-1} R_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 2\lambda\pi q^{-1} R_1 & 2\lambda\pi q^{-1} R_2 & \cdots & 2\lambda\pi q^{-1} R_{nq} \end{vmatrix} = (2\lambda\pi q^{-1})^{nq} R_1 R_2 \cdots R_{nq}.$$

The limits of integration for u_{nq} are 0 to ∞ and for u_m ($i = m, \dots, nq - 1$) they are 0 to u_{m+1} . So (18) becomes

$$\begin{aligned} E \left[\frac{nq}{\pi q^{-1} \sum_{m=1}^{nq} R_m^2} \right] & = E \left[\frac{\lambda nq}{u_{nq}} \right] = \int_0^\infty \cdots \int_0^{u_3} \int_0^{u_2} \frac{\lambda nq}{u_{nq}} e^{-u_{nq}} du_1 du_2 \cdots du_{nq} \\ & = \int_0^\infty \cdots \int_0^{u_3} \frac{\lambda nq u_2}{1 \cdot u_{nq}} e^{-u_{nq}} du_2 \cdots du_{nq} \\ & = \int_0^\infty \cdots \int_0^{u_4} \frac{\lambda nq u_3^2}{2 \cdot 1 \cdot u_{nq}} e^{-u_{nq}} du_3 \cdots du_{nq} \\ & \quad \vdots \\ & = \int_0^\infty \frac{\lambda nq u_{nq}^{nq-1}}{(nq-1)! u_{nq}} e^{-u_{nq}} du_{nq} \\ & = \frac{\lambda nq}{(nq-1)!} \int_0^\infty u_{nq}^{nq-2} e^{-u_{nq}} du_{nq} \\ & = \frac{\lambda nq}{nq-1}. \end{aligned} \quad (19)$$

So the reciprocal of the mean area occupied by a tree is also a biased estimate of λ , but the bias is easily corrected. An unbiased estimate of the density is

$$\hat{\lambda} = \frac{nq - 1}{nq} \cdot \frac{nq}{\pi q^{-1} \sum_{m=1}^{nq} R_m^2} = \frac{q(nq - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}. \quad (20)$$

For the point-centered quarter method method where $q = 4$ we have that an unbiased estimate of the density is

$$\hat{\lambda} = \frac{4(4n - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2},$$

which is Formula 5.1.

It is worth mentioning the interpretation of (20) when $q = 1$. In this case the distance from each sample point to the nearest individual is measured and an unbiased estimate of the density is given by the simpler formula

$$\hat{\lambda} = \frac{n - 1}{\pi \sum_{i=1}^n R_i^2}. \quad (21)$$

Confidence Intervals and the Derivation of Formula 5.2

Next, recall that the probability density function of the chi-square distribution for $x \geq 0$ is

$$f(x; k) = \frac{\left(\frac{1}{2}\right)^{k/2} x^{k/2-1}}{\Gamma(k/2)} e^{-x/2}, \quad (22)$$

where k denotes degrees of freedom and $\Gamma(z)$ is the gamma function.⁴ If we let $y = 2\lambda\pi r^2 q^{-1}$, then $dy = 4\lambda\pi r q^{-1} dr$ so (13) may be written as

$$\int_{\pi a^2}^{\pi b^2} \frac{1}{2} e^{-y/2} dy.$$

In other words, using (22) with $k = 2$ and (13) we see that $2\lambda\pi r^2 q^{-1}$ is distributed as $\chi_{(2)}^2$.

To generalize, assume as before that we have selected n random sampling points along a transect and that there are q equiangular sectors centered at each such point. For $i = 1, \dots, n$ and $j = 1, \dots, q$ let R_{ij} denote the distance from the i th sample point to the nearest individual in the j sector. From (16) the probability of their joint occurrence is the product

$$(2\lambda\pi q^{-1})^{nq} (R_{11} R_{12} \dots R_{nq}) e^{-\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}.$$

Since the distances are independent and since each $2\lambda\pi R_{ij}^2 q^{-1}$ is distributed as $\chi_{(2)}^2$, then

$$2\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2 \sim \chi_{(2nq)}^2. \quad (23)$$

Consequently, a $(1 - \alpha)100\%$ confidence interval for λ is determined by the inequalities

$$\chi_{\frac{\alpha}{2}(2nq)} < 2\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2 < \chi_{1-\frac{\alpha}{2}(2nq)}.$$

Solving for λ we obtain the following result.

FORMULA B.1. Assume n random sampling points have been selected along a transect and that there are q equiangular sectors centered at each such point. For $i = 1, \dots, n$ and $j = 1, \dots, q$ let R_{ij} denote the distance

⁴In particular, if z is a positive integer, then $\Gamma(z) = (z - 1)!$.

from the i th sample point to the nearest individual in the j th sector. A $(1 - \alpha)100\%$ confidence interval for the density λ is given by (C_1, C_2) , where

$$C_1 = \frac{q\chi_{\frac{\alpha}{2}}(2nq)}{2\pi \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2} \quad \text{and} \quad C_2 = \frac{q\chi_{1-\frac{\alpha}{2}}(2nq)}{2\pi \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}.$$

In particular, for the point-centered quarter method where $q = 4$, we have

$$C_1 = \frac{2\chi_{\frac{\alpha}{2}}(8n)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} \quad \text{and} \quad C_2 = \frac{2\chi_{1-\frac{\alpha}{2}}(8n)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2}.$$

For convenience, for 95% confidence intervals, Table 15 provides the required χ^2 values for up to $n = 240$ sample points (960 quarters).

EXAMPLE B.1. Return to Example 5.2 and calculate a confidence interval for the density using Formula B.1.

SOLUTION. From Formula B.1,

$$C_1 = \frac{2\chi_{\frac{\alpha}{2}}(8n)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{2\chi_{\frac{\alpha}{2}}(120)}{\pi \sum_{i=1}^{15} \sum_{j=1}^4 R_{ij}^2} = \frac{183.15}{1092.11} = 0.1677.$$

and

$$C_2 = \frac{2\chi_{1-\frac{\alpha}{2}}(8n)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} = \frac{2\chi_{1-\frac{\alpha}{2}}(120)}{\pi \sum_{i=1}^{15} \sum_{j=1}^4 R_{ij}^2} = \frac{304.42}{1092.11} = 0.2787.$$

This interval is nearly identical to the one computed in Example 5.2 using a normal approximation.

Normal Approximation

A difficulty with calculating confidence intervals using Formula B.1 is that $2nq$ is often greater than the degrees of freedom listed in a typical χ^2 -table. For larger values of $2nq$, the appropriate χ^2 values can be obtained from a spreadsheet program or other statistical or mathematical software.

Alternatively, one can use a normal approximation. It is a well-known result due to Fisher that if $X \sim \chi^2(k)$, then $\sqrt{2X}$ is approximately normally distributed with mean $\sqrt{2k-1}$ and unit variance. In other words, $\sqrt{2X} - \sqrt{2k-1}$ has approximately a standard normal distribution.

In the case at hand, $2\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2 \sim \chi^2(2nq)$. Therefore, the endpoints for a $(1 - \alpha)100\%$ confidence interval for λ are determined as follows:

$$\begin{aligned} z_{\alpha/2} &< \sqrt{2 \left(2\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2 \right)} - \sqrt{2(2nq) - 1} < z_{1-\alpha/2} \\ \iff z_{\alpha/2} + \sqrt{4nq - 1} &< \sqrt{4\lambda\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2} < z_{1-\alpha/2} + \sqrt{4nq - 1} \\ \iff \frac{z_{\alpha/2} + \sqrt{4nq - 1}}{\sqrt{4\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}} &< \sqrt{\lambda} < \frac{z_{1-\alpha/2} + \sqrt{4nq - 1}}{\sqrt{4\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}}. \end{aligned}$$

Squaring, we find:

FORMULA B.2. For $nq > 30$, the endpoints of a $(1 - \alpha)100\%$ confidence interval for the density λ are well-approximated by

$$C_1 = \frac{\left(z_{\frac{\alpha}{2}} + \sqrt{4nq - 1} \right)^2}{4\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2} \quad \text{and} \quad C_2 = \frac{\left(z_{1-\frac{\alpha}{2}} + \sqrt{4nq - 1} \right)^2}{4\pi q^{-1} \sum_{i=1}^n \sum_{j=1}^q R_{ij}^2}.$$

For the point-centered quarter method where $q = 4$ we obtain

$$C_1 = \frac{\left(z_{\frac{\alpha}{2}} + \sqrt{16n - 1} \right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2} \quad \text{and} \quad C_2 = \frac{\left(z_{1-\frac{\alpha}{2}} + \sqrt{16n - 1} \right)^2}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2}.$$

Note that the later formula above is Formula 5.2.

Further Generalizations: Order Methods

Order methods describe the estimation of the density λ by measuring the distances from the sample point to the first, second, third, etc. closest individuals. Note: The data collected during point-centered quarter method sampling (as in Table 1) do *not* necessarily measure the first through fourth closest individuals to the sample point because any two, three, or four closest individuals may lie in a single quadrant or at least be spread among fewer than all four quadrants.

The derivation that follows is an adaptation of Moore (1954), Seber (1982), Eberhardt (1967), and Morisita (1954). We continue to assume, as above, that the population is randomly distributed with density λ so that the number of individuals x in a circle of radius r chosen at random has a Poisson distribution

$$P(x) = \frac{(\lambda\pi r^2)^x e^{-\lambda\pi r^2}}{x!}.$$

Let $R_{(k)}$ denote the distance to the k th nearest tree from a random sampling point. Then

$$\begin{aligned} P(R_{(k)} \leq r) &= P(\text{finding at least } k \text{ individuals in a circle of area } \pi r^2) \\ &= \sum_{i=k}^{\infty} e^{-\lambda\pi r^2} \left[\frac{(\lambda\pi r^2)^i}{i!} \right]. \end{aligned} \quad (24)$$

Taking the derivative of (24), the corresponding pdf for r is

$$\begin{aligned} f_k(r) &= \sum_{i=k}^{\infty} \left(-2\lambda\pi r e^{-\lambda\pi r^2} \left[\frac{(\lambda\pi r^2)^i}{i!} \right] + e^{-\lambda\pi r^2} \left[\frac{2i\lambda\pi r (\lambda\pi r^2)^{(i-1)}}{i!} \right] \right) \\ &= 2\lambda\pi r e^{-\lambda\pi r^2} \sum_{i=k}^{\infty} \left(-\frac{(\lambda\pi r^2)^i}{i!} + \frac{(\lambda\pi r^2)^{(i-1)}}{(i-1)!} \right) \\ &= \frac{2\lambda\pi r e^{-\lambda\pi r^2} (\lambda\pi r^2)^{(k-1)}}{(k-1)!} \\ &= \frac{2(\lambda\pi)^k r^{2k-1} e^{-\lambda\pi r^2}}{(k-1)!}, \end{aligned} \quad (25)$$

which generalizes (12). In other words, the probability that the k th closest tree to the sample point lies in the interval between a and b is

$$\int_a^b \frac{2(\lambda\pi)^k r^{2k-1} e^{-\lambda\pi r^2}}{(k-1)!} dr. \quad (26)$$

If we use the substitution $y = 2\lambda\pi r^2$ and $dy = 4\lambda\pi r dr$, then (26) becomes

$$\int_{2\lambda\pi a^2}^{2\lambda\pi b^2} \frac{\left(\frac{1}{2}\right)^k y^{k-1} e^{-y/2}}{(k-1)!} dy.$$

In other words, the pdf for y is

$$g_k(y) = \frac{\left(\frac{1}{2}\right)^k y^{k-1} e^{-y/2}}{(k-1)!}$$

and so it follows from (22) that

$$2\lambda\pi R_{(k)}^2 \sim \chi_{(2k)}^2. \quad (27)$$

Now assume that n independent sample points are chosen at random. Similar to the derivation of (20), we have that an unbiased estimate of the density is

$$\hat{\lambda} = \frac{kn - 1}{\pi \sum_{i=1}^n R_{(k)i}^2}. \quad (28)$$

Moreover, from (27) it follows that

$$2\lambda\pi \sum_{i=1}^n R_{(k)i}^2 \sim \chi_{(2kn)}^2. \quad (29)$$

Consequently, a $(1 - \alpha)100\%$ confidence interval for λ is determined by the inequalities

$$\chi_{\frac{\alpha}{2}(2kn)} < 2\lambda\pi \sum_{i=1}^n R_{(k)i}^2 < \chi_{1-\frac{\alpha}{2}(2kn)}.$$

Solving for λ , a $(1 - \alpha)100\%$ confidence interval is given by (C_1, C_2) , where

$$C_1 = \frac{\chi_{\frac{\alpha}{2}(2kn)}}{2\pi \sum_{i=1}^n R_{(k)i}^2} \quad \text{and} \quad C_2 = \frac{\chi_{1-\frac{\alpha}{2}(2kn)}}{2\pi \sum_{i=1}^n R_{(k)i}^2}. \quad (30)$$

A special case. Notice that when $k = 1$ only the nearest individual to the sample point is being measured. This is the same as taking only $q = 1$ sector (the entire circle) in the two preceding sections. In particular, when $k = q = 1$, the unbiased estimates for λ in (28) and (20) agree as do the confidence interval limits in (30) and Formula B.1.

EXAMPLE B.2. Use the closest trees to the 15 sample points in Example 5.2 to estimate the density and find a 95% confidence interval for this estimate.

SOLUTION. From Example 5.2 we have

R_i	1.2	0.7	2.3	1.0	0.9	0.7	0.7	1.1	1.0	0.7	1.0	0.6	0.2	1.1	1.2
$\pi R_{(1)i}^2$	4.52	1.54	16.62	3.14	2.54	1.54	1.54	3.80	3.14	1.54	3.14	1.13	0.13	3.80	4.52

Check that $\pi \sum_{i=1}^{15} R_{(1)i}^2 = 52.64$. Since $n = 15$ and $k = 1$, then from (28)

$$\hat{\lambda} = \frac{kn - 1}{\pi \sum_{i=1}^n R_{(1)i}^2} = \frac{1(15) - 1}{52.64} = 0.2660 \text{ trees/m}^2$$

or 2660 trees/ha. From (30) we find

$$C_1 = \frac{\chi_{\frac{\alpha}{2}(2kn)}}{2\pi \sum_{i=1}^n R_{(1)i}^2} = \frac{\chi_{0.025(30)}}{2(52.64)} = \frac{16.2}{105.28} = 0.1596$$

and

$$C_2 = \frac{\chi_{1-\frac{\alpha}{2}(2kn)}}{2\pi \sum_{i=1}^n R_{(1)i}^2} = \frac{\chi_{0.975(30)}}{2(52.64)} = \frac{47.0}{105.28} = 0.4464.$$

This is equivalent to a confidence interval of (1596, 4464) trees/ha. With fewer estimates this confidence interval is wider than the one originally calculated in Example 5.2.

Normal Approximation

For larger values of $2kn$, one can use a normal approximation. In the case at hand, $2\lambda\pi \sum_{i=1}^n R_{(k)i}^2 \sim \chi_{(2kn)}^2$. Adapting the argument that precedes Formula B.2 the endpoints for a $(1 - \alpha)100\%$ confidence interval for λ are determined as follows:

$$\begin{aligned} z_{\alpha/2} &< \sqrt{2 \left(2\lambda\pi \sum_{i=1}^n R_{(k)i}^2 \right) - \sqrt{2(2kn) - 1}} < z_{1-\alpha/2} \\ &\iff z_{\alpha/2} + \sqrt{4kn - 1} < \sqrt{4\lambda\pi \sum_{i=1}^n R_{(k)i}^2} < z_{1-\alpha/2} + \sqrt{4kn - 1} \\ &\iff \frac{z_{\alpha/2} + \sqrt{4kn - 1}}{\sqrt{4\pi \sum_{i=1}^n R_{(k)i}^2}} < \sqrt{\lambda} < \frac{z_{1-\alpha/2} + \sqrt{4kn - 1}}{\sqrt{4\pi \sum_{i=1}^n R_{(k)i}^2}} \end{aligned}$$

Squaring, we find that the endpoints of a $(1 - \alpha)100\%$ confidence interval for λ are

$$C_1 = \frac{(z_{\alpha/2} + \sqrt{4kn - 1})^2}{4\pi \sum_{i=1}^n R_{(k)i}^2} \quad \text{and} \quad C_2 = \frac{(z_{1-\alpha/2} + \sqrt{4kn - 1})^2}{4\pi \sum_{i=1}^n R_{(k)i}^2}. \quad (31)$$

Typically, $kn > 30$ before one would use a normal approximation.

Again note that when $k = q = 1$, (31) and Formula B.2 agree. For comparison purposes only, we now use (31) to determine a 95% confidence interval for the density in Example B.2. We obtain

$$C_1 = \frac{(z_{0.025} + \sqrt{4kn - 1})^2}{4\pi \sum_{i=1}^n R_{(k)i}^2} = \frac{(-1.96 + \sqrt{60 - 1})^2}{4(52.64)} = 0.1554$$

$$C_2 = \frac{(z_{0.975} + \sqrt{4kn - 1})^2}{4\pi \sum_{i=1}^n R_{(k)i}^2} = \frac{(1.96 + \sqrt{60 - 1})^2}{4(52.64)} = 0.4414,$$

or (1554, 4414) trees/ha. This is not that different from the interval calculated in Example B.2

Angle-Order Methods

The angle and order methods may be combined by dividing the region about each sampling point into q equiangular sectors and recording the distance to the k th nearest individual in each sector. Morisita (1957) seems to have been the first to propose such a method.

Randomly Distributed Populations

Though Morisita's paper concerns methods to estimate the density of non-randomly distributed populations, he first describes a combination of the angle and order methods that may be used to estimate density when a population is randomly distributed (Morisita, 1957, equation (15) of the translation). Assume that the distances to the k th closest individual in each of the q sectors are measured at each sample point. In particular, let $R_{(k)ij}$ denote the distance from the i th sample point to the k th closest individual in the j th sector. Then Morisita (1957, equation 15) shows that unbiased estimate of the density⁵ is

$$\hat{\lambda} = \frac{q(kqn - 1)}{\pi \sum_{i=1}^n \sum_{j=1}^q R_{(k)ij}^2} \quad (32)$$

with variance

$$\text{Var}(\hat{\lambda}) = \frac{\hat{\lambda}^2}{\pi^2(kqn - 2)}. \quad (33)$$

Note: If $k = 1$, then this estimate for $\hat{\lambda}$ is the same as (20). Instead, if $q = 1$, then this estimate is the same as (28). And if $k = q = 1$, then this estimate is using the closest individual at each sample point and is (21)

Non-Randomly Distributed Populations

When populations are not randomly distributed, Morisita (1957) proposed two unbiased estimates of the density and gave guidelines governing when and how each estimate was to be used. Paraphrasing Morisita, to deal with aggregated (clumped) populations, divide the total area into subplots with areas sufficiently small so that no further aggregation exists in each. Then within each subplot, either the population is distributed (1) randomly, possibly with different densities for each subplot; or (2) uniformly, again possibly with different densities for each subplot.

⁵In the original Japanese manuscript, equation 15 is missing a factor of q and is stated incorrectly, in the notation of this paper, as

$$\hat{\lambda} = \frac{kqn - 1}{\pi \sum_{i=1}^n \sum_{j=1}^q R_{(k)ij}^2}.$$

The English translation corrects this to the formula for $\hat{\lambda}$ in (32).

For the random case, Morisita showed that an unbiased estimate of the overall density is given by

$$\hat{\lambda}_1 = \frac{k-1}{\pi n} \sum_{i=1}^n \sum_{j=1}^q \frac{1}{R_{(k)ij}^2}. \quad (34)$$

Note: It is clear from the formula above that k must be at least 2. Though not apparent from the formula, the estimate $\hat{\lambda}_1$ actually requires measuring the distances to the k th closest individual in each sector, where $k \geq 3$. This follows from the complicated formula for the variance (see Morisita (1957)) that involves a factor of $k-2$ in the denominator. This estimate is also discussed by Eberhardt (1967) and Seber (1982).

For the more uniform case, Morisita showed that an unbiased estimate of the density is given by

$$\hat{\lambda}_2 = \frac{kq-1}{\pi n} \sum_{i=1}^n \frac{q}{\sum_{j=1}^q R_{(k)ij}^2} = \frac{q(kq-1)}{\pi n} \sum_{i=1}^n \frac{1}{\sum_{j=1}^q R_{(k)ij}^2}. \quad (35)$$

Not apparent from the formula above, the estimate $\hat{\lambda}_2$ requires that $kq \geq 3$ because the variance (see Morisita (1957)) involves a factor of $kq-2$ in the denominator.

Be careful to note the difference in order of operations (reciprocals and summations) in these two estimates. In particular,

$$\sum_{i=1}^n \frac{1}{\sum_{j=1}^q R_{(k)ij}^2} \neq \sum_{i=1}^n \sum_{j=1}^q \frac{1}{R_{(k)ij}^2} \quad \text{and} \quad \sum_{i=1}^n \sum_{j=1}^q \frac{1}{R_{(k)ij}^2} \neq \frac{1}{\sum_{i=1}^n \sum_{j=1}^q R_{(k)ij}^2}.$$

Notice that (35) is valid for $q=4$ and $k=1$, which corresponds to the using data collected in the ‘standard’ point-centered quarter method, and in that case simplifies to

$$\hat{\lambda}_2 = \frac{12}{\pi n} \sum_{i=1}^n \frac{1}{\sum_{j=1}^4 R_{ij}^2}. \quad (36)$$

This equation differs from the earlier biased estimate of λ for the point-centered quarter method in (1) and the unbiased estimate in Formula 5.1. Equation (36) appears to have been rediscovered by Jost (1993).

Guidelines

Morisita (1957) summarizes the difference between the estimates as follows. In (34), the density in each sector is estimated first, by computing $\frac{1}{\pi R_{(k)ij}^2}$, and then the density of the total area is estimated using the mean of the densities of all of the sectors of all of the sample points. In contrast, in (35), the density at each sample point is calculated first, by computing $\frac{q}{\pi \sum_{j=1}^q R_{ij}^2}$, and then the density of the total area is estimated using the mean of densities of all of the sample points.

At first it appears that one needs to know a lot about the distribution of the population before applying one of these methods. However, Morisita makes the following observations. When the distribution is more uniform, the variance in r is smaller than expected. So for two populations with the same density λ , the value of $\sum_{j=1}^q R_j^2$ for a uniform distribution is smaller than expected for a random distribution. (The sum of squares is minimized when all the values are the same.) The reciprocal of this sum appears in (35) for $\hat{\lambda}_2$, which tends to make $\hat{\lambda}_2$ an overestimate of the true density in the uniform case.

Similar reasoning applies to the sum of squares of the reciprocals: $\sum_{j=1}^q \frac{1}{R_j^2}$, too, will be smaller for a uniform distribution than expected. Since exactly this sum appears in (34) for $\hat{\lambda}_1$, it will tend to make $\hat{\lambda}_1$ an underestimate of the true density in the uniform case. Thus, for the uniform case, averaging $\hat{\lambda}_1$ and $\hat{\lambda}_2$ should provide a reasonable estimate.

Consequently, Morisita (1957) suggests the following ‘practical protocol’ to determine which density estimate is most appropriate, even when the distribution of the population is unknown. Assuming that $k \geq 3$ (so that $\hat{\lambda}_1$ may be computed)

1. Calculate both $\hat{\lambda}_1$ and $\hat{\lambda}_2$.
2. If $\hat{\lambda}_1 \leq \hat{\lambda}_2$, use their average

$$\hat{\lambda}_0 = \frac{\hat{\lambda}_1 + \hat{\lambda}_2}{2} \quad (37)$$

as the density estimate. (The distribution is may be uniform, at least locally.)

3. If $\hat{\lambda}_1 > \hat{\lambda}_2$, use $\hat{\lambda}_1$ as the density estimate. (The distribution is may be random, at least locally.)

Derivation of Equation (35). Given our previous work, it is relatively easy to derive (35) for the case $k = 1$, that is, measuring the closest individual to the sample point in each sector (quarter). The motivating idea is to estimate the density at each point along the transect separately and then average these estimates. As usual, the density is measured by taking the reciprocal of the mean area occupied by individuals near each sample point. With $k = 1$, the mean of the q estimates of the area occupied by an individual near the i th sample point is

$$\frac{\sum_{j=1}^q \pi q^{-1} R_{ij}^2}{q}.$$

The reciprocal gives an estimate of the density (near the i th point):

$$\frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2}.$$

Averaging all n density estimates along the transect, yields the estimate

$$\frac{1}{n} \sum_{i=1}^n \frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2}.$$

However, using (19), we find that

$$\begin{aligned} E \left[\frac{1}{n} \sum_{i=1}^n \frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2} \right] &= \frac{1}{n} \sum_{i=1}^n E \left[\frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2} \right] \\ &= \frac{1}{n} \sum_{i=1}^n \left[\int_0^\infty \cdots \int_0^\infty \frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2} (2\lambda\pi q^{-1})^q (R_{i1} \cdots R_{iq}) e^{-\lambda\pi q^{-1} \sum_{j=1}^q R_{ij}^2} dR_{i1} \cdots dR_{iq} \right] \\ &= \frac{1}{n} \sum_{i=1}^n \frac{\lambda q}{q-1} \\ &= \frac{\lambda q}{q-1}, \end{aligned}$$

which means that the estimate is biased. An unbiased estimate of the density is

$$\hat{\lambda} = \frac{q-1}{q} \left[\frac{1}{n} \sum_{i=1}^n \frac{q}{\pi q^{-1} \sum_{j=1}^q R_{ij}^2} \right] = \frac{q-1}{n} \sum_{i=1}^n \frac{q}{\pi \sum_{j=1}^q R_{ij}^2}.$$

This is the same as (35) with $k = 1$ or (36) with $q = 4$.

EXAMPLE B.3. If we use (36) and the data in Example 5.2 (where $k = 1$) we obtain

$$\hat{\lambda}_2 = \frac{12}{15\pi} \sum_{i=1}^{15} \frac{1}{\sum_{j=1}^4 R_{ij}^2} = 0.2078 \text{ trees/m}^2. \quad (38)$$

Table 12 compares this estimate to the estimates with the other applicable methods in this paper. In short, though most estimates are similar, it is important to specify which formula one is using to estimate density when the point-centered quarter method is employed.

TABLE 12. The various density estimates using the data in Example 5.2.

Equation	Formula	$\hat{\lambda}$	Source
Equation (1)	$\frac{1}{\bar{r}^2} = \frac{16n^2}{\left(\sum_{i=1}^n \sum_{j=1}^4 R_{ij}\right)^2}$	0.2201	Cottam et al. (1953), Morisita (1954)
Formula 5.1	$\frac{4(4n-1)}{\pi \sum_{i=1}^n \sum_{j=1}^4 R_{ij}^2}$	0.2161	Pollard (1971); Seber (1982)
Equation (28)	$\frac{kn-1}{\pi \sum_{i=1}^n R_{(k)i}^2}$	0.2660	Pollard (1971)
Equation (36)	$\frac{12}{\pi n} \sum_{i=1}^n \frac{1}{\sum_{j=1}^4 R_{ij}^2}$	0.2078	Morisita (1957)

Engeman et al. (1994) examined a large number of methods to estimate density⁶ including those suggested above in (28), (34), and (35). Of the estimators discussed in this paper, they concluded that the best performing ones were the angle-order methods with $q = 4$ (that is, quarters) and $k = 3$ followed by $q = 4$ and $k = 2$ and then the two order methods with $k = 3$ and then $k = 2$. However, notice that the efficiency is decreased in the angle-order methods since in the first case 12 trees must be located at each sample point and in the second case 8 trees.

C A Non-parametric Estimate

Most of the distance method density estimates discussed so far have the disadvantage of assuming complete spatial randomness (CSR) in the distribution of the population in the area sampled. This assumption justifies the use of the Poisson distribution in developing the various density estimates. However, many authors (e.g., see Engeman et al., 1994) suggest that plant distributions are seldom random and are often aggregated. In contrast, the use of non-parametric statistics to develop a density estimate would require no assumption about the underlying distribution of organisms.

Patil et al. (1979) and Patil et al. (1982) developed a distance-based, non-parametric estimate of plant density. It is beyond the scope of this paper to derive these formulæ. The latter paper revises their earlier work and the estimates, which we state without proof, come from the suggested formulæ in Patil et al. (1982).

Non-parametric Estimates

Data are collected as in the special case of the order method described above. That is, at each of the n sample points along the transect, the distance to the closest individual is recorded (there are no quarters). These n distances are then ordered from smallest to largest. Let $R_{(k)}$ denote the k th order statistic, that is, the k th smallest such distance. Next, for any real number r , let $[r]$ denote the floor function, that is, the greatest integer less than or equal to r . Then

$$\hat{\lambda} = \frac{n^{2/3} - 1}{n\pi R_{([n^{2/3}])}^2}. \quad (40)$$

⁶A word of caution: The formulæ for angle-order density estimates are notationally complex and it is easy to make an error in copying or using them. The formula for the angle-order method density estimate $\hat{\lambda}_2$ in (35), which is really Morisita (1957, equation 31), is given in Engeman et al. (1994, pp. 1771, 1773) as

$$[nq(kq-1)/\pi] \sum 1/R_{(k)ij}^2. \quad (39)$$

That is, they multiply by n rather than divide by n in the first factor. Based on (39), they then write (36) as

$$\text{AO1Q:} \quad [12n/\pi] \sum 1/R_{(1)ij}^2,$$

and for $k = 2$ and $k = 3$, they write

$$\text{AO2Q:} \quad [28n/\pi] \sum 1/R_{(1)ij}^2,$$

$$\text{AO3Q:} \quad [44n/\pi] \sum 1/R_{(1)ij}^2.$$

This error for AO2Q and AO3Q occurs again in White et al. (2008, Table 1).

An estimate of the variance is given by

$$\text{Var}(\hat{\lambda}) = \frac{\hat{\lambda}^2}{n^{2/3}} \tag{41}$$

and so the the standard deviation is $\frac{\hat{\lambda}}{n^{1/3}}$. For large samples, a confidence interval is developed in the usual way: The endpoints of a $(1 - \alpha)100\%$ confidence interval for the density λ are well-approximated by

$$C_1 = \hat{\lambda} + \frac{z_{\frac{\alpha}{2}} \hat{\lambda}}{n^{1/3}} \quad \text{and} \quad C_2 = \hat{\lambda} + \frac{z_{1-\frac{\alpha}{2}} \hat{\lambda}}{n^{1/3}}. \tag{42}$$

EXAMPLE C.1. The data in Example B.2 lists the distances to the closest trees at $n = 15$ sample points. Estimate the density non-parametrically.

SOLUTION. The ordered data are

$R_{(k)}$	0.2	0.6	0.7	0.7	0.7	0.7	0.9	1.0	1.0	1.0	1.1	1.1	1.2	1.2	2.3
$\pi R_{(k)}^2$	0.13	1.13	1.54	1.54	1.54	1.54	2.54	3.14	3.14	3.14	3.80	3.80	4.52	4.52	16.62

Now use (40) and (41). Since $[n^{2/3}] = [15^{2/3}] = [6.08] = 6$, then $R_{([15^{2/3}])} = R_{(6)} = 0.7$. Thus,

$$\hat{\lambda} = \frac{n^{2/3} - 1}{n\pi R_{([n^{2/3}])}^2} = \frac{15^{2/3} - 1}{15(1.54)} = 0.2201 \text{ trees/m}^2.$$

This estimate of λ compares favorably with those given by the parametric formulæ in Table 12.

An estimate of the variance is given by

$$\text{Var}(\hat{\lambda}) = \frac{\hat{\lambda}^2}{n^{2/3}} = \frac{(0.2201)^2}{15^{2/3}} = 0.0080$$

and for the standard deviation by $\sqrt{\text{Var}(\hat{\lambda})} = \sqrt{0.0080} = 0.0894$. Though the sample size is not large, we illustrate the calculation of a 95% confidence interval for λ .

$$C_1 = \hat{\lambda} + \frac{z_{0.025} \hat{\lambda}}{n^{1/3}} = 0.2201 - 1.96(0.0894) = 0.0449 \text{ trees/m}^2$$

and

$$C_2 = \hat{\lambda} + \frac{z_{0.975} \hat{\lambda}}{n^{1/3}} = 0.2201 + 1.96(0.0894) = 0.3953 \text{ trees/m}^2.$$

This confidence interval is wider than the one calculated in Example B.2 using parametric methods. In the discussion section of Patil et al. (1982), the authors note that the price for a robust density estimate “is the considerable increase in variance as compared to a parametric estimator which assumes a specific spatial distribution of plants.”

Truncated Sampling

For truncated sampling, that is, when a consistent upper limit is placed on the search radius used about each sample point, Patil et al. (1979) derived formulæ for the density and its variance. Using these formulæ with the modifications in Patil et al. (1982) leads to the following. Let w be the upper limit for the radius beyond which one does not search. Let n be the number of sample points and let n_1 denote the number of sample points with observations, that is, points where the distance to the nearest individual does not exceed w . (So there are $n_0 = n - n_1$ sample points without observations.) The data are the order statistics $R_{(k)}$, where $k = 1, \dots, n_1$.

Then

$$\hat{\lambda}_t = \frac{n_1}{n} \left(\frac{n_1^{2/3} - 1}{n_1 \pi R_{([n_1^{2/3}])}^2} \right). \tag{43}$$

An estimate of the variance is given by

$$\text{Var}(\hat{\lambda}_t) = \frac{\hat{\lambda}_t^2}{n_1^{2/3}} + \hat{\lambda}_t^2 \left(\frac{1}{n_1} - \frac{1}{n} \right) \left(1 + \frac{1}{n_1^{2/3}} \right). \tag{44}$$

For large samples, the endpoints of a $(1 - \alpha)100\%$ confidence interval for the density λ are well-approximated by

$$C_1 = \hat{\lambda}_t + z_{\frac{\alpha}{2}} \sqrt{\text{Var}(\hat{\lambda}_t)} \quad \text{and} \quad C_2 = \hat{\lambda}_t + z_{1-\frac{\alpha}{2}} \sqrt{\text{Var}(\hat{\lambda}_t)}. \quad (45)$$

EXAMPLE C.2. To illustrate these calculations return once more to the data in Example C.1. Suppose that the students who collected the data only brought a 1 meter stick with them and so did not search for trees beyond a meter from each sampling point. Then the data would consist of the $n_1 = 10$ observations that were no greater than 1.0 m. Determine a density estimate non-parametrically.

SOLUTION. We have $n = 15$ sampling points, $\lfloor n_1^{2/3} \rfloor = \lfloor 10^{2/3} \rfloor = 4$, and from the table in Example C.1, $R_{(4)} = 0.7$. Using (43), (44) we obtain

$$\hat{\lambda}_t = \frac{n_1}{n} \left(\frac{n_1^{2/3} - 1}{n_1 \pi R_{(\lfloor n_1^{2/3} \rfloor)}^2} \right) = \frac{10}{15} \left(\frac{10^{2/3} - 1}{10 \pi R_{(4)}^2} \right) = \frac{2}{3} \left(\frac{3.6416}{10 \pi (0.7)^2} \right) = 0.1577 \text{ trees/m}^2$$

and

$$\begin{aligned} \text{Var}(\hat{\lambda}_t) &= \frac{\hat{\lambda}_t^2}{n_1^{2/3}} + \hat{\lambda}_t^2 \left(\frac{1}{n_1} - \frac{1}{n} \right) \left(1 + \frac{1}{n_1^{2/3}} \right) \\ &= \frac{(0.1577)^2}{10^{2/3}} + (0.1577)^2 \left(\frac{1}{10} - \frac{1}{15} \right) \left(1 + \frac{1}{10^{2/3}} \right) \\ &= 0.00637. \end{aligned}$$

So a 95% confidence interval for λ using these data would be

$$C_1 = \hat{\lambda}_t + z_{\frac{\alpha}{2}} \sqrt{\text{Var}(\hat{\lambda}_t)} = 0.1577 - 1.96 \sqrt{0.00637} = 0.0013 \text{ trees/m}^2$$

and

$$C_2 = \hat{\lambda}_t + z_{1-\frac{\alpha}{2}} \sqrt{\text{Var}(\hat{\lambda}_t)} = 0.1577 + 1.96 \sqrt{0.00637} = 0.3141 \text{ trees/m}^2.$$

D R Scripts

This appendix provides links to R scripts to carry out the various calculations described earlier in this article. Examples illustrate how these scripts may be used and to verify that they work as expected.

What is R?

R is a language and environment for statistical computing and graphics. It is available as Free Software at <http://www.r-project.org> under the terms of the Free Software Foundation's GNU General Public License in source code form. It compiles and runs on a wide variety of operating systems such as Windows, MacOS, and most UNIX platforms.

There are many online resources to help you learn about R. Start with the R-project homepage at <http://www.r-project.org>. Here are a few others written for those just beginning to use R.

1. John Verzani's "simpleR" at <http://cran.r-project.org/doc/contrib/Verzani-SimpleR.pdf>
2. "Software Resources for R" at <http://courses.statistics.com/software/R/Rhome.htm>
3. "R: A self-learn tutorial" at <http://www.nceas.ucsb.edu/files/scicomp/Dloads/RProgramming/BestFirstRTutorial.pdf>
4. Kelly Black's extensive "R Tutorial" at <http://www.cyclismo.org/tutorial/R/index.html>

Downloading the Basic Scripts

I have written four basic functions to carry out the calculations previously described that are contained in a single file. They may be downloaded (once per session) using R's `source()` command as shown.

```
source("http://math.hws.edu/pcqm/pcqm.txt")

## Downloaded: importance.val( )
## Downloaded: density.est( )
## Downloaded: angle.order.est( )
## Downloaded: np.density.est( )
```

Note: Lines that begin with `##` consist of output from the command that precedes them. Examples in the following sections describe what data these functions require, how this data should be formatted, how the functions are used, and verify that the functions work as expected.

Script to Calculate Importance Value

The function `importance.val()` may be used to calculate the importance value of various species from data collected using the point-centered quarter method. The function has the following form:

```
importance.val(z = dataframe)
```

Details: `z` is a data frame in which each row contains the following data in the order listed.

- The first column identifies the sample point along the transect. This may be a number or other descriptor.
- The second column identifies the quarter in which the observation was made. Typically quarters are designated 1, 2, 3, and 4. But other designations, such as orientation (NW, NE, SE, SW) are possible. There must be four quarters associated with each sample point and the same four quarter descriptors should (but not must) be used at each sample point.
- The third column lists the species name or other descriptor of the closest individual to the sample point in the current quarter.
- The fourth column contains the distance (in meters) of the nearest individual to the sample point in the current quarter.
- The fifth column contains a single diameter at breast height (in centimeters) of the nearest individual to the sample point in the current quarter. Multi-stem data are not allowed.

The columns may have headers. The expectation is that the data have been recorded in a spreadsheet in csv format or in a text file in five columns in the order just described. There can be no missing data (no blank cells) in the file.

The function returns the Relative Density, Relative Cover, Relative Frequency, Importance Value, and Relative Importance of each species observed along the transect(s). It also returns an estimate of the overall Absolute Density per hectare, as well as an estimate of the Absolute Density of each species. The species are listed in descending order of Importance Value.

Examples D.1 and D.2 illustrate the use of `importance.val()` and verify its accuracy by comparing its output to calculations that appear in the literature. Note: The data files used in all of the examples are publicly accessible.

EXAMPLE D.1. To illustrate how calculate importance values, (Mueller-Dombois and Ellenberg, 1974, Table 7.4) use the data collected at five sample points at intervals of 5 m in a tropical insular rainforest near Honolulu, HI in 1972. The authors emphasize that these data are for illustrative purposes only and that a sample of at least 20 points per stand is recommended. The data are located in a csv file (click on the link) at <http://math.hws.edu/pcqm/PauoaFlats.csv>. Here are the first two lines of the data file to show the format.

```
Sample Pt,Qtr No,Species,Distance m,DBH cm
1,1,Psidium guajava,0.7,5.5
1,2,Acacia koa,1.6,42.5
```

To read and list the data with R, and then calculate the importance value of each species, use

```

PauoaFlats <- read.csv("http://math.hws.edu/pcqm/PauoaFlats.csv", header = TRUE)
PauoaFlats                                     # list the data

##      Sample.Pt Qtr.No      Species Distance.m DBH.cm
## 1           1     1      Psidium guajava      0.7   5.5
## 2           1     2      Acacia koa         1.6  42.5
## 3           1     3  Metrosideros collina      3.5  17.0
## 4           1     4  Metrosideros tremuloides  2.0  25.0
## 5           2     1      Psidium guajava      1.1   4.0
## 6           2     2      Psidium guajava      0.8   5.0
## 7           2     3      Psidium guajava      1.9   5.0
## 8           2     4      Psidium guajava      1.8   4.0
## 9           3     1      Acacia koa         1.3  75.0
## 10          3     2      Psidium guajava      0.7   3.0
## 11          3     3  Metrosideros collina      1.5   9.0
## 12          3     4  Metrosideros collina      2.0  23.0
## 13          4     1      Acacia koa         3.1  14.0
## 14          4     2      Psidium guajava      1.7   6.0
## 15          4     3      Psidium guajava      1.1   5.0
## 16          4     4      Acacia koa         1.9  12.0
## 17          5     1      Acacia koa         2.5  23.0
## 18          5     2      Acacia koa         2.2  18.0
## 19          5     3      Psidium guajava      1.4   5.0
## 20          5     4  Metrosideros collina      2.8  25.0

importance.val(PauoaFlats)                    # do the calculations

## Number of sample points: n = 5
## Overall Absolute Density per Hectare (Cottam & Curtis): 3156.17
##
##              Rel Density  R Cover  R Freq  Importance  R Import  Abs Density
## Acacia koa              30.00   78.54   30.77    139.31    46.44    946.85
## Psidium guajava         45.00    1.89   38.46    85.35    28.45   1420.28
## Metrosideros collina    20.00   13.88   23.08    56.96    18.99    631.23
## Metrosideros tremuloides  5.00    5.69    7.69    18.38    6.13    157.81

```

Up to rounding, the results are the same as in Mueller-Dombois and Ellenberg (1974), pages 113 and 119.

EXAMPLE D.2. The scripts may be used with large files. Baltzer (2007) used 105 sample points to determine importance values at Yuhus Woods, a botanically rich and diverse area in east-central Indiana.

```

Yuhas <- read.csv("http://math.hws.edu/pcqm/Baltzer2007.csv", header = TRUE)
tail(Yuhas, n = 4)                             # list the observations at the last sample point

##      Point Quarter      Species Distance.m DBH.cm
## 417    105      a  Acer saccharum      0.70  42.6
## 418    105      b  Prunus serotina      7.37  19.0
## 419    105      c  Prunus serotina      9.40  13.8
## 420    105      d   Quercus alba      7.52  49.8

importance.val(Yuhas)

## Number of sample points: n = 105
## Overall Absolute Density per Hectare (Cottam & Curtis): 433.61
##
##              Rel Density  R Cover  R Freq  Importance  R Import  Abs Density
## Acer saccharum          31.67   21.17   23.65    76.49    25.49   137.31
## Quercus alba            9.05   18.06   10.14    37.25    12.41    39.23
## Ulmus rubra             9.76    6.90   11.15    27.81    9.27    42.33
## Carya ovata             7.38    5.88    7.77    21.03    7.01    32.00

```


## Prunus serotina	7.38	3.17	7.09	17.64	5.88	32.00
## Carya cordiformis	5.95	5.88	5.41	17.24	5.75	25.81
## Aesculus glabra	5.00	2.08	4.73	11.81	3.94	21.68
## Fraxinus pennsylvanica	2.86	5.00	3.04	10.90	3.63	12.39
## Juglans nigra	1.90	4.74	2.70	9.34	3.11	8.26
## Liriodendron tulipifera	2.14	3.60	2.36	8.10	2.70	9.29
## Quercus rubra	1.90	3.75	2.36	8.01	2.67	8.26
## Quercus muehlenbergii	1.43	2.81	2.03	6.27	2.09	6.19
## Acer saccharinum	1.19	4.10	0.68	5.97	1.99	5.16
## Celtis occidentalis	2.38	0.88	2.70	5.96	1.99	10.32
## Ulmus Americana	2.14	0.55	3.04	5.73	1.91	9.29
## Fraxinus americana	1.90	1.01	2.70	5.61	1.87	8.26
## Carya glabra	1.43	1.86	2.03	5.32	1.77	6.19
## Quercus palustris	0.24	3.13	0.34	3.71	1.24	1.03
## Ostrya virginiana	1.19	0.27	1.69	3.15	1.05	5.16
## Fagus grandifolia	0.48	1.36	0.68	2.52	0.84	2.06
## Quercus velutina	0.48	0.73	0.68	1.89	0.63	2.06
## Tilia americana	0.48	0.35	0.68	1.51	0.50	2.06
## Gymnocladus dioica	0.24	0.88	0.34	1.46	0.49	1.03
## Nyssa sylvatica	0.24	0.65	0.34	1.23	0.41	1.03
## Acer rubra	0.24	0.48	0.34	1.06	0.35	1.03
## Populus Deltoides	0.24	0.40	0.34	0.98	0.33	1.03
## Carya laciniata	0.24	0.19	0.34	0.77	0.26	1.03
## Cercis canadensis	0.24	0.09	0.34	0.67	0.22	1.03
## Carpinus caroliniana	0.24	0.04	0.34	0.62	0.21	1.03

The results agree with those reported in Baltzer (2007) and Baltzer et al. (2007).

EXERCISE D.1. Create a csv file for the data in Table 1. Verify that the analysis in Table 9 is correct. You will have to make one modification to Table 1. The multi-stem DBH at one of the quarters must be converted to an equivalent single stem DBH of 10 cm.

EXERCISE D.2. Ten sample points were used to survey a forest plot in the northwestern United States. Determine the relative importance and density estimate for each of the four species in the data set at <http://math.hws.edu/pcqm/fir.csv>. Species key: AGR = *Abies grandis*, PSME = *Pseudotsuga menziesii*, PIPO = *Pinus ponderosa*, and LAOC = *Larix occidentalis*. (Answer. Relative importance (in the order above): 77.17, 12.98, 6.51, and 3.34; Density: 17.80, 2.78, 1.11, 0.56.)

EXERCISE D.3. Analyze a large data set of 255 sample points recorded in Alaska in 2000 by Hollingsworth (2005). The data are the first 51 transects listed in http://www.lter.uaf.edu/ascii/files/138_pcqbs_ht_diam.txt. Species key: picmar = *Picea mariana*, picgla = *Picea glauca*, alncri = *Alnus crispa*, betneo = *Betula neolaskana*, larlar = *Larix laricina*, and salgla = *Salix glauca*. Determine the relative importance and density estimate for each species. (Partial answer: Relative Importance: picmar 92.08, betneo 1.27. Density: picmar 3125.34, betneo 29.00.)

Script to Estimate Density

The function `density.est()` may be used to calculate densities of organisms from data collected using the point-centered quarter method. The function has the following form:

```
density.est(z = dataframe, method = c("pollard", "cottam", "warde"), conf.level = 0.95)
```

Details: `z` is a data frame where each row contains the distances from the sample point to the nearest individual in each sector. The argument `method` specifies how the calculation is made:

"pollard" uses Formula 5.1 on page 11;

"cottam" uses the formula in equation (1) on page 5;

"warde" uses the formula in equation (8) on page 14.

When `method = "pollard"`, a fixed number q of equiangular sectors must be used at each sample point. For methods `"cottam"` and `"warde"` quarters, that is, four equiangular sectors, are required at each sample point.

The default method is `"pollard"`. The method `"warde"` should be used for data sets containing vacant quarters, that is, quarters in which no individual was found. If methods `"pollard"` or `"cottam"` are used with missing observations (NA), the calculation method automatically defaults to `"warde"`, assuming that quarters were used.

`conf.level` specifies the confidence level of the interval and has a default value of 0.95. A confidence interval is computed only when `method = "pollard"`.

EXAMPLE D.3. The data in Example 5.2 (see <http://math.hws.edu/pcqm/lamington.csv> for format) measured the distance to the nearest tree in each quarter for 15 sample points. After reading and listing the data, to estimate the density and calculate a 95% confidence interval using Pollard's method, use the `density.est()` function with its default arguments `method = "pollard"` and `conf.level = 0.95`, which need not appear in the function call.

```
lamington <- read.csv("http://math.hws.edu/pcqm/lamington.csv")
lamington

##      Qtr.1 Qtr.2 Qtr.3 Qtr.4
## 1      1.5  1.2  2.3  1.9
## 2      3.3  0.7  2.5  2.0
## 3      3.3  2.3  2.3  2.4
## 4      1.8  3.4  1.0  4.3
## 5      0.9  0.9  2.9  1.4
## 6      2.0  1.3  1.0  0.7
## 7      0.7  2.0  2.7  2.5
## 8      2.6  4.8  1.1  1.2
## 9      1.0  2.5  1.9  1.1
## 10     1.6  0.7  3.4  3.2
## 11     1.8  1.0  1.4  3.6
## 12     4.2  0.6  3.2  2.6
## 13     4.1  3.9  0.2  2.0
## 14     1.7  4.2  4.0  1.1
## 15     1.8  2.2  1.2  2.8

density.est(lamington)

##
## Pollard's estimate of density using 4 sectors per point
##
## data: lamington
## No. of sample pts: n = 15
## 95 percent confidence interval:
## 1676.98 2787.47
## sample estimates:
## density per hectare
##                2160.95
```

The density estimate is identical to that calculated in Example 5.2, but the confidence interval is narrower. The confidence interval calculated by `density.est()` is exact, using the chi-squared distribution as in Example B.1, rather than using a normal approximation. To just calculate a 99% confidence interval for the density, use `conf.level = 0.99` and display the result as a vector. The interval widens with an increase in confidence.

```
as.vector(density.est(lamington, conf.level = 0.99)$conf.int)

## [1] 1535.59 2996.91
```

To use the density estimate proposed in Cottam et al. (1953), set `method = "cottam"`.

```
density.est(lamington, method = "cottam")

##
## Cottam, Curtis, & Hale Point-Centered Quarter Method density estimate
##
## data: lamington
## No. of sample pts: n = 15
## sample estimates:
## density per hectare
##                2200.7
```

Suppose that we remove two of the observations from the `lamington` data set to simulate that there were two quarters in which an individual could not be found. It is now appropriate to use the method described by Warde and Petranka (1981) to estimate the density. The data are located at <http://math.hws.edu/pcqm/lamington.vacant.csv>. Notice that the missing values are in rows 9 (trailing comma) and 13 (consecutive commas).

```
Qtr 1,Qtr 2,Qtr 3,Qtr 4
1.5,1.2,2.3,1.9
3.3,0.7,2.5,2
3.3,2.3,2.3,2.4
1.8,3.4,1,4.3
0.9,0.9,2.9,1.4
2,1.3,1,0.7
0.7,2,2.7,2.5
2.6,4.8,1.1,1.2
1,2.5,1.9,
1.6,0.7,3.4,3.2
1.8,1,1.4,3.6
4.2,0.6,3.2,2.6
4.1,,0.2,2
1.7,4.2,4,1.1
1.8,2.2,1.2,2.8
```

```
lamington.vacant <- read.csv("http://math.hws.edu/pcqm/lamington.vacant.csv", header = TRUE)
lamington.vacant      # list the data; note that empty numerical cells are replaced with NA
```

```
##      Qtr.1 Qtr.2 Qtr.3 Qtr.4
## 1      1.5  1.2  2.3  1.9
## 2      3.3  0.7  2.5  2.0
## 3      3.3  2.3  2.3  2.4
## 4      1.8  3.4  1.0  4.3
## 5      0.9  0.9  2.9  1.4
## 6      2.0  1.3  1.0  0.7
## 7      0.7  2.0  2.7  2.5
## 8      2.6  4.8  1.1  1.2
## 9      1.0  2.5  1.9   NA
## 10     1.6  0.7  3.4  3.2
## 11     1.8  1.0  1.4  3.6
## 12     4.2  0.6  3.2  2.6
## 13     4.1   NA  0.2  2.0
## 14     1.7  4.2  4.0  1.1
## 15     1.8  2.2  1.2  2.8
```

```
density.est(lamington.vacant, method = "warde")

##
## Warde & Petranka (1981) estimate of density using 4 sample quarters per point
##
## data: lamington.vacant
```

```
## No. of sample pts: n = 15, No. of vacant quarters: = 2
## sample estimates:
## density per hectare
##                2024.03
```

EXAMPLE D.4. Pollard's method requires the use of equiangular sectors at each point, not necessarily quarters. In Example 5.2, that is, Example D.3, quarters 1 and 2 were on the eastern side of the transect while quarters 3 and 4 were on the western side. Instead of using quarters at each sample point, assume we divided the world into east and west halves and selected the nearest individual in each half. We can use the original data to obtain this information and then calculate the corresponding density estimate.

```
lamington.2 <- data.frame(East = apply(lamington[,1:2],1,min), West = apply(lamington[,3:4],1,min))
tail(lamington.2, n = 3) # check that the data is as expected

##      East West
## 13  3.9  0.2
## 14  1.7  1.1
## 15  1.8  1.2

density.est(lamington.2)

##
## Pollard's estimate of density using 2 sectors per point
##
## data: lamington.2
## No. of sample pts: n = 15
## 95 percent confidence interval:
## 1414.93 2911.44
## sample estimates:
## density per hectare
##                2027.23
```

The density estimate is within 6% of the original estimate of 2160.95 trees/ha in Example D.3, but required about half the sampling effort. However, with less data, the confidence interval is wider.

EXERCISE D.4. A problem in Krebs (1999) asks to estimate the population density and find a 95% confidence interval for the density for Amabilis fir in the Coast Range of British Columbia using point-quarter data collected at $n = 10$ points. The data may be found at <http://math.hws.edu/pcqm/Krebs.csv>. Use an appropriate R function to determine the answer. (Answer: Density per hectare: 192.958; confidence interval: [141.387, 263.780].)

EXERCISE D.5. From (Pierce et al., 2012, pp. 299–300): To estimate the number of active bird nests in a study area during breeding season, a transect with five sample points spaced 100 m apart was used and the distances (in m) to the nearest nest in each quarter were recorded. I: 0, 15, 15, 15; II: 10, 7, 7, 5; III: 1, 12, 3, 11; IV: 10, 10, 12, 1; V: 11, 9, 9, 7. Estimate the number of nests per hectare and determine a 95% confidence interval for the density. (Answer: Density per hectare 130.77; confidence interval: [84.08, 204.21].)

Script to Estimate Density Using Angle-Order Methods

Morisita (1957) combined the angle and order methods by dividing the region about each sample point into q equiangular sectors and recording the distance to the k th nearest individual in each sector. The function `angle.order.est()` calculates densities of organisms from data collected in this way.

```
angle.order.est(z = dataframe, k = 3, method = c("auto", "morisita1", "morisita2",
"morisita"), conf.level = 0.95)
```

Details: `z` is a data frame where each row contains the q observations for a single sample point. The argument `k` specifies that the observations are distances to the k th nearest individual in each of the q equiangular sectors. No missing observations are allowed. The default is `k = 3`. The argument `method` specifies how the calculation is made:

"auto" is the default method and uses Morisita's guidelines (see page 26) to estimate the density.

If $\hat{\lambda}_1 > \hat{\lambda}_2$, then $\hat{\lambda}_1$ is used. Otherwise $\hat{\lambda}_0 = \frac{\hat{\lambda}_1 + \hat{\lambda}_2}{2}$ is used. This method requires that $k \geq 3$.

"morisita1" uses equation (34): $\hat{\lambda}_1 = \frac{k-1}{\pi n} \sum_{i=1}^n \sum_{j=1}^q \frac{1}{R_{(k)ij}^2}$. This method requires that $k \geq 3$.

"morisita2" uses equation (35): $\hat{\lambda}_2 = \frac{kq-1}{\pi n} \sum_{i=1}^n \frac{q}{\sum_{j=1}^q R_{(k)ij}^2}$. This method requires that $kq \geq 2$.

"morisita" uses equation (32): $\hat{\lambda} = \frac{q(kqn-1)}{\pi \sum_{i=1}^n \sum_{j=1}^q R_{(k)ij}^2}$. Note: If $k = 1$, then this estimate is the same as (20), which is computed when `method = "pollard"` in the function `density.est()`. Instead, if $q = 1$, then this estimate is the same as (28).

`conf.level` specifies the confidence level of the interval and has a default value of 0.95. A confidence interval is computed only when `method = "morisita"`.

EXAMPLE D.5. Redo Example B.2 that used the closest trees to the 15 sample points in Example 5.2 to estimate the density and find a 95% confidence interval for this estimate. This requires using `method = "morisita"` and `k = 1` in the `angle.order.est()` function. Re-use the `lamington` data from Example D.3. The results, up to rounding, are the same as calculated earlier in Example B.2.

```
lamington.closest <- data.frame(min.dist = apply(lamington, 1, min)) # closest individual
angle.order.est(lamington.closest, k = 1, method = "morisita")

##
## Morisita angle-order density estimate for randomly distributed populations with 1 sector
## at each sample point using the closest individuals.
##
## data: lamington.closest
## Number of sample points: n = 15
## 95 percent confidence interval:
## 1594.47 4461.20
## sample estimates:
## density per hectare
## 2658.91
```

EXAMPLE D.6. In Example B.3 we used (36) and the `lamington` data in Example 5.2 with $k = 1$ to obtain a density estimate of 2078 trees/ha. Equation (36) corresponds to `method = "morisita2"` and `k = 1`.

```
angle.order.est(lamington, k = 1, method = "morisita2")

##
## Morisita 2 density estimate with 4 sectors at each sample point using the closest
## individual in each sector.
##
## data: lamington
## Number of sample points: n = 15
## sample estimates:
## density per hectare
## 2078.42
```

Script to Estimate Density Non-parametrically

Appendix C described a distance-based, non-parametric estimate of plant density developed by Patil et al. (1982). The data for this method consist of the distances of the nearest individual to each sample point. The function `np.density.est()` may be used to calculate densities in this way.

```
np.density.est(z = dataframe, conf.level = 0.95)
```

Details: `z` is a data frame comprising a single column of distances of the nearest individual to each sample point. Missing observations should be indicated by `NA`, though the function should automatically detect blank entries. `conf.level` specifies the confidence level of the interval and has a default value of `0.95`.

EXAMPLE D.7. Example C.1 used the method of Patil et al. (1982) to non-parametrically estimate density and locate a 95% confidence interval. It employed the `lamington.closest` data set from Example D.5 that listed the distances to the nearest trees from 15 sample points. The calculations below agree with those in Example C.1.

```
np.density.est(lamington.closest)

##
## Patil, et. al. (1982) non-parametric density estimate using the closest individual at
## each sample point.
##
## data: lamington.closest
## No. of sample pts: n = 15
## 95 percent confidence interval:
## 451.802 3950.144
## sample estimates:
## density per hectare
## 2200.97
```

Example C.2 also used the data in Example C.1 (that is, `lamington.closest`), but omitted all five distances greater than 1.0 m. The results using the truncated data agree with those in Example C.2.

```
lamington.trunc <- lamington.closest
lamington.trunc[lamington.trunc > 1] <- NA # substitute NA for distances greater than 1 m
np.density.est(lamington.trunc)

##
## Patil, et. al. (1982) non-parametric density estimate using the closest individual at
## each sample point.
##
## data: lamington.trunc
## No. of sample pts: n = 15, No. of truncated points: = 5
## 95 percent confidence interval:
## 13.2614 3140.8984
## sample estimates:
## density per hectare
## 1577.08
```

EXAMPLE D.8. To illustrate their method, Patil et al. (1982) used data from a 100-point transect in Batcheler (1971). These data may be found at <http://math.hws.edu/pcqm/Batcheler1971.csv>. The original data were recorded in feet and must be converted to meters before calculation. Further, the density was given in acres, so the output of `np.density.est()`, which is in hectares, must be converted to acres.

```
Batcheler <- read.csv("http://math.hws.edu/pcqm/Batcheler1971.csv", header = TRUE)
tail(Batcheler, n = 3) # list the last three data values

## Batcheler.1971
## 98 25.7
## 99 20.6
## 100 25.6

BatchelerMeters <- 0.30480 * Batcheler # convert feet to meters
np.density.est(BatchelerMeters)
```

```
##
## Patil, et. al. (1982) non-parametric density estimate using the closest individual at
## each sample point.
##
## data: BatchelerMeters
## No. of sample pts: n = 100
## 95 percent confidence interval:
## 200.826 494.387
## sample estimates:
## density per hectare
## 347.606

cat("Density estimate:", 0.404686*np.density.est(BatchelerMeters)$est) # convert to acres

## Density estimate: 140.671

cat("Confidence interval:", 0.404686*np.density.est(BatchelerMeters)$conf.int)

## Confidence interval: 81.2713 200.071
```

Up to rounding, these results agree with (Patil et al., 1982, page 247) where the density is given as 140 plants per acre. The standard deviation is given as 30 plants. From (42), the confidence interval limits using 140 and 30 are shown below, and agree with those calculated above, given rounding.

```
140 + 1.96 * c(-30, 30) # confidence limits
## [1] 81.2 198.8
```

For comparison, we estimate the density with Pollard's method.

```
cat("Density estimate:", 0.404686*density.est(BatchelerMeters, method = "pollard")$est)

## Density estimate: 142.485

cat("Confidence interval:", 0.404686*density.est(BatchelerMeters, method = "pollard")$conf.int)

## Confidence interval: 117.103 173.47
```

The two density estimates differ by 1.5%. However, the 95% confidence interval is nearly twice as wide using the non-parametric method, as Patil et al. (1982) warned.

Suppose that the sampling effort is truncated with a maximum search radius of 7.8 ft. That is, if no plant is found within that radius of the sample point, then the search is terminated. (The value of 7.8 ft was used in Patil et al. (1979) because it eliminates half the data.) To carry out the analysis, first truncate the data.

```
BatchelerMeters[BatchelerMeters > 0.30480 * 7.8] <- NA # substitute NA if > 7.8 ft
np.density.est(BatchelerMeters)

##
## Patil, et. al. (1982) non-parametric density estimate using the closest individual at
## each sample point.
##
## data: BatchelerMeters
## No. of sample pts: n = 100, No. of truncated points: = 50
## 95 percent confidence interval:
## 170.299 620.798
## sample estimates:
## density per hectare
## 395.548

cat("Density estimate:", 0.404686*np.density.est(BatchelerMeters)$est) # convert to acres
```

```
## Density estimate: 160.073
cat("Confidence interval:", 0.404686*np.density.est(BatchelerMeters)$conf.int)
## Confidence interval: 68.9176 251.228
```

The result is within 15% of the original density estimate and would have required just half the sampling effort. However, the confidence interval is about two-thirds wider than before.

Re-analyzing Data

The following functions may be used to further analyze survey data that consists of the rectangular coordinates of all the trees in a particular plot. This might be done to determine which methods provide accurate density estimates for particular forest types. These functions may be downloaded using `source("http://math.hws.edu/pcqm/survey.txt")`.

```
convex.hull(z = dataframe, lcolor = "orange", display = TRUE)
```

Details: `z` specifies a data frame with two columns containing the x and y coordinates, in meters, of all individuals in the area surveyed; `lcolor` specifies the color used to draw the convex hull (smallest convex polygon, i.e., ‘rubber band’) containing the surveyed individuals, with default set to "orange".

Output: The area of the convex hull and the density calculated using the hull area are reported. The area of the smallest rectangle, with sides parallel to the axes, that contains the data and the corresponding density are also reported. If `display = TRUE`, a plot of the data, its convex hull, and bounding rectangle are drawn.

```
manual.survey <- function(z = dataframe, t.coords = c(0, 0, 10, 10), points = 10,
  transects = 2, k = 1, horizontal = TRUE, display = TRUE)
```

Details: `manual.survey()` takes the locations of all individuals in a specified area and produces the data required to estimate density using the functions described earlier in this section. `z` specifies a data frame with two columns containing the x and y coordinates, in meters, of all individuals in the area surveyed; `t.coords` is a vector of the form $(x_1, y_1, x_2, y_2, \dots)$ containing the coordinates of either two or four points that are used to determine either one or more transects, respectively. If four points are used, they should be listed counter-clockwise starting from the lower left. `points` specifies the number of sample points; `transects` specifies the number of transects; `k` specifies that the k th closest individual is sampled in each quarter with default `k = 1`; `display` is the logical value specifying whether the forest is shown, with default `TRUE`; and `horizontal` is a logical value specifying whether the orientation of the transects is horizontal (by default `TRUE`) or not (vertical).

Transects: If `t.coords` contains four components specifying two points, then these two points are used as the endpoints of a single transect with the specified number of sample points distributed evenly along its length. If `t.coords` contains eight components specifying four points and `horizontal = TRUE`, then the first two points are used as the endpoints of the bottommost transect and the remaining two points are used as the endpoints of the uppermost transect. Any remaining transects are interpolated between these two with the sample points distributed evenly along them. If `horizontal = FALSE`, the first and fourth points and second and third points determine the outermost transects. Note: The lines defining the quarters are always parallel to the axes regardless of whether the transects are.

Output: The area of the convex hull and the density calculated using the hull area are reported, as are the area of the bounding rectangle the corresponding density. A data frame comprised of the distances to the k th closest individual in each quarter is returned. If `display = TRUE` a plot of the data, its convex hull and bounding rectangle, and the transects with sample points as specified are drawn, with the k th closest individual in each quarter highlighted.

EXAMPLE D.9. In a study measuring the impact of deer browsing on tree regeneration, Newell (2015) collected coordinate data for all 257 trees in a plot between Snell and PreEmption Roads in Geneva, NY (see <http://people.hws.edu/mitchell/PCQM.pdf>):

//math.hws.edu/pcqm/NewellSouth.csv). To determine the site's convex hull and bounding rectangle areas and the corresponding densities, use the `convex.hull()` function. A plot is shown later in this example.

```
source("http://math.hws.edu/pcqm/survey.txt")

## Downloaded convex.hull( )
## Downloaded manual.survey( )

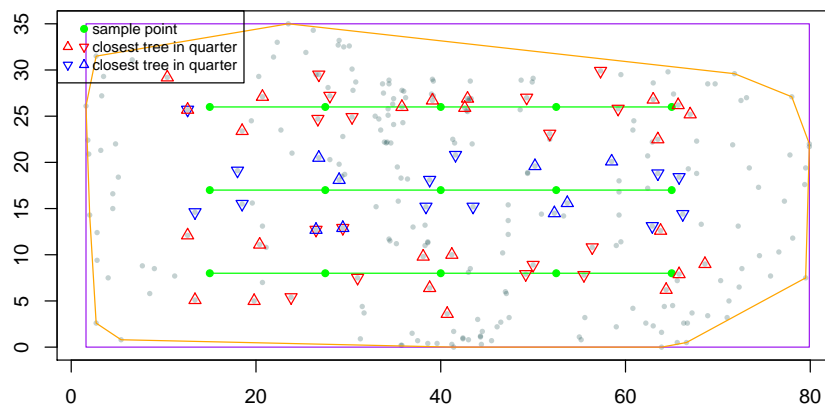
NewellSouth <- read.csv("http://math.hws.edu/pcqm/NewellSouth.csv")
convex.hull(NewellSouth, display = FALSE)

## Data: NewellSouth
##              Area (ha) Density (per ha)
## Convex Hull      0.241      1056.00
## Bounding Rectangle 0.274      930.50
```

The actual density is known, so there would seem to be no reason to estimate it. However, if one now wanted to sample, rather than completely survey, other similar areas, then it would be useful to know which sampling techniques provide accurate estimates. One can test these techniques using the previously collected data. To place transects on the site and then see how various density estimates compare to the actual density, use the `manual.survey()` function. Its output can be analyzed with an appropriate density function. To illustrate the idea, we use three horizontal transects with a total of 15 sample points to which are measured the closest individuals in each quarter. We then use Pollard's method to analyze the data.

```
Newell.horiz <- manual.survey(z = NewellSouth, t.coords = c(15, 8, 65, 8, 65, 26, 15, 26),
                             points = 15, transects = 3, k = 1)

## Data: NewellSouth
##              Area (ha) Density (per ha)
## Convex Hull      0.241      1056.00
## Bounding Rectangle 0.274      930.50
```



```
tail(Newell.horiz, n = 2)      # distances for the last two sample points

##      Qtr 1  Qtr 2  Qtr 3  Qtr 4
## 14 6.184658 3.35261 2.98329 6.70298
## 15 0.728011 2.15407 3.80789 2.15407

density.est(z = Newell.horiz, conf.level = 0.95)
```

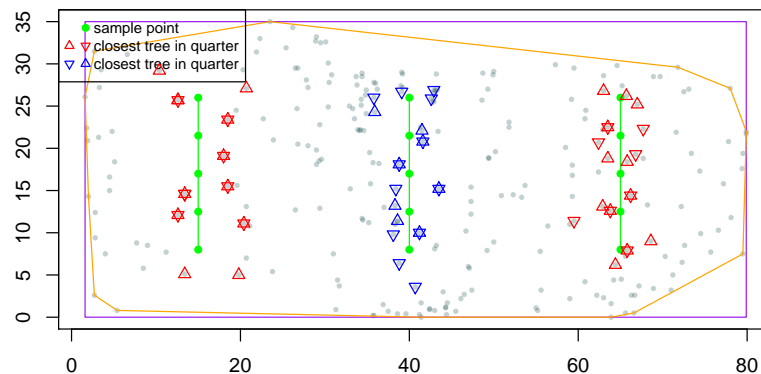
```
##
## Pollard's estimate of density using 4 sectors per point
##
## data: Newell.horiz
## No. of sample pts: n = 15
## 95 percent confidence interval:
## 639.291 1062.625
## sample estimates:
## density per hectare
## 823.787
```

The transects and sample points are depicted in green. The nearest trees to each sample point are indicated with up or down triangles whose color alternates between red and blue corresponding to the transect. This may be used to identify whether the same tree is resampled from different points. The distances from the sample points to the nearest tree in each quarter can be listed and then analyzed using techniques discussed earlier. In this example, the 95% confidence interval for Pollard's method contains the actual density using the convex hull.

If the same corner points are used with vertical transects (`horizontal = FALSE`), the array of sample points is different. There are three points in each of five horizontal rows rather than five points in each of three horizontal rows as above. The density estimate using these vertical transects happens to be more accurate in this case.

```
Newell.vert <- manual.survey(z = NewellSouth, t.coords = c(15, 8, 65, 8, 65, 26, 15, 26),
  points = 15, transects = 3, k = 1, horizontal = FALSE)

## Data: NewellSouth
##              Area (ha) Density (per ha)
## Convex Hull      0.241      1056.00
## Bounding Rectangle 0.274      930.50
```



```
density.est(z = Newell.vert, conf.level = 0.95)

##
## Pollard's estimate of density using 4 sectors per point
##
## data: Newell.vert
## No. of sample pts: n = 15
## 95 percent confidence interval:
## 679.46 1129.39
## sample estimates:
## density per hectare
## 875.548
```

Morisita (1957) suggested measuring the distance to the third closest tree in each quarter ($k = 3$). For these data, this method gives quite a good estimate of the actual density of 1056 trees/ha.

```
Newell.third <- manual.survey(z = NewellSouth, t.coords = c(15, 8, 65, 8, 65, 26, 15, 26),
  points = 15, transects = 3, k = 3, display = FALSE)
angle.order.est(z = Newell.third, k = 3, method = "auto")

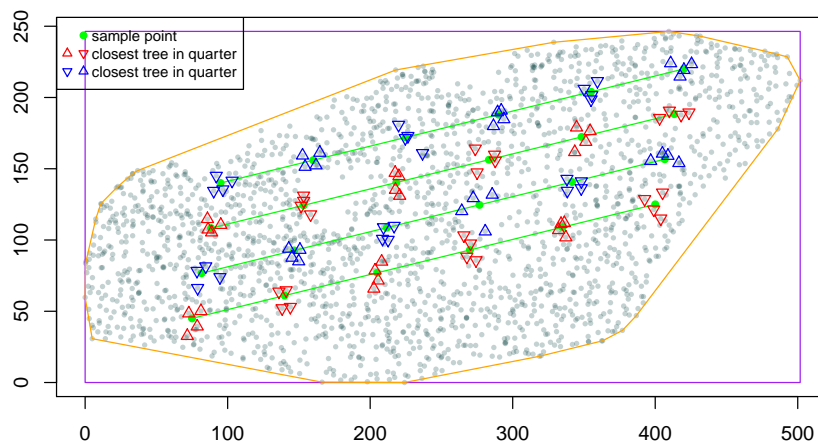
##
## Morisita Practical Procedure for density estimate with 4 sectors at each sample point
## using the third closest individuals. m1 > m2 (1045.75 > 968.82). Use m1.
##
## data: Newell.third
## Number of sample points: n = 15
## sample estimates:
## density per hectare
##          1045.75
```

EXAMPLE D.10 (Susquehanna Shale Hills Critical Zone Observatory). The Susquehanna Shale Hills Critical Zone Observatory is an 8 hectare, first-order catchment in the Susquehanna River basin (see <http://criticalzone.org/shale-hills/infrastructure/field-area/susquehanna-shale-hills-critical-zone-observatory/>).

Among its publicly available resources is a data set of the locations of all trees in the basin (see Eissenstat and Kaye (2015)). The (x, y) -location data are available at <http://math.hws.edu/pcqm/czo.csv>. The data used below were modified (translated) by subtracting the minimum values of x and y from their respective coordinates to simplify the plot.

```
czo <- read.csv("http://math.hws.edu/pcqm/czoNormalized.csv")
czo.horiz <- manual.survey(z = czo, t.coords = c(75, 45, 400, 125, 420, 220, 95, 140),
  points = 24, transects = 4, k = 1)

## Data: czo
##          Area (ha) Density (per ha)
## Convex Hull          8.507         243.80
## Bounding Rectangle   12.361         167.80
```



```
density.est(z = czo.horiz)
```

```
##
```

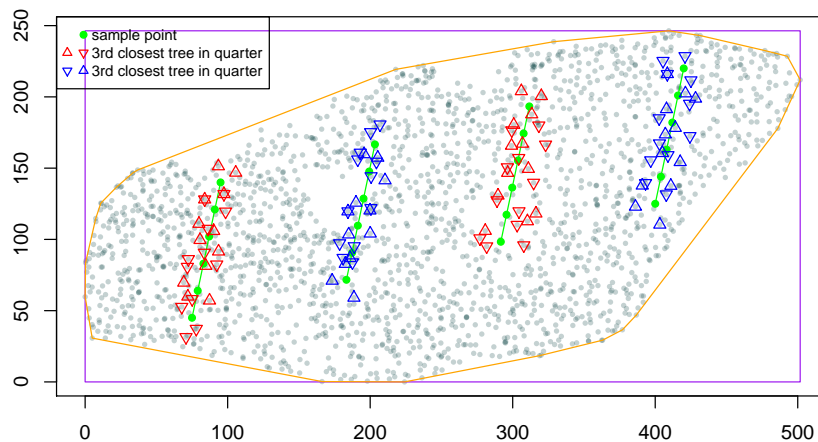
```
## Pollard's estimate of density using 4 sectors per point
##
## data:  czo.horiz
## No. of sample pts: n = 24
## 95 percent confidence interval:
## 177.898 265.685
## sample estimates:
## density per hectare
## 217.339
```

Because of the shape of the plot, the bounding rectangle is not useful. The confidence interval for the density contains the actual density of 243.8 trees/ha determined by the convex hull.

The next analysis uses the same four corner points for the transects but with a vertical orientation and Morisita's recommendation for a third-order analysis. The resulting estimate is within 4% of the actual value.

```
czo.third.vert <- manual.survey(z = czo, t.coords = c(75, 45, 400, 125, 420, 220, 95, 140),
  points = 24, transects = 4, k = 3, horizontal = FALSE)
```

```
## Data: czo
##
##          Area (ha) Density (per ha)
## Convex Hull      8.507      243.80
## Bounding Rectangle 12.361      167.80
```



```
angle.order.est(z = czo.third.vert, k = 3, method = "auto")
##
## Morisita Practical Procedure for density estimate with 4 sectors at each sample point
## using the third closest individuals. m1 > m2 (234.65 > 232.19). Use m1.
##
## data:  czo.third.vert
## Number of sample points: n = 24
## sample estimates:
## density per hectare
## 234.651
```

EXAMPLE D.11 (Barro Colorado Forest Census Data). Barro Colorado Island (BCI), a 1560-hectare island, is the Smithsonian Tropical Research Institute's primary site for the study of lowland moist tropical forests. It contains

a 50-hectare rectangular forest plot (1000 × 500-m) in which all woody trees and shrubs with stem diameters of at least 1 cm have been censused. Every stem in the plot was permanently numbered with an aluminum tag in 1982, and every individual has been revisited six times since: in 1985, 1990, 1995, 2000, 2005, and 2010. In each census, every stem was measured, mapped, and identified to species; see Condit et al. (2012).

Conditions for the use of BCI Forest Census Plot Data do not permit my sharing the raw data with other parties. However, access to the entire database may be requested at <http://ctfs.si.edu/webatlas/datasets/bci/> or see <http://dx.doi.org/10.5479/data.bci.20130603>. Once the entire data set was downloaded, a file named `bci.2010` was created containing just the recordings from the 2010 census of all main stems of live trees with a DBH of at least 10 cm. To begin, we sample the 100 m × 100 m (1-ha) plot in the southwest corner of the entire site using five horizontal transects with four sample points each. Using Morisita's recommended third-order analysis, we obtain

```
bci <- subset(bci.2010, x <= 100 & y <= 100)           # obtain subplot
cat("Actual density per hectare:", nrow(bci))         # trees in 1 ha subplot

## Actual density per hectare: 441

bci.dist.morisita <- manual.survey(z = bci, t.coords = c(15, 15, 85, 15, 85, 85, 15, 85),
  points = 20, transects = 5, k = 3, display = FALSE)
angle.order.est(z = bci.dist.morisita, k = 3, method = "auto")

##
## Morisita Practical Procedure for density estimate with 4 sectors at each sample point
## using the third closest individuals. m1 < m2 (424.19 < 462.77). Use m0 = (m1 + m2)/2.
##
## data: bci.dist.morisita
## Number of sample points: n = 20
## sample estimates:
## density per hectare
## 443.481
```

The estimate is nearly identical to the actual density of 441 trees/ha. Using the nearest point in each quarter instead yields an overestimate of 11.7%, but the confidence interval does contain the true density.

```
bci.dist.pollard <- manual.survey(z = bci, t.coords = c(15, 15, 85, 15, 85, 85, 15, 85),
  points = 20, transects = 5, k = 1, display = FALSE)
density.est(z = bci.dist.pollard)

##
## Pollard's estimate of density using 4 sectors per point
##
## data: bci.dist.pollard
## No. of sample pts: n = 20
## 95 percent confidence interval:
## 395.680 614.136
## sample estimates:
## density per hectare
## 492.768
```

The remainder of this example illustrates how more extensive sampling might allow us to determine which methods provide accurate density estimates in similar forests. Most of the sampling techniques that we have discussed assume complete spatial randomness (CSR) in the distribution of the population, which is not always true of natural populations (see Engeman et al. (1994)).

One method to measure spatial randomness is the Clark-Evans test. Assume that a population of some plot has n individuals and density ρ . Let r_i denote the distance from the i th individual to its nearest neighbor. The mean distance to the nearest neighbor is

$$\bar{r}_a = \frac{\sum_{i=1}^n r_i}{n}.$$

Clark and Evans (1954) showed that under the CSR assumption, the expected mean nearest-neighbor distance

is

$$\bar{r}_e = \frac{1}{2\sqrt{\rho}}.$$

The deviation of the actual mean from the expected mean is measured by the ratio

$$R = \frac{\bar{r}_a}{\bar{r}_e},$$

and is called the **index of aggregation**. If the spatial pattern is random, $R = 1$. When clustering or aggregation is present, $R < 1$ and approaches 0 in the most extreme cases. In a regular (dispersed) pattern, $R > 1$ and has an upper limit of just less than 2.15.

Comparing plotless density estimators using simulated populations, Engeman et al. (1994) found that angle-order methods tended to underestimate the true density when the spatial distribution was aggregated and overestimate the density when the distribution was regular. Using actual field data and Cottam and Curtis's method, Bryant et al. (2005) also observed this bias of underestimating density in aggregated populations. This tendency was less pronounced for angle-order methods in a study by Kiani et al. (2013) using actual field data. In a study involving a wide range of densities, White et al. (2008) found that angle-order methods using the second- and third-nearest trees to the sample points were among the best of the eight plotless density estimators tested when censusing aggregated populations, but performed poorly for regular (dispersed) populations.

We use $N = 966$ square 1-ha subplots laid out in a overlapping grid of 21 rows and 46 columns. The horizontal distance between the columns is $h = \frac{890}{45} \approx 19.78$ m and the vertical distance between the rows is $v = \frac{390}{21} = 19.5$ m. The lower-left corners of the plots are situated at coordinates $(hi + 5, vj + 5)$, where $0 \leq i \leq 45$ and $0 \leq j \leq 20$. These points form a grid with initial point (5, 5) and final point (895, 395).

For the Clark-Evans test to be unbiased, a guard (boundary) strip is required to surround the each subplot. Without a guard strip, trees closest to the original boundary would tend to have larger nearest-neighbor distances than those that are more interior to the plot. We use a strip 5 m wide about each sample plot that results in square guard plots with edges of 110 m. The coordinates of the 1-hectare plots were determined to ensure that any surrounding guard plot with lower-left corner (hi, vj) and upper-right corner $(hi + 110, vj + 110)$ would lie entirely within the Barro Colorado Forest site.

As with the 1-ha plot earlier in this example, we sample each plot using Morisita's third-order practical method and Pollard's method with five transects of four points each. We also carry out the Clark-Evans test on each plot.

Code. The code used for sampling the Barro Colorado Forest site and the simulated forest is listed below. The corresponding plots and results follow the code.

```
require (spatstat, quietly = TRUE) # install package
N <- 966
act.density <- R <- P.Val <- est.pollard <- est.morisita <- rep(0, N) # initialize variables
y <- rep(0, N) # lower-left plot corners
for (j in 1:N) y[j] <- 19.5*(floor((j-1)/46)) + 5
  cpt <- data.frame("x" = rep((0:45),21)*890/45 + 5, y)
  for (ct in 1:N){
    px <- c(cpt$x[ct], cpt$x[ct] + 100) # plot coordinates
    py <- c(cpt$y[ct], cpt$y[ct] + 100)
    guard <- subset(bci.2010, x >= px[1] - 5 & x <= px[2] + 5
      & y >= py[1] - 5 & y <= py[2] + 5) # guard plot for c-e test
    guard.ppp <- ppp(guard$x, guard$y, px + c(-5, 5), py + c(-5, 5))
    subplot <- subset(guard, x >= px[1] & x <= px[2] & y >= py[1] & y <= py[2])
    act.density[ct] <- nrow(subplot) # actual density of 1-ha plot
    ce <- clarkevans.test(guard.ppp, clipregion = erosion(guard.ppp$window, 5),
      alternative = "regular", correction = "guard", nsim = 99)
    R[ct] <- ce$statistic
    P.Val[ct] <- ce$p.val
    coords <- c(px[1] + 15, py[1] + 15, px[2] - 15, py[1] + 15,
      px[2] - 15, py[2] - 15, px[1] + 15, py[2] - 15)
    dist.pollard <- manual.survey(z = guard, t.coords = coords, points = 20,
      transects = 5, k = 1, display = FALSE)
    dist.morisita <- manual.survey(z = guard, t.coords = coords, points = 20,
      transects = 5, k = 3, display = FALSE)
```

```

est.pollard[ct] <- density.est(dist.pollard, method = "pollard")$estimate
est.morisita[ct] <- angle.order.est(dist.morisita, k = 3, method = "auto")$estimate
err.pollard <- (est.pollard - act.density) / act.density * 100
err.morisita <- (est.morisita - act.density) / act.density * 100
Pollard <- data.frame(Act.Dens = act.density, Est.Dens = est.pollard,
  Pct.Err = err.pollard, Abs.Err = abs(err.pollard))
Morisita <- data.frame(Act.Dens = act.density, Est.Dens = est.morisita,
  Pct.Err = err.morisita, Abs.Err = abs(err.morisita))
}

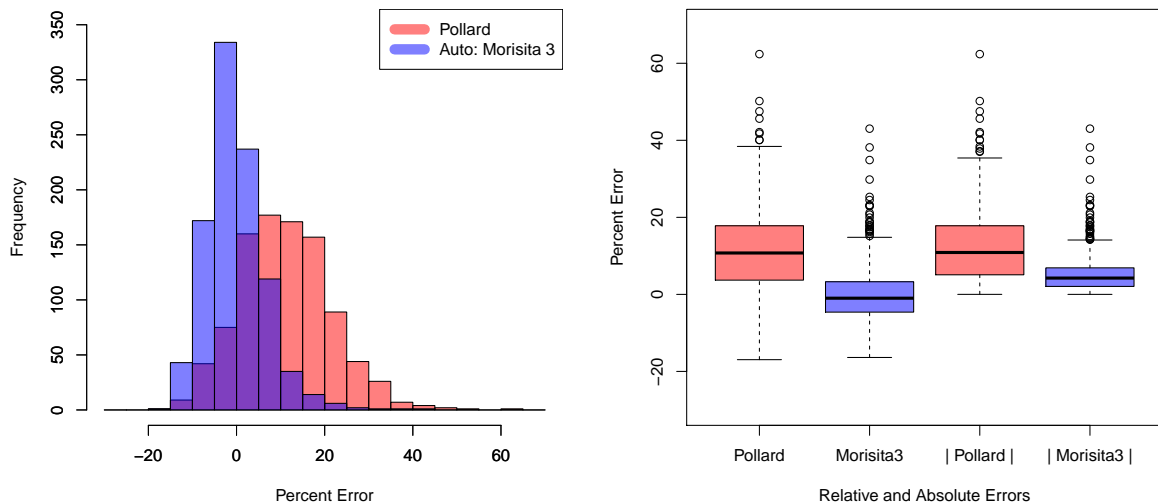
```

Histograms and Box Plots. Histograms and box plots for the BCI data show that Morisita's method to estimate density using the third nearest tree in each quarter, in general, provides better estimates of the actual density than using the nearest tree to the sample point. Pollard's method significantly overestimates the true density of the BCI samples. In contrast, the median error for Morisita's method is nearly 0 and the errors have a smaller spread than with Pollard's method.

```

Col = c(rgb(1, 0, 0, 0.5), rgb(0, 0, 1, 0.5)) # colors for plots
par(mfrow = c(1, 2))
hist(Pollard$Pct.Err, xlim = c(-30, 70), breaks = seq(-30, 70, by = 5), ylim = c(0, 350),
  main = "", xlab = "Percent Error", col = Col[1])
legend("topright", c("Pollard", "Auto: Morisita 3"), col=c(Col[1], Col[2]), lwd=10)
par(new = TRUE)
hist(Morisita$Pct.Err, xlim = c(-30, 70), breaks = seq(-30, 70, by = 5), ylim = c(0, 350),
  main = "", xlab = "", ylab = "", col = Col[2])
boxplot(Pollard$Pct.Err, Morisita$Pct.Err, abs(Pollard$Pct.Err), abs(Morisita$Pct.Err),
  names = c("Pollard", "Morisita3", "| Pollard |", "| Morisita3 |"), ylim = c(-30, 70),
  col = rep(Col, 2))
title(xlab = "Relative and Absolute Errors", ylab = "Percent Error", main = "")

```



Summary Data. The tables below summarize the data for the BCI samples. The basic summary statistics confirm that Pollard's method overestimates the true density for the BCI samples; the mean error of the estimates is 11.1%. The mean error for Morisita's method is just -0.23% . More importantly the mean size of the error is 12.3% for Pollard's method compared to 5.1% for Morisita's method. Just 47% of the Pollard estimates lie within 10% of the actual density compared to 89% of the Morisita estimates. Additionally, t tests show that there is a significant difference between the actual plot densities and the Pollard estimates ($p \approx 0$), but no difference between plot densities and the Morisita estimates ($p = 0.389$).

```
summary(Pollard)

##      Act.Dens      Est.Dens      Pct.Err      Abs.Err
## Min.   :330   Min.   :315   Min.   :-16.9   Min.   : 0.005
## 1st Qu.:389   1st Qu.:419   1st Qu.: 3.7   1st Qu.: 5.095
## Median :409   Median :454   Median : 10.7   Median :10.879
## Mean   :412   Mean   :457   Mean   : 11.1   Mean   :12.268
## 3rd Qu.:430   3rd Qu.:489   3rd Qu.: 17.8   3rd Qu.:17.802
## Max.   :587   Max.   :739   Max.   : 62.4   Max.   :62.382

summary(Morisita)

##      Act.Dens      Est.Dens      Pct.Err      Abs.Err
## Min.   :330   Min.   :311   Min.   :-16.377   Min.   : 0.0035
## 1st Qu.:389   1st Qu.:379   1st Qu.: -4.610   1st Qu.: 2.0692
## Median :409   Median :406   Median : -0.990   Median : 4.2362
## Mean   :412   Mean   :411   Mean   : -0.231   Mean   : 5.0773
## 3rd Qu.:430   3rd Qu.:435   3rd Qu.: 3.272   3rd Qu.: 6.8877
## Max.   :587   Max.   :713   Max.   : 43.030   Max.   :43.0299

cat("Abs Err <= 10%. Pollard:", 100*nrow(subset(Pollard, Abs.Err <= 10))/N,
    " Morisita:", 100*nrow(subset(Morisita, Abs.Err <= 10))/N)

## Abs Err <= 10%. Pollard: 46.9979 Morisita: 89.234

t.test(Pollard$Act.Dens, Pollard$Est.Dens, alternative= "two.sided", paired = TRUE)$p.val

## [1] 2.14391e-160

t.test(Morisita$Act.Dens, Morisita$Est.Dens, alternative= "two.sided", paired = TRUE)$p.val

## [1] 0.388538
```

For the BCI site, the mean Clark-Evans aggregation index for the sample plots is $R = 1.09$ with all R -values greater than 1.0. This indicates some regularity (dispersion) in the distribution. In fact, for 91% of the plots the corresponding p -value is no greater than 0.05 for the Clark-Evans one-tailed test of dispersion.

```
rbind("Aggregation index R" = summary(R), "Clark-Evans p value" = summary(P.Val))

##           Min. 1st Qu. Median  Mean 3rd Qu. Max.
## Aggregation index R 1.01  1.07  1.09 1.0900  1.11 1.16
## Clark-Evans p value 0.01  0.01  0.01 0.0248  0.02 0.49

100 * length(P.Val[P.Val <= 0.05])/N # pct rejection of C-E 1-sided null hypothesis

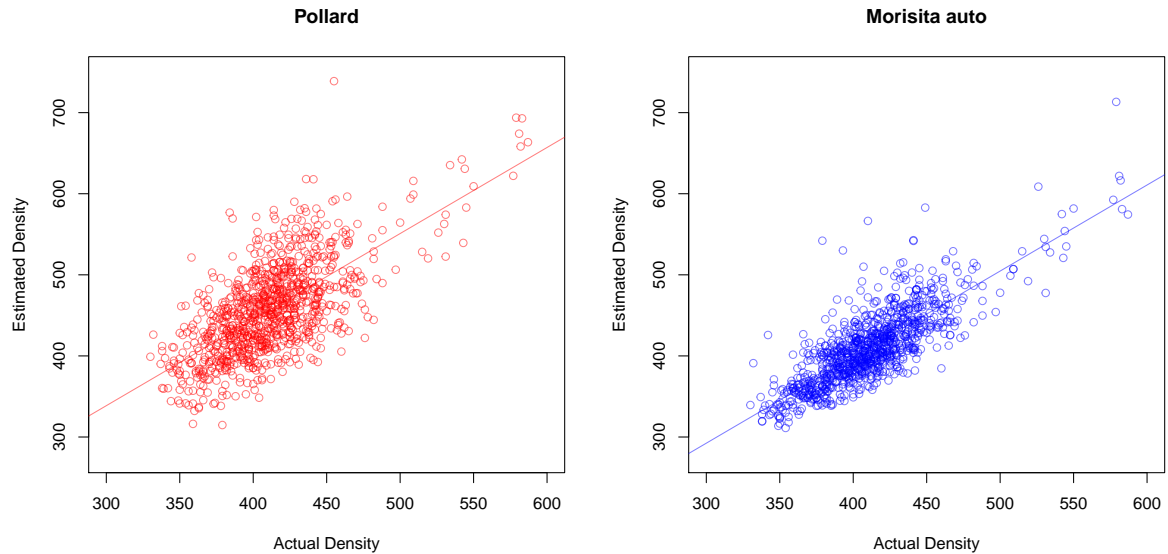
## [1] 91.3043
```

Correlations. The scatterplots below indicate that the two density estimates for the BCI plots are correlated to the corresponding actual plot densities, with a higher correlation for Morisita's method. The Pearson correlation coefficients for Pollard's and Morisita's methods are $r = 0.66$ and $r = 0.81$, respectively. The slopes of the corresponding regression lines are both 1.06 with intercepts 20.2 and -26.0 , respectively.

```
lm.pollard <- lm(Est.Dens ~ Act.Dens, data = Pollard) # regressions
lm.morisita <- lm(Est.Dens ~ Act.Dens, data = Morisita)
par(mfrow = c(1, 2))
plot(Pollard$Act.Dens, Pollard$Est.Dens, xlab = "Actual Density", xlim = c(300, 600),
     ylim = c(275, 750), ylab = "Estimated Density", col = Col[1], pch = 1, main = "Pollard")
abline(lm.pollard, col = Col[1])
plot(Morisita$Act.Dens, Morisita$Est.Dens, xlab = "Actual Density", xlim = c(300, 600),
```



```
ylim = c(275, 750), ylab = "Estimated Density", col = Col[2], pch = 1, main = "Morisita auto")
abline(lm.morisita, col = Col[2])
```



```
cor.pol <- cor.test(Pollard$Est.Dens, Pollard$Act.Dens, method = "pearson")
cor.mor <- cor.test(Morisita$Est.Dens, Morisita$Act.Dens, method = "pearson")
Pollard.cor <- c(cor.pol$est, lm.pollard$coefficients[1:2])
Morisita.cor <- c(cor.mor$est, lm.morisita$coefficients[1:2])
Linear <- data.frame("Pollard" = Pollard.cor, "Morisita" = Morisita.cor)
rownames(Linear) <- c("Pearson r", "Regr Intercept", "Regr Slope")
format(Linear, scientific = FALSE)

##           Pollard  Morisita
## Pearson r    0.664983  0.807623
## Regr Intercept 20.238899 -25.970712
## Regr Slope    1.061315  1.061218

ci <- rbind(confint(lm.pollard), confint(lm.morisita))
rownames(ci) <- c("Pollard Intercept", "Pollard Slope", "Morisita Intercept", "Morisita Slope")
ci      # confidence intervals for the regression coefficients

##           2.5 %  97.5 %
## Pollard Intercept -10.887547  51.36535
## Pollard Slope     0.985975  1.13666
## Morisita Intercept -46.204839 -5.73659
## Morisita Slope    1.012242  1.11019
```

The confidence intervals indicate that the estimates for both methods give results that are reasonably close to the ideal regression with slope 1 and intercept 0, with Morisita's estimates more strongly correlated to the actual densities.

Conclusion. There is some regularity (dispersion) present in the distribution of trees with DBH of at least 10 cm at the Barro Colorado Forest site. At this site, Pollard's method has a tendency to overestimate the actual density. Morisita's practical procedure using third order data performs better (80% of all estimates are within 10% of the actual density) at the cost of somewhat more effort.

EXAMPLE D.12 (Sherman 6-ha Plot). The Sherman plot is another Smithsonian Tropical Research Institute site is located near the Atlantic end of the Panama Canal, south of the Chagres River, close to Fort Sherman, a former U.S. Army Base. The plot is 5.96 ha, has an inverted L-shape: a 400×100 -m rectangle plus a 140

× 140-m square set to the lower left side. See <http://www.ctfs.si.edu/site/Sherman>. The Sherman plot has been censused three times. All free-standing woody plants with stem diameter 1 cm or above at breast height were tagged, measured, mapped, and identified to species. Access to the entire database may be requested at <http://ctfs.si.edu/webatlas/datasets/sherman/>.

The data used below are from the first census in 1996 and consist of all live trees with a minimum DBH of at least 10 cm. We estimate the density of the smaller, square plot by using a subset of the data. Because of suspected similarity to the Barro Colorado Island site, the preceding example indicates that Morisita's method should be used. We use 6 transects with 5 points each to sample this larger 1.96-ha plot.

```
temp <- tempfile()
download.file("http://ctfs.si.edu/webatlas/datasets/sherman/sherman.zip", temp)
data <- read.csv(unz(temp, "sherman.txt"), head = TRUE, sep = "\t") # unzip and extract data
unlink(temp)
data <- subset(data, dbh1 >= 100) # trees with dbh >= 100 mm in 1996 survey
sherman.1996 <- data.frame(x = data$x, y = data$y) # extract tree coordinates
sh <- subset(sherman.1996, x <= 140 & y <= 140) # obtain subplot
sherman.square <- manual.survey(z = sh, t.coords = c(15, 15, 125, 15, 125, 125, 15, 125),
  points = 30, transects = 6, k = 3, display = FALSE)
nrow(sh) / 1.96 # actual density (number of trees in 1.96 ha plot)

## [1] 508.673

angle.order.est(sherman.square, k = 3, method = "auto")

##
## Morisita Practical Procedure for density estimate with 4 sectors at each sample point
## using the third closest individuals. m1 < m2 (487.04 < 537.93). Use m0 = (m1 + m2)/2.
##
## data: sherman.square
## Number of sample points: n = 30
## sample estimates:
## density per hectare
## 512.483
```

The estimate is almost identical to actual density of 508.7 trees/ha. We end by estimating the density of the rectangular 4-ha subplot of the Sherman site using 30 sample points and Morisita's third-order procedure. Since the rectangle is vertically oriented, we set `horizontal = FALSE`. The result is also a very good estimate.

```
shr <- subset(sherman.1996, x >= 140 & y >= 40) # obtain subplot
nrow(shr) / 4 # actual density (number of trees in 4 ha plot)

## [1] 624

sherman.rectangle <- manual.survey(z = shr, points = 30, transects = 6, k = 3,
  t.coords = c(155, 55, 225, 55, 225, 425, 155, 425), display = FALSE, horizontal = FALSE)
angle.order.est(z = sherman.rectangle, k = 3, method = "auto")

##
## Morisita Practical Procedure for density estimate with 4 sectors at each sample point
## using the third closest individuals. m1 < m2 (656.80 < 662.17). Use m0 = (m1 + m2)/2.
##
## data: sherman.rectangle
## Number of sample points: n = 30
## sample estimates:
## density per hectare
## 659.486
```

EXERCISE D.6. Compare the results in Example D.12 to similar estimates using Pollard's method. Are they better or worse? (Answer: Slightly worse, but the 95% confidence intervals contain the true densities.)

References

- H. Baltzer. Point-centered-quarter analyses of two woodlands in east-central Indiana, 2007. URL http://cardinalscholar.bsui.edu/bitstream/handle/handle/189367/B35_2007BaltzerHolly.pdf.
- Holly Baltzer, Donald Ruch, Benjamin Hess, and Byron Torke. Point-centered-quarter analysis of the upland forest at Yuhas Woods in Randolph County, Indiana. *Proc of the Indiana Academy of Science*, 116(1):108–109, 2007. URL <http://journals.iupui.edu/index.php/ias/article/view/8740/8800>.
- C. L. Batcheler. Estimation of density from a sample of joint point and nearest-neighbor distances. *Ecology*, 52(4):703–709, July 1971. URL <http://www.jstor.org/discover/10.2307/1934161>.
- Samuel L. Beasom and Harry H. Haucke. A comparison of four distance sampling techniques in South Texas live oak mottes. *Journal of Range Management*, 28(2):142–144, March 1975. URL <http://www.jstor.org/stable/3897447>.
- Nicholas Brokaw and Jill Thompson. The H for DBH. *Forest Ecology and Management*, 129(1–3):89–91, 2000. URL <http://www.sciencedirect.com/science/article/pii/S0378112799001413>.
- David M. Bryant, Mark J. Ducey, James C. Innes, Thomas D. Lee, Robert T. Eckert, and Daniel J. Zarin. Forest community analysis and the point-centered quarter method. *Plant Ecology*, 175(2):193–203, 2005. doi: 10.1007/s11258-005-0013-0. URL <http://dx.doi.org/10.1007/s11258-005-0013-0>.
- Philip J. Clark and Francis C. Evans. Distance to nearest neighbor as a measure of spatial relationships in populations. *Ecology*, 35(4):445–453, 1954. URL <http://www.jstor.org/discover/10.2307/1931034>.
- R. Condit, S. Lao, R. Pérez, S.B. Dolins, R.B. Foster, and S.P. Hubbell. Barro Colorado Forest census plot data, 2012 version. Center for Tropical Forest Science Databases. Technical report, Smithsonian Tropical Research Institute, 2012. URL <https://repository.si.edu/handle/10088/20925>. Accessed 10 March 2015.
- Grant Cottam and J. T. Curtis. The use of distance measures in phytosociological sampling. *Ecology*, 37(3):451–460, 1956. URL <http://www.jstor.org/stable/1930167>.
- Grant Cottam, J. T. Curtis, and B. Wilde Hale. Some sampling characteristics of a population of randomly dispersed individuals. *Ecology*, 34(4):741–757, 1953. URL <http://www.jstor.org/stable/1931337>.
- Farid Dahdouh-Guebas and Nico Koedam. Empirical estimate of the reliability of the use of the point-centred quarter method (PCQM): Solutions to ambiguous field situations and description of the PCQM+ protocol. *Forest Ecology and Management*, 228(1–3):1–18, 2006. URL <http://www.sciencedirect.com/science/article/pii/S0378112706000776>.
- H. Díaz, J. E. Conde, and B. Orihuela. Estimating the species number and cover of a mangrove-root community: a comparison of methods. *J Marine and Freshwater Research*, 43(4):707–713, 1975. URL <http://dx.doi.org/10.1071/MF9920707>.
- Ralph L. Dix. An application of the point-centered quarter method to the sampling of grassland vegetation. *J Range Management*, 14(2):63–69, March 1961. URL <http://www.jstor.org/stable/3894717>.
- L. L. Eberhardt. Some developments in ‘distance sampling’. *Biometrics*, 23(2):207–216, June 1967. URL <http://www.jstor.org/stable/2528156>.
- David Eissenstat and Margot Kaye. CZO Dataset: Shale Hills—Vegetation (2012) tree survey. Online, 2015. URL <http://criticalzone.org/shale-hills/data/dataset/2648/>. Retrieved 01 Mar 2015.
- Richard M. Engeman, Robert T. Sugihara, Larry F. Pank, and William E. Dusenberry. A comparison of plotless density estimators using Monte Carlo simulation. *Ecology*, 75(6):1769–1779, September 1994. ISSN 00129658. URL <http://www.jstor.org/stable/1939636>.

- Ralph E. Good and Norma Frauendorf Good. Vegetation of a Minnesota prairie and a comparison of methods. *American Midland Naturalist*, 85(1):228–231, 1971. URL <http://www.jstor.org/stable/2423926>.
- Teresa Hollingsworth. Point-center quarter method black spruce heights, diameter, and location for 150 mature black spruce sites in interior Alaska. Bonanza Creek LTER, University of Alaska Fairbanks. BNZ:138, http://www.lter.uaf.edu/data_detail.cfm?datafile_pkey=138, 2005.
- Lou Jost. A simple distance estimator for plant density in nonuniform stands, mathematical appendix. <http://www.loujost.com/Statistics%20and%20Physics/PCQ/PCQJournalArticle.htm>, 1993.
- Bahman Kiani, Asghar Fallah, Masoud Tabari, Sayed Mohsen Hosseini, and Mohammad-Hossein In Parizi. A comparison of distance sampling methods in saxaul (*Halloxylon ammodendron C.A. Mey Bunge*) shrub-lands. *Polish Journal of Ecology*, 61(2):207–219, 2013. URL http://www.pje.miiz.waw.pl/article/ar61_2_02.pdf.
- Charles J. Krebs. *Ecological Methodology, Second Edition*. Benjamin/Cummings, New York, 1999.
- P. G. Moore. Spacing in plant populations. *Ecology*, 35(2):222–227, 1954. URL <http://www.jstor.org/stable/1931120>.
- Masaaki Morisita. Estimation of population density by spacing method. *Memoirs Fac. Sci. Kyushu Univ.*, 1:187–197, 1954.
- Masaaki Morisita. A new method for the estimation of density by the spacing method applicable to nonrandomly distributed populations. *Physiology and Ecology*, 7:134–144, 1957. In Japanese; USDA English translation available at <http://math.hws.edu/~mitchell/Morisita1957.pdf>.
- Dieter Mueller-Dombois and Heinz Ellenberg. *Aims and Methods of Vegetation Ecology*. Wiley, 1974.
- Elizabeth Newell. Coordinates of all woody plants in two areas of forested land owned by Rob Poole, Geneva, NY. Personal communication, 2015. URL <http://math.hws.edu/aitb/NewellSouth.csv>.
- S. A. Patil, K. P. Burnham, and J. L. Kovner. Nonparametric estimation of plant density by the distance method. *Biometrics*, 35(3):597–604, September 1979. URL <http://www.jstor.org/stable/2530250>.
- S. A. Patil, J. L. Kovner, and K. P. Burnham. Optimum nonparametric estimation of population density based on ordered distances. *Biometrics*, 38(1):243–248, March 1982. URL <http://www.jstor.org/stable/2530307>.
- William T. Penfound. A modification of the point-centered quarter method for grassland analysis. *Ecology*, 44(1):175–176, 1963. URL <http://www.jstor.org/stable/1933199>.
- Brian L. Pierce, Roel R. Lopez, and Nova J. Silvy. *The Wildlife Techniques Manual*, volume 1: Research, chapter 11. Estimating Animal Abundance, pages 284–310. Johns Hopkins University Press, 7th edition, 2012. Nova J. Silvy, editor.
- J. H. Pollard. On distance estimators of density in randomly distributed forests. *Biometrics*, 27(4):991–1002, December 1971. URL <http://www.jstor.org/stable/2528833>.
- R. Rheinhardt, Mark M. Brinson, N. Eric Fleming, and J. Glenn Sandifer, Jr. Deciduous wetland flats interim HGM model. 1997. URL <ftp://ftp-fc.sc.egov.usda.gov/WLI/121201dWLIfromUSGS/wlistates/secoast.htm>.
- Paul G. Risser and Paul H. Zedler. An evaluation of the grassland quarter method. *Ecology*, 49(5):1006–1009, September 1968. URL <http://www.jstor.org/stable/1936556>.
- G. A. F. Seber. *The Estimation of Animal Abundance and Related Parameters*. MacMillan, New York, 1982.

Forest W. Stearns. Ninety years change in a northern hardwood forest in Wisconsin. *Ecology*, 30(3): 350–358, July 1949. URL <http://www.jstor.org/stable/1932615>.

William Warde and James W. Petranka. A correction factor table for missing point-center quarter data. *Ecology*, 62(2):491–494, 1981. URL <http://www.jstor.org/stable/1936723>.

Neil A. White, Richard M. Engeman, Robert T. Sugihara, and Heather W. Krupa. A comparison of plotless density estimators using Monte Carlo simulation on totally enumerated field data sets. *BioMed Central Ecology*, 8(6), April 2008. doi: 10.1186/1472-6785-8-6. URL <http://www.biomedcentral.com/1472-6785/8/6>.

E Reference Tables

TABLE 13. The cumulative standard normal distribution.

z	0.00	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
−3.9	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
−3.8	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
−3.7	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
−3.6	0.0002	0.0002	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
−3.5	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002
−3.4	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0002
−3.3	0.0005	0.0005	0.0005	0.0004	0.0004	0.0004	0.0004	0.0004	0.0004	0.0003
−3.2	0.0007	0.0007	0.0006	0.0006	0.0006	0.0006	0.0006	0.0005	0.0005	0.0005
−3.1	0.0010	0.0009	0.0009	0.0009	0.0008	0.0008	0.0008	0.0008	0.0007	0.0007
−3.0	0.0013	0.0013	0.0013	0.0012	0.0012	0.0011	0.0011	0.0011	0.0010	0.0010
−2.9	0.0019	0.0018	0.0018	0.0017	0.0016	0.0016	0.0015	0.0015	0.0014	0.0014
−2.8	0.0026	0.0025	0.0024	0.0023	0.0023	0.0022	0.0021	0.0021	0.0020	0.0019
−2.7	0.0035	0.0034	0.0033	0.0032	0.0031	0.0030	0.0029	0.0028	0.0027	0.0026
−2.6	0.0047	0.0045	0.0044	0.0043	0.0041	0.0040	0.0039	0.0038	0.0037	0.0036
−2.5	0.0062	0.0060	0.0059	0.0057	0.0055	0.0054	0.0052	0.0051	0.0049	0.0048
−2.4	0.0082	0.0080	0.0078	0.0075	0.0073	0.0071	0.0069	0.0068	0.0066	0.0064
−2.3	0.0107	0.0104	0.0102	0.0099	0.0096	0.0094	0.0091	0.0089	0.0087	0.0084
−2.2	0.0139	0.0136	0.0132	0.0129	0.0125	0.0122	0.0119	0.0116	0.0113	0.0110
−2.1	0.0179	0.0174	0.0170	0.0166	0.0162	0.0158	0.0154	0.0150	0.0146	0.0143
−2.0	0.0228	0.0222	0.0217	0.0212	0.0207	0.0202	0.0197	0.0192	0.0188	0.0183
−1.9	0.0287	0.0281	0.0274	0.0268	0.0262	0.0256	0.0250	0.0244	0.0239	0.0233
−1.8	0.0359	0.0351	0.0344	0.0336	0.0329	0.0322	0.0314	0.0307	0.0301	0.0294
−1.7	0.0446	0.0436	0.0427	0.0418	0.0409	0.0401	0.0392	0.0384	0.0375	0.0367
−1.6	0.0548	0.0537	0.0526	0.0516	0.0505	0.0495	0.0485	0.0475	0.0465	0.0455
−1.5	0.0668	0.0655	0.0643	0.0630	0.0618	0.0606	0.0594	0.0582	0.0571	0.0559
−1.4	0.0808	0.0793	0.0778	0.0764	0.0749	0.0735	0.0721	0.0708	0.0694	0.0681
−1.3	0.0968	0.0951	0.0934	0.0918	0.0901	0.0885	0.0869	0.0853	0.0838	0.0823
−1.2	0.1151	0.1131	0.1112	0.1093	0.1075	0.1056	0.1038	0.1020	0.1003	0.0985
−1.1	0.1357	0.1335	0.1314	0.1292	0.1271	0.1251	0.1230	0.1210	0.1190	0.1170
−1.0	0.1587	0.1562	0.1539	0.1515	0.1492	0.1469	0.1446	0.1423	0.1401	0.1379
−0.9	0.1841	0.1814	0.1788	0.1762	0.1736	0.1711	0.1685	0.1660	0.1635	0.1611
−0.8	0.2119	0.2090	0.2061	0.2033	0.2005	0.1977	0.1949	0.1922	0.1894	0.1867
−0.7	0.2420	0.2389	0.2358	0.2327	0.2296	0.2266	0.2236	0.2206	0.2177	0.2148
−0.6	0.2743	0.2709	0.2676	0.2643	0.2611	0.2578	0.2546	0.2514	0.2483	0.2451
−0.5	0.3085	0.3050	0.3015	0.2981	0.2946	0.2912	0.2877	0.2843	0.2810	0.2776
−0.4	0.3446	0.3409	0.3372	0.3336	0.3300	0.3264	0.3228	0.3192	0.3156	0.3121
−0.3	0.3821	0.3783	0.3745	0.3707	0.3669	0.3632	0.3594	0.3557	0.3520	0.3483
−0.2	0.4207	0.4168	0.4129	0.4090	0.4052	0.4013	0.3974	0.3936	0.3897	0.3859
−0.1	0.4602	0.4562	0.4522	0.4483	0.4443	0.4404	0.4364	0.4325	0.4286	0.4247
−0.0	0.5000	0.4960	0.4920	0.4880	0.4840	0.4801	0.4761	0.4721	0.4681	0.4641

TABLE 14. The cumulative standard normal distribution (continued).

<i>z</i>	0.00	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
0.0	0.5000	0.5040	0.5080	0.5120	0.5160	0.5199	0.5239	0.5279	0.5319	0.5359
0.1	0.5398	0.5438	0.5478	0.5517	0.5557	0.5596	0.5636	0.5675	0.5714	0.5753
0.2	0.5793	0.5832	0.5871	0.5910	0.5948	0.5987	0.6026	0.6064	0.6103	0.6141
0.3	0.6179	0.6217	0.6255	0.6293	0.6331	0.6368	0.6406	0.6443	0.6480	0.6517
0.4	0.6554	0.6591	0.6628	0.6664	0.6700	0.6736	0.6772	0.6808	0.6844	0.6879
0.5	0.6915	0.6950	0.6985	0.7019	0.7054	0.7088	0.7123	0.7157	0.7190	0.7224
0.6	0.7257	0.7291	0.7324	0.7357	0.7389	0.7422	0.7454	0.7486	0.7517	0.7549
0.7	0.7580	0.7611	0.7642	0.7673	0.7704	0.7734	0.7764	0.7794	0.7823	0.7852
0.8	0.7881	0.7910	0.7939	0.7967	0.7995	0.8023	0.8051	0.8078	0.8106	0.8133
0.9	0.8159	0.8186	0.8212	0.8238	0.8264	0.8289	0.8315	0.8340	0.8365	0.8389
1.0	0.8413	0.8438	0.8461	0.8485	0.8508	0.8531	0.8554	0.8577	0.8599	0.8621
1.1	0.8643	0.8665	0.8686	0.8708	0.8729	0.8749	0.8770	0.8790	0.8810	0.8830
1.2	0.8849	0.8869	0.8888	0.8907	0.8925	0.8944	0.8962	0.8980	0.8997	0.9015
1.3	0.9032	0.9049	0.9066	0.9082	0.9099	0.9115	0.9131	0.9147	0.9162	0.9177
1.4	0.9192	0.9207	0.9222	0.9236	0.9251	0.9265	0.9279	0.9292	0.9306	0.9319
1.5	0.9332	0.9345	0.9357	0.9370	0.9382	0.9394	0.9406	0.9418	0.9429	0.9441
1.6	0.9452	0.9463	0.9474	0.9484	0.9495	0.9505	0.9515	0.9525	0.9535	0.9545
1.7	0.9554	0.9564	0.9573	0.9582	0.9591	0.9599	0.9608	0.9616	0.9625	0.9633
1.8	0.9641	0.9649	0.9656	0.9664	0.9671	0.9678	0.9686	0.9693	0.9699	0.9706
1.9	0.9713	0.9719	0.9726	0.9732	0.9738	0.9744	0.9750	0.9756	0.9761	0.9767
2.0	0.9772	0.9778	0.9783	0.9788	0.9793	0.9798	0.9803	0.9808	0.9812	0.9817
2.1	0.9821	0.9826	0.9830	0.9834	0.9838	0.9842	0.9846	0.9850	0.9854	0.9857
2.2	0.9861	0.9864	0.9868	0.9871	0.9875	0.9878	0.9881	0.9884	0.9887	0.9890
2.3	0.9893	0.9896	0.9898	0.9901	0.9904	0.9906	0.9909	0.9911	0.9913	0.9916
2.4	0.9918	0.9920	0.9922	0.9925	0.9927	0.9929	0.9931	0.9932	0.9934	0.9936
2.5	0.9938	0.9940	0.9941	0.9943	0.9945	0.9946	0.9948	0.9949	0.9951	0.9952
2.6	0.9953	0.9955	0.9956	0.9957	0.9959	0.9960	0.9961	0.9962	0.9963	0.9964
2.7	0.9965	0.9966	0.9967	0.9968	0.9969	0.9970	0.9971	0.9972	0.9973	0.9974
2.8	0.9974	0.9975	0.9976	0.9977	0.9977	0.9978	0.9979	0.9979	0.9980	0.9981
2.9	0.9981	0.9982	0.9982	0.9983	0.9984	0.9984	0.9985	0.9985	0.9986	0.9986
3.0	0.9987	0.9987	0.9987	0.9988	0.9988	0.9989	0.9989	0.9989	0.9990	0.9990
3.1	0.9990	0.9991	0.9991	0.9991	0.9992	0.9992	0.9992	0.9992	0.9993	0.9993
3.2	0.9993	0.9993	0.9994	0.9994	0.9994	0.9994	0.9994	0.9995	0.9995	0.9995
3.3	0.9995	0.9995	0.9995	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9997
3.4	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9998
3.5	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998
3.6	0.9998	0.9998	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999
3.7	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999
3.8	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999
3.9	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

TABLE 15. Table of chi-square values for 95% confidence intervals for $n = 1$ to 240 transect sample points.

n	$8n$	$\chi^2_{0.025}$	$\chi^2_{0.975}$	n	$8n$	$\chi^2_{0.025}$	$\chi^2_{0.975}$	n	$8n$	$\chi^2_{0.025}$	$\chi^2_{0.975}$	n	$8n$	$\chi^2_{0.025}$	$\chi^2_{0.975}$
1	8	2.18	17.53	61	488	428.68	551.10	121	968	883.67	1056.12	181	1448	1344.43	1555.36
2	16	6.91	28.85	62	496	436.18	559.60	122	976	891.32	1064.47	182	1456	1352.14	1563.65
3	24	12.40	39.36	63	504	443.69	568.10	123	984	898.96	1072.83	183	1464	1359.85	1571.94
4	32	18.29	49.48	64	512	451.20	576.59	124	992	906.61	1081.18	184	1472	1367.56	1580.23
5	40	24.43	59.34	65	520	458.71	585.08	125	1000	914.26	1089.53	185	1480	1375.27	1588.52
6	48	30.75	69.02	66	528	466.22	593.56	126	1008	921.91	1097.88	186	1488	1382.99	1596.80
7	56	37.21	78.57	67	536	473.74	602.04	127	1016	929.56	1106.23	187	1496	1390.70	1605.09
8	64	43.78	88.00	68	544	481.27	610.52	128	1024	937.21	1114.58	188	1504	1398.41	1613.38
9	72	50.43	97.35	69	552	488.79	619.00	129	1032	944.87	1122.92	189	1512	1406.13	1621.66
10	80	57.15	106.63	70	560	496.32	627.47	130	1040	952.52	1131.27	190	1520	1413.84	1629.95
11	88	63.94	115.84	71	568	503.85	635.93	131	1048	960.18	1139.61	191	1528	1421.56	1638.23
12	96	70.78	125.00	72	576	511.39	644.40	132	1056	967.84	1147.95	192	1536	1429.27	1646.51
13	104	77.67	134.11	73	584	518.93	652.86	133	1064	975.50	1156.29	193	1544	1436.99	1654.80
14	112	84.60	143.18	74	592	526.47	661.31	134	1072	983.16	1164.63	194	1552	1444.71	1663.08
15	120	91.57	152.21	75	600	534.02	669.77	135	1080	990.82	1172.97	195	1560	1452.43	1671.36
16	128	98.58	161.21	76	608	541.57	678.22	136	1088	998.48	1181.31	196	1568	1460.15	1679.64
17	136	105.61	170.18	77	616	549.12	686.67	137	1096	1006.15	1189.64	197	1576	1467.87	1687.92
18	144	112.67	179.11	78	624	556.67	695.11	138	1104	1013.81	1197.98	198	1584	1475.59	1696.20
19	152	119.76	188.03	79	632	564.23	703.56	139	1112	1021.48	1206.31	199	1592	1483.31	1704.48
20	160	126.87	196.92	80	640	571.79	712.00	140	1120	1029.15	1214.64	200	1600	1491.03	1712.75
21	168	134.00	205.78	81	648	579.35	720.43	141	1128	1036.82	1222.97	201	1608	1498.76	1721.03
22	176	141.16	214.63	82	656	586.92	728.87	142	1136	1044.49	1231.30	202	1616	1506.48	1729.31
23	184	148.33	223.46	83	664	594.49	737.30	143	1144	1052.16	1239.63	203	1624	1514.21	1737.58
24	192	155.52	232.27	84	672	602.06	745.73	144	1152	1059.83	1247.96	204	1632	1521.93	1745.86
25	200	162.73	241.06	85	680	609.63	754.16	145	1160	1067.50	1256.28	205	1640	1529.66	1754.13
26	208	169.95	249.83	86	688	617.21	762.58	146	1168	1075.18	1264.61	206	1648	1537.38	1762.41
27	216	177.19	258.60	87	696	624.79	771.00	147	1176	1082.86	1272.93	207	1656	1545.11	1770.68
28	224	184.44	267.35	88	704	632.37	779.42	148	1184	1090.53	1281.26	208	1664	1552.84	1778.95
29	232	191.71	276.08	89	712	639.95	787.84	149	1192	1098.21	1289.58	209	1672	1560.57	1787.22
30	240	198.98	284.80	90	720	647.54	796.25	150	1200	1105.89	1297.90	210	1680	1568.30	1795.49
31	248	206.27	293.51	91	728	655.12	804.66	151	1208	1113.57	1306.22	211	1688	1576.03	1803.76
32	256	213.57	302.21	92	736	662.71	813.07	152	1216	1121.25	1314.54	212	1696	1583.76	1812.03
33	264	220.89	310.90	93	744	670.31	821.48	153	1224	1128.93	1322.85	213	1704	1591.49	1820.30
34	272	228.21	319.58	94	752	677.90	829.89	154	1232	1136.62	1331.17	214	1712	1599.22	1828.57
35	280	235.54	328.25	95	760	685.50	838.29	155	1240	1144.30	1339.49	215	1720	1606.95	1836.84
36	288	242.88	336.90	96	768	693.10	846.69	156	1248	1151.99	1347.80	216	1728	1614.68	1845.10
37	296	250.23	345.55	97	776	700.70	855.09	157	1256	1159.67	1356.11	217	1736	1622.42	1853.37
38	304	257.59	354.19	98	784	708.30	863.49	158	1264	1167.36	1364.43	218	1744	1630.15	1861.64
39	312	264.96	362.83	99	792	715.91	871.88	159	1272	1175.05	1372.74	219	1752	1637.89	1869.90
40	320	272.34	371.45	100	800	723.51	880.28	160	1280	1182.74	1381.05	220	1760	1645.62	1878.17
41	328	279.72	380.07	101	808	731.12	888.67	161	1288	1190.43	1389.36	221	1768	1653.36	1886.43
42	336	287.11	388.68	102	816	738.73	897.06	162	1296	1198.12	1397.67	222	1776	1661.09	1894.69
43	344	294.51	397.28	103	824	746.35	905.44	163	1304	1205.81	1405.97	223	1784	1668.83	1902.96
44	352	301.92	405.87	104	832	753.96	913.83	164	1312	1213.51	1414.28	224	1792	1676.57	1911.22
45	360	309.33	414.46	105	840	761.58	922.21	165	1320	1221.20	1422.59	225	1800	1684.31	1919.48
46	368	316.75	423.04	106	848	769.19	930.59	166	1328	1228.90	1430.89	226	1808	1692.05	1927.74
47	376	324.17	431.62	107	856	776.81	938.97	167	1336	1236.59	1439.19	227	1816	1699.79	1936.00
48	384	331.60	440.18	108	864	784.44	947.35	168	1344	1244.29	1447.50	228	1824	1707.53	1944.26
49	392	339.04	448.75	109	872	792.06	955.73	169	1352	1251.99	1455.80	229	1832	1715.27	1952.52
50	400	346.48	457.31	110	880	799.69	964.10	170	1360	1259.69	1464.10	230	1840	1723.01	1960.78
51	408	353.93	465.86	111	888	807.31	972.48	171	1368	1267.39	1472.40	231	1848	1730.75	1969.04
52	416	361.38	474.40	112	896	814.94	980.85	172	1376	1275.09	1480.70	232	1856	1738.49	1977.30
53	424	368.84	482.95	113	904	822.57	989.22	173	1384	1282.79	1489.00	233	1864	1746.24	1985.55
54	432	376.31	491.48	114	912	830.20	997.58	174	1392	1290.49	1497.30	234	1872	1753.98	1993.81
55	440	383.77	500.01	115	920	837.84	1005.95	175	1400	1298.20	1505.59	235	1880	1761.72	2002.07
56	448	391.25	508.54	116	928	845.47	1014.32	176	1408	1305.90	1513.89	236	1888	1769.47	2010.32
57	456	398.73	517.06	117	936	853.11	1022.68	177	1416	1313.60	1522.18	237	1896	1777.21	2018.58
58	464	406.21	525.58	118	944	860.75	1031.04	178	1424	1321.31	1530.48	238	1904	1784.96	2026.83
59	472	413.70	534.09	119	952	868.39	1039.40	179	1432	1329.02	1538.77	239	1912	1792.70	2035.08
60	480	421.19	542.60	120	960	876.03	1047.76	180	1440	1336.72	1547.06	240	1920	1800.45	2043.34

TABLE 16. Table of 2025 Random Digits.

1	60082	84894	87580	22864	25331	54562	44686	40649	51483
2	22224	12938	28165	75805	68172	80673	17717	53236	68851
3	60285	32511	72012	82652	34342	78292	76543	20885	73190
4	88812	28748	21729	61863	68489	21822	56358	52501	89453
5	44576	55744	46672	14593	64783	37256	93146	88197	76405
6	28890	23523	93040	14691	29545	74989	95987	28891	21203
7	33248	36833	92299	67498	42777	26268	17589	92760	46627
8	06486	93538	12667	83088	04615	65794	66354	60781	84674
9	17475	62049	17297	39937	65459	75082	78141	12139	89131
10	15274	37983	98317	94216	67221	93399	85141	77546	67711
11	68879	51475	98386	75048	29674	75489	12385	05994	63650
12	83496	72984	23660	95481	60220	39281	58264	52018	27812
13	26744	36792	72255	76361	19424	98679	36742	18622	19857
14	62711	87719	67049	44892	52839	15490	46973	74915	46364
15	31414	85454	16495	40617	02926	45817	96356	52240	47116
16	34554	98863	34967	85013	27775	14375	89156	21919	76635
17	95462	96714	49735	87824	97419	33554	17134	49235	97579
18	48093	46752	93317	37664	45035	72983	80716	30263	64913
19	60969	95257	40274	60833	74771	73456	27750	10135	49899
20	01096	16749	75350	87705	72326	68094	23155	91453	74633
21	39062	42448	18988	93694	57797	34517	10748	74680	21585
22	88966	87249	77126	01433	94406	15789	07692	17558	33372
23	55472	54559	42499	98779	34668	77150	04338	70459	31650
24	77115	91315	70052	14534	76386	18211	42522	31774	52762
25	68296	65967	27859	36237	03758	02576	31417	79768	23853
26	11891	92132	43614	25173	37475	92684	07525	12754	52073
27	67845	41815	87539	63773	33269	96363	83893	13684	54758
28	80715	03333	36746	42279	63932	91413	13015	45479	96152
29	93614	88328	22103	21134	73295	22175	46254	11747	36284
30	28017	18124	61320	52542	35362	27681	58562	53691	96599
31	95114	73345	78448	17128	94266	82197	10938	42871	39309
32	29631	61790	17394	87012	80142	12916	43588	88044	07429
33	72439	22965	22452	89352	84598	40162	51112	99370	58994
34	43206	76531	23736	90099	16631	62425	23619	94864	28797
35	19266	29669	79345	01827	15147	85505	58666	84693	65570
36	95222	14122	54382	71115	93771	35510	79567	96455	67252
37	17310	48813	33458	54178	34773	29541	75989	11419	81253
38	72494	45082	88616	80699	59886	36329	69658	71891	03236
39	89818	68866	13858	32642	41924	08469	14327	84551	47068
40	73182	66270	93939	45159	28426	43253	42189	61174	77953
41	41648	15786	24517	80227	79184	72866	96071	36856	92714
42	86633	67816	43550	00765	88497	46434	10767	27709	14374
43	60762	91378	18649	96638	85675	33142	79869	18443	24879
44	29283	77878	61353	89214	72140	29236	11476	82552	47777
45	78114	48491	51326	68205	52576	54212	46363	61776	97791