Sampling Trees Using the Point-quarter Method

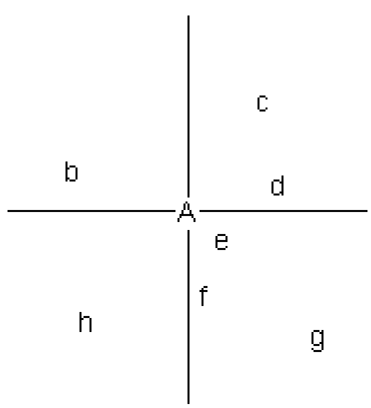
modified from:
http://faculty.clintoncc.suny.edu/faculty/michael.gregory/files/BIO%20206/206%20Laboratory/Point-Quarter%20Method/point-quarter%20instructions.htm

Introduction

Ecologists often need to estimate the number of individuals present in a population or community. If there are a few, large individuals, this can be done directly by counting each individual. If there are many individuals, the community is large, or the individuals are small, it may be impractical to count all of the individuals. In these cases it is easier to take samples of the community and then estimate density the population size based on the samples. For example, suppose that you wanted to know how many sugar maple trees are in the Adirondack Park. It would be impossible to count every tree in the 2.4 million hectare (6,000,000 acre) park. Instead, randomly-located samples can be taken. Suppose that 100 one-hectare samples were taken at random locations in the park and in each of these samples, the number of Maple trees was counted. The average number of maples per one-hectare sample was 500. From this we can estimate the number of maples in the entire park by multiplying 500 X 2,400,000.

Plot sampling as described above may be difficult for sampling trees, particularly if a large area is to be sampled. It may be easiest to sample trees using a plotless technique. Plotless techniques are best used with stationary organisms because sometimes they involve measuring distances to organisms.

The point-quarter technique is perhaps the most popular of the plotless sampling techniques. Each sample is taken at a random location in the area to be sampled. This is frequently done by choosing random points along a transect, but any randomization technique may be used. The area near each random point (sample point) is divided into four imaginary quadrants as indicated below. Within each quadrant, the nearest tree is included in the field sample. There are four quadrants, so you will measure a total of four trees at each sample point. In the diagram below, point A represents a random point (sample point) and the letters b through h represent trees. The tees b, d, e and h would be included as the four nearest trees within each quadrant that are nearest to A.



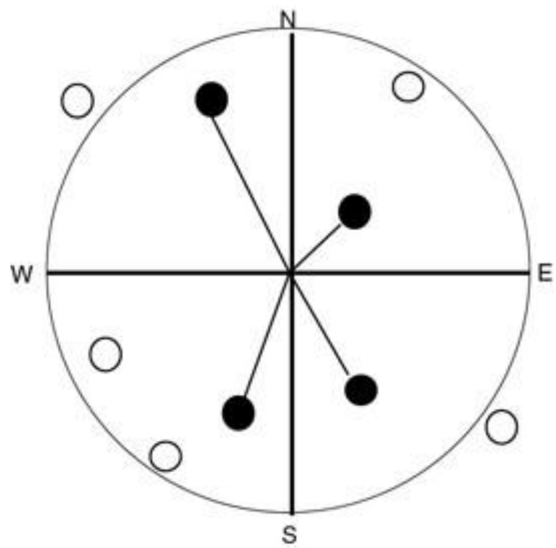
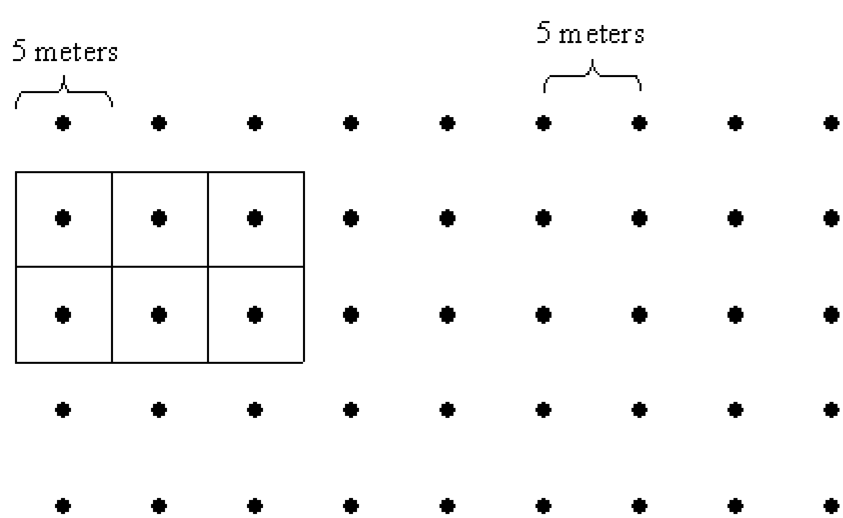


Diagram of point-centered quarter sampling. Sampled trees are indicated by solid (black) circles; trees not sampled are indicated by white circles. Within each of the four quadrants, the researcher locates the nearest tree to the sampling point in the center.

If you wish to measure tree density and/or basal area, you should also measure the distance from your sampling point to each tree, and the DBH of each tree. DBH is measured using a diameter tape wrapped around the tree at 1.3m above the ground. These measurements can then be used to calculate basal area by converting diameter to area and summing the measurements for all trees within a given area.

Calculations

The diagram of a hypothetical forest below will be used to explain the rationale for density calculations. Each dot in the diagram represents a tree. The distance between each tree is 5 meters.



If you were to draw a square around each tree, the sides of each square would also be 5 meters (see diagram). The area occupied by each tree is therefore 5 m X 5 m (or 5^2) sq. m = 25 sq. m. This gives you the number of square meters per tree. We want to calculate density, which is the number of trees per square meter. Density is therefore the inverse. Density = 1/(distance between trees)^2.

In nature, organisms are seldom distributed in such a regular pattern. The distance between each tree in a forest, for example varies. The formula for density calculations given above can still be used if we use the average (mean) distance between each tree.

To calculate the density of all species, it is necessary to sum the point-to-organism distances for all species and calculate a mean. The square of this number is equal to the mean area occupied per organism.

Mean area per organism = mean point-to-plant distance^2

Density is equal to the inverse of the area per organism as shown below.

$$\textbf{Density} \text{ (all species)} = \frac{1}{\text{Mean point-to-plant distance}^2} \quad \textbf{Equation \#1}$$

Note that the above formula computes the density of ***all species combined***. The unit of density is the same unit as the mean point-to-organism. For example, if the point-to-organism distance is in meters and you want density calculated in individuals per square meter, then use the equation given above. If you want to know the number of individuals per 100 sq. meters, then D = 100/mean point-to-plant distance^2. In our samples, we will measure distance in meters but calculate the number of individuals per hectare. The numerator in the equation becomes 10,000 because there are 10,000 square meters in one hectare.

The equations below show calculations for relative density, dominance, relative dominance frequency, relative frequency, and importance value.

$$\textbf{Relative Density} = \frac{\text{\# individuals of a species}}{\text{Total \# of individuals (all species)}} \times 100 \quad \textbf{Equation \#2}$$

$$\textbf{Density} = \frac{\text{Relative density of a species}}{100} \times \text{Density (all species)} \quad \textbf{Equation \#3}$$

The units for density will be the same units that you used for measuring the distance from the sample points to the trees. For example, if you measured these distances in meters, the calculation for density will be trees per square meter. If you measured these distances in centimeters, density will be given as trees per square centimeter. It is usually to convert these measurements to trees per ***hectare***. There are 10,000 square meters in one hectare.

Dominance = density for a species X average basal area for species **Equation #4**

$$\textbf{Relative Dominance} = \frac{\text{Dominance}}{\text{Total dominance of all species}} \times 100$$ **Equation #5**

Frequency = number of sample points at which species occurs* **Equation #6**

*Important- This is not equal to the number of individuals in your samples. There are 4 measurements taken (4 trees measured) at each sample point. Regardless of how many times a species occurs at that point (1, 2, 3, or 4), it's frequency for that point is still 1. For example, if you sampled 5 points (20 trees), there may have been 6 maples. If these maples occurred at two sample points, the frequency for maple is 2.

If your samples are obtained from 5 sample points, the maximum value that a species can have for frequency is 5.

$$\textbf{Relative Frequency} = \frac{\text{Frequency}}{\text{Total frequency of all species}} \times 100$$ **Equation #7**

Importance Value = relative density + relative dominance + relative frequency
Equation #8