Catch up

- Need everyone's email address.
- Readings are on reserve via ERes:
  http://eres.uaf.edu,
  click on "Electronic Reserves and Course Materials",
  searching for "Skip Walker" or "Biol 475".
  Password is vegetation "vegetation"
- Do we have all the data sheets, soil samples, and plant vouchers from the relevé sampling? Still need from Emily for relevé 06-3?
- Next week I am on travel:
  Meet here and go directly to the field for the Plot-Count lab, which will be taught by Dr. Patrick Kuss.
  Do all the calculations from today's Point-Center Quarter lab before next week.
- The write ups for Labs 4 and 5 will be combined into a single Lab Report due on Oct 16 and worth 200 points. (More on this at the end of the lecture.)

Lesson 4

Plot-count method and Point-centered-quarter method

Review of basic terms

- **Cover:** The area of ground covered by the vertical projection of the aerial parts of plants of one or more species.

- **Density:** The number of plants of a species per unit area (e.g., individuals/m^2, or individuals/ha).

- **Frequency:** A measure of the degree of uniformity with which individuals of a species are distributed in an area. The percentage of samples in which at least one individual of the species occurs.

- **Basal area (= dominance in calculating importance values):** The area of the stems of trees per unit area.

Count-plot method

- Used for determining density and basal area of trees.
- Species are counted and measured within a specifically defined area (belt transect or quadrat).
- Widely used method for forest inventory.
- The main reason for doing a plot as opposed to a plotless methods are:
  - It can also be used to sample the understory, and thus is useful for vegetation classification
  - Record a wide variety of other properties, such as soils, site factors, and the plot can be mapped for spatial studies
  - Useful for long-term studies where the same plot will be revisited in future years.

Data obtained in the plot-count method

In the United States this is usually done in plots or belt transects (e.g., a 10 x 20-m plot.

<u>All</u> the trees in the plot are measured.

Sampling often includes:

(1) ***Number of individuals for each tree species*** above a predetermined minimum diameter. From these data **density** of each species is determined.

(2) ***Tree diameters*** at breast height (dbh) using a Biltmore stick or diameter tape and grouped in diameter classes. From these data **basal area (cross-sectional area of tree stems at breast height/ha)** for each species is determined.

(3) ***Tree heights*** (e.g., with an clinometer).

(4) Trees less than the minimum diameter or height are classed as ***saplings.***

Distance Methods for determining density, frequency and dominance

- Developed by Cottam and Curtis in the 1950s to describe the forests of Wisconsin.
- A quick method for determining key forest variables without the time-consuming task of laying out plots of fixed dimension in a forest.
- Called "distance methods" because density can be determined by calculating the average distance between trees.
- **Density** can be determined by first finding the average distance between trees, and then squaring this distance to find the average area occupied per tree. To find the number of trees per unit area, divide the unit area (e.g., a hectare) by the area per tree.
- **Frequency** is determined by counting the number of points (sample sites) at which a tree occurs.
- **Dominance** is calculated by first determining the mean basal area per tree species and then multiplying by the density of that species.

Importance Value

$$IV_i = Dr_i + Fr_i + Br_i$$

IV = importance value

i = species i

Dr_i = relative density of species i = (density of species i)/ (density of all species)

Fr_i = relative frequency of species i = (frequency of species i)/ (frequency of all species)

Br_i = relative dominance of species i = (dominance of species i)/ (dominance of all species)

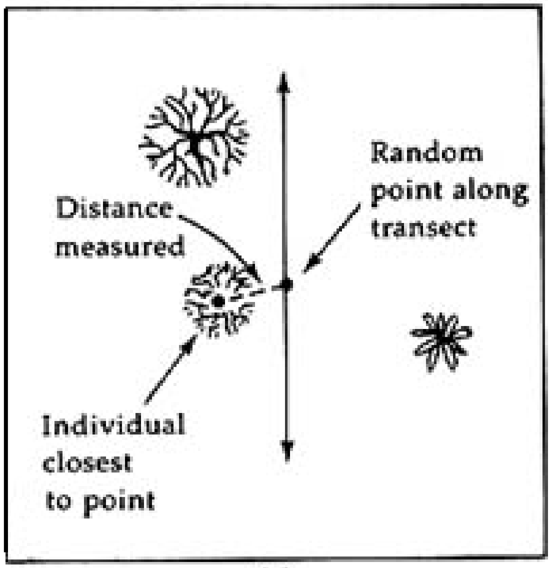
Four distance methods for determining density

- **Nearest individual -** measure distance to the nearest tree at each point (correction factor = 2).
- **Nearest neighbor -** the nearest tree is selected and the distance between it and its nearest neighbor is measured. (correction factor = 1.47).
- **Random pairs -** a line from a random point to the nearest tree is made and a 90˚ exclusion is erected on either side of the line. The distance to the nearest tree outside the exclusion angle is measured. (Correction factor = 0.8)
- **Pont-centered quarter (PCQ) -** a pair of perpendicular lines are erected at the random point, forming a cross with four quadrants. The distances to the nearest tree in each quadrant are measured. This method can also yield a measure of frequency (the number of sample points at which a species occurs).

Again:

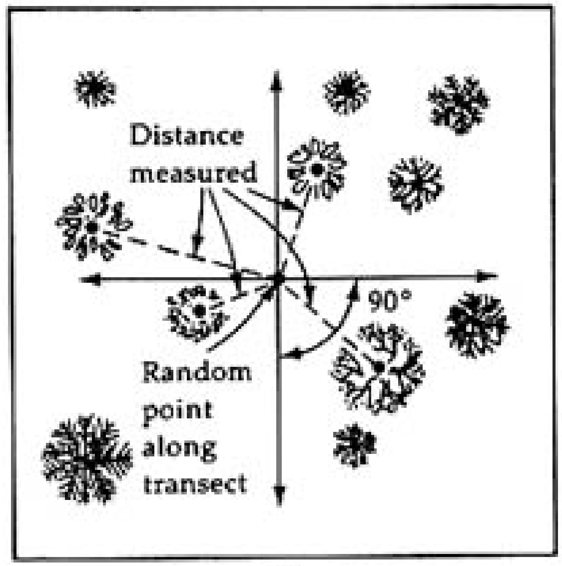
1. The distances are calculated separately for each tree species.
2. The squared distances are the areas occupied by each tree.
3. If the average area per tree is divided into a unit of area (e.g. ha), this will give the **density** of the trees.

Distance methods



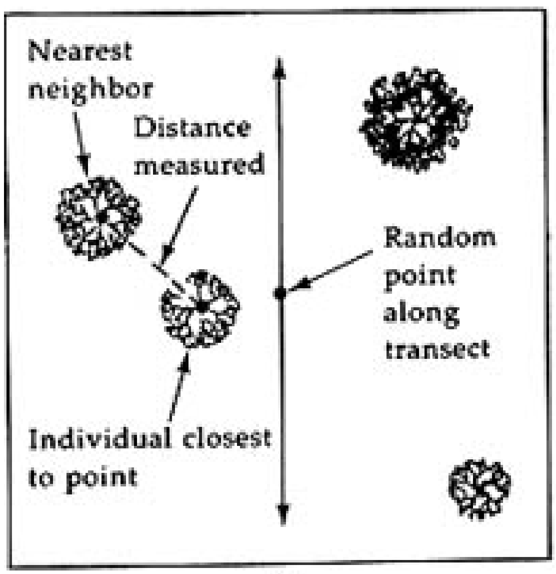
(a)

Nearest individual



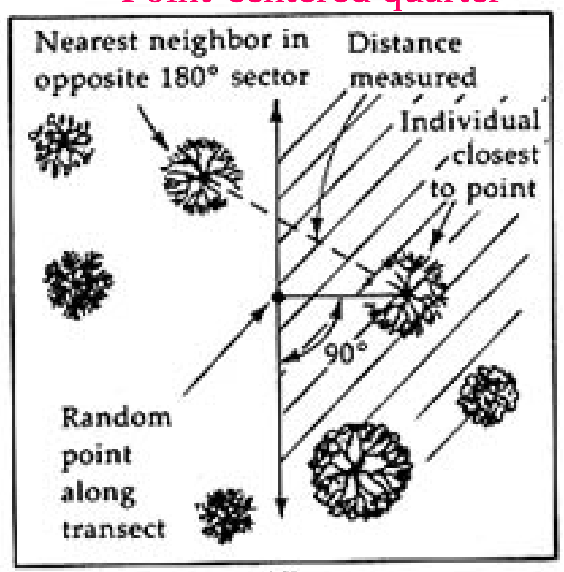
(b)

Point-centered quarter



(c)

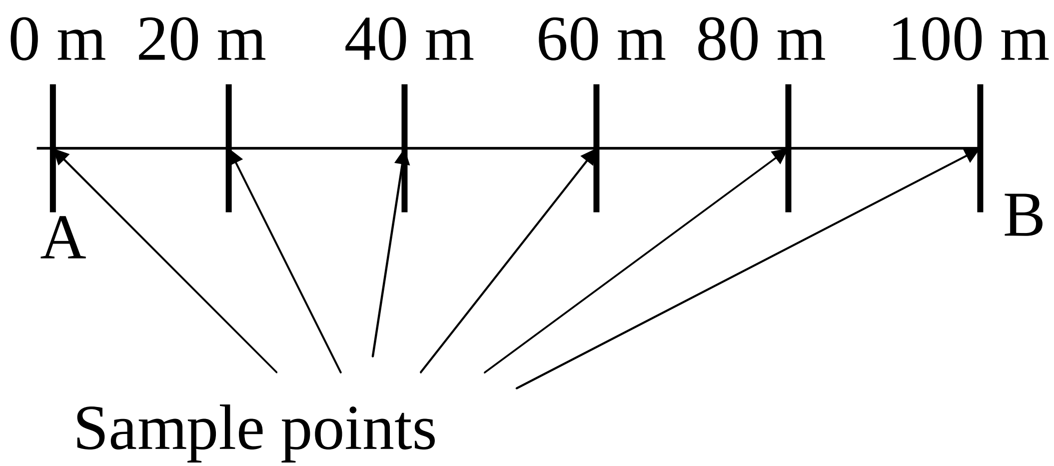
Nearest neighbor



(d)

Random pairs

Point-centered quarter method



- Layout random transect (AB)
- Sample at regular intervals along the transect.
- At each sample point, lay a meter stick down perpendicular to the transect to define 4 quarters (quadrants).
- Many shorter transects (rather than a few long ones) are less susceptible to problems related to clumped distribution patterns.

Point-centered quarter method (Cont')

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are needed to

- At each sample point (P_t), measure the distance (d) to the nearest tree in each quadrant.
- Also measure dbh and record the tree species.

Example using 1994 Flagstaff Mountain data

- North-facing slope of Flagstaff Mountain, Colorado
- *Pinus ponderosa - Pseudotsuga menzeisii* forest
- Sampled using point-centered quarter method

Sample data for Point-centered quadrat method from Flagstaff Mtn. Colorado, 1994

Sample point	Quadrant No.	Species code	Distance (m)	Dbh (cm)	Basal Area (cm^2)
1	1	Psemen	2.1	2	3
	2	Psemen	3.9	8	50
	3	Psemen	2.3	2	3
	4	Psemen	3.1	20	314
2	1	Psemen	1.6	3	7
	2	Psemen	4.9	36	1018
	3	Psemen	1.4	22	380
	4	Psemen	3.1	35	962
3	1	Psemen	1	17	227
	2	Psemen	2.5	16	201
	3	Psemen	4.3	5	20
	4	Pinpon	2.1	36	1018
4	1	Psemen	2.4	8	50
	2	Psemen	0.25	35	962
	3	Psemen	3.3	7	38
	4	Psemen	3.3	2	3
5	1	Psemen	2.2	2	3
	2	Psemen	0.71	31	755
	3	Psemen	3.6	3	7
	4	Psemen	4.3	32	84
6	1	Psemen	7	38	1075
	2	Pinpon	5	18	254
	3	Psemen	5.3	2	3
	4	Psemen	6.6	18	227

Sum = 76. 3 m

Conversion of dbh to basal area

(1) $Ba = \pi\,(dbh/2)^2$ or

(2) Tables of basal areas

Table 3. Conversion of dbh to basal area.

dbh (cm)	BA (cm2)	dbh (cm)	BA (cm2)	dbh (cm)	BA (cm2)	dbh (cm)	BA (cm2)
1	0.8	26	530.9	51	2042.8	76	4536.5
2	3.1	27	572.6	52	2123.7	77	4656.6
3	7.1	28	615.8	53	2206.2	78	4778.4
4	12.6	29	660.5	54	2290.2	79	4901.7
5	19.6	30	706.9	55	2375.8	80	5026.5
6	28.3	31	754.8	56	2463.0	81	5153.0
7	38.5	32	804.2	57	2551.8	82	5281.0
8	50.3	33	855.3	58	2642.1	83	5410.6
9	63.6	34	907.9	59	2734.0	84	5541.8
10	78.5	35	962.1	60	2827.4	85	5674.5
11	95.0	36	1017.9	61	2922.5	86	5808.8
12	113.1	37	1075.2	62	3019.1	87	5944.7
13	132.7	38	1134.1	63	3117.2	88	6082.1
14	153.9	39	1194.6	64	3217.0	89	6221.1
15	176.7	40	1256.6	65	3318.3	90	6361.7
16	201.1	41	1320.3	66	3421.2	91	6503.9
17	227.0	42	1385.4	67	3525.7	92	6647.6
18	254.5	43	1452.2	68	3631.7	93	6792.9
19	283.5	44	1520.5	69	3739.3	94	6939.8
20	314.2	45	1590.4	70	3848.5	95	7088.2
21	346.4	46	1661.9	71	3959.2	96	7238.2
22	380.1	47	1734.9	72	4071.5	97	7389.8
23	415.5	48	1809.6	73	4185.4	98	7543.0
24	452.4	49	1885.7	74	4300.8	99	7697.7
25	490.9	50	1963.5	75	4417.9	100	7854.0

Relative density, frequency, and dominance and importance value

- **Relative density** of a species is the absolute density of a species in a plot or set of samples divided by the sum of the absolute densities of *all* species. (Similarly, **relative dominance** of a species is the absolute dominance of a species divided by the sum of dominances for all species; and relative **frequency** is the frequency of an individual species divided by the sum of frequences for all species in a plot.)
- **Importance value (I.V.):** a measure of the relative importance of a species. It is the sum of the relative density, relative dominance, and relative frequency. The maximum value of I.V. is 300. This is often converted to **percentage importance** by dividing by 3.

$I.V._j = Dr_j + Fr_j + Br_j$,

where: $I.V._j$ = Importance value of species j,

Dr_j = Relative density of species j,

Fr_j = Relative frequency of species j,

Br_j = Relative dominance (basal area) of species j.

Step 1. Calculation of relative density (Dr_j) for Flagstaff Mtn. data

Species designation:

$_{pm}$ = *Pseudotsuga menziesii*,

$_{pp}$ = *Pinus ponderosa*

$Dr_j = n_j/N \times 100\%$,

where n_j = number of trees of species j, and N = Total number of trees.

$Dr_{pm} = 22/24 \times 100\% = 91.7\%$

$Dr_{pp} = 2/24 \times 100\% = 8.3\%$.

Sample point	Quadrant No.	Species code	Distance (m)	Dbh (cm)	Basal Area (cm^2)
1	1	Psemen	2.1	2	3
	2	Psemen	3.9	8	50
	3	Psemen	2.3	2	3
	4	Psemen	3.1	20	314
2	1	Psemen	1.6	3	7
	2	Psemen	4.9	36	1018
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	4	Psemen	3.3	2	3
5	1	Psemen	2.2	2	3
	2	Psemen	0.71	31	755
	3	Psemen	3.6	3	7
	4	Psemen	4.3	32	84
6	1	Psemen	7	38	1075
	2	Pinpon	5	18	254
	3	Psemen	5.3	2	3
	4	Psemen	6.6	18	227

Sum = 76. 3 m

Step 2. Calculation of absolute density (*Da*)

Da = unit area (e.g. ha)/ A, where Da is the total number of trees per unit area, and A = average area occupied by a tree.

d_i = distance from sample point to individual tree i.

d_t = total of all distance measurements (column 4 in sample data table).

$\bar{d}$ = average distance between trees.

N = total number of trees.

$$d_t = \sum_{i=1}^{N} d_i = 76.3 \text{ m}$$

$\bar{d} = d_t/N = 76.3/24 = 3.2$ m/tree

$A = \bar{d}^2 = (3.2)^2$/tree = 10.1 m^2/tree

Da = 1 ha/10.1 m^2/tree

= (10^4 m^2/ha)/(10.1 m^2/tree) **= <u>990 trees/ha</u>**

Denstiy of each tree species:

$Da_j = Dr_j \times Da$, where Da_j is the absolute density of species j. Dr_j is relative density of species j (from Step 1).

Da_{pm} = .917 x 990 = **<u>908 trees/ha</u>**

Da_{pp} = 0.83 x 990 = **<u>82 trees/ha</u>**

Sample point	Quadrant No.	Species code	Distance (m)	Dbh (cm)	Basal Area (cm^2)
1	1	Psemen	2.1	2	3
	2	Psemen	3.9	8	50
	3	Psemen	2.3	2	3
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	3	Psemen	5.3	2	3
	4	Psemen	6.6	18	227

Sum = 76. 3 m

Step 3. Calculation of absolute frequency (*Fa*)

$Fa_j = m_j/m$, where j is the total number of sample points where species j occurs, and m is the total number of sample points.

$\boldsymbol{Fa_{pm}} = m_{pm}/m = 6/6 = \underline{\mathbf{1.00}}$

$\boldsymbol{Fa_{pp}} = m_{pp}/m = 2/6 = \underline{\mathbf{0.33}}$

Sample point	Quadrant No.	Species code	Distance (m)	Dbh (cm)	Basal Area (cm^2)
1	1	Psemen	2.1	2	3
	2	Psemen	3.9	8	50
	3	Psemen	2.3	2	3
	4	Psemen	3.1	20	314
2	1	Psemen	1.6	3	7
	2	Psemen	4.9	36	1018
	3	Psemen	1.4	22	380
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	3	Psemen	5.3	2	3
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Sum = 76. 3 m

Step 4. Relative frequency (*Fr*)

$$Fr_j = Fa_j / (\sum_{i=1}^{k} Fa_i) \times 100\%$$, where *k* is the total number of species.

$\boldsymbol{Fr_{pm}}$ = 1.00/1.33 x 100% = **<u>75.2%</u>**

$\boldsymbol{Fr_{pp}}$ = 0.33/1.33 x 100% = **<u>24.8%</u>**

Step 5. Calculation of absolute dominance (*Ba*)

$Ba_j = \overline{Ba_j} \times Da_j$, where is Ba_j the absolute dominance of species *j*. $\overline{Ba_j}$ is the average basal area for species *j*, and Da_j is the absolute density of species *j*.

$\mathbf{Ba_{pm}} = \overline{Ba_{pm}} \times Da$

$= (7112\ cm^2/(22\ trees)) \times 990\ trees/ha$

(7112 is the sum of basal areas for *Pseudotsuga menziesii*, *22* is the number of sampled PSEMEN)

$= 293{,}284\ cm^2/ha =$ **<u>29.3 m²/ha</u>**

$\mathbf{Ba_{pm}} = (1272\ cm^2 / (2\ trees)) \times 82\ trees/ha$

$= 52{,}152\ cm^2/ha =$ **<u>5.2 m²/ha</u>**

Sample point	Quadrant No.	Species code	Distance (m)	Dbh (cm)	Basal Area (cm^2)
1	1	Psemen	2.1	2	3
	2	Psemen	3.9	8	50
	3	Psemen	2.3	2	3
	4	Psemen	3.1	20	314
2	1	Psemen	1.6	3	7
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	3	Psemen	5.3	2	3
	4	Psemen	6.6	18	227

Sum = 76. 3 m

Step 6. Calculation of relative dominance (Br)

$Br_j = Ba_j / (\sum_{i=1}^{k} Ba_i) \times 100\%$, where k is the total number of species.

$\boldsymbol{Br_{pm}} = 29.3/(29.3 + 5.2) \times 100\%$
$= 29.3/ 34.5$
$= \underline{\mathbf{85.6\%}}$

$\boldsymbol{Br_{pp}} = 5.2/34.5 \times 100\%$
$= \underline{\mathbf{14.4\%}}$

Step 7. Calculation of importance value (*I.V.*)

$I.V._j = Dr_j + Fr_j + Br_j$

$\mathbf{I.V.}_{pm}$ = 75.2% + 91.7% + 85.6% = **252.5%**
$\mathbf{I.V.}_{pp}$ = 24.8% + 8.3% +14.4% = **47.5%**

Step 8. Calculation of relative importance value (*IVr*)

$IVr_j = IV_j / (\sum_{i=1}^{k} IV_i) \times 100\%$, where k is the total number of species.

$\mathbf{IVr}_{pm}$ = (252.5/300) x 100%
= **84.2%**
$\mathbf{Br}_{pp}$ = (47.5/300) x 100%
= **15.8%**

Armed with this bit of knowledge the Biol 475 teams are ready to attack any forest!

QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Labs 4 and 5: Forest sampling methods

- Lab 4 (Oct 2): Point-centered-quarter method
- Lab 5 (Oct 9): Plot-count method
- Write-up for both Labs will be due Oct 16.
- Be sure to have the calculations done for Lab 4 before class next week. Each student will be responsible for doing the calculations from one PCQ transect. We will share the calculations with other members of the class so we all have data and calculations from all six transects.