BIOL 410 Population and Community Ecology

Population sampling

Calculating vital rates

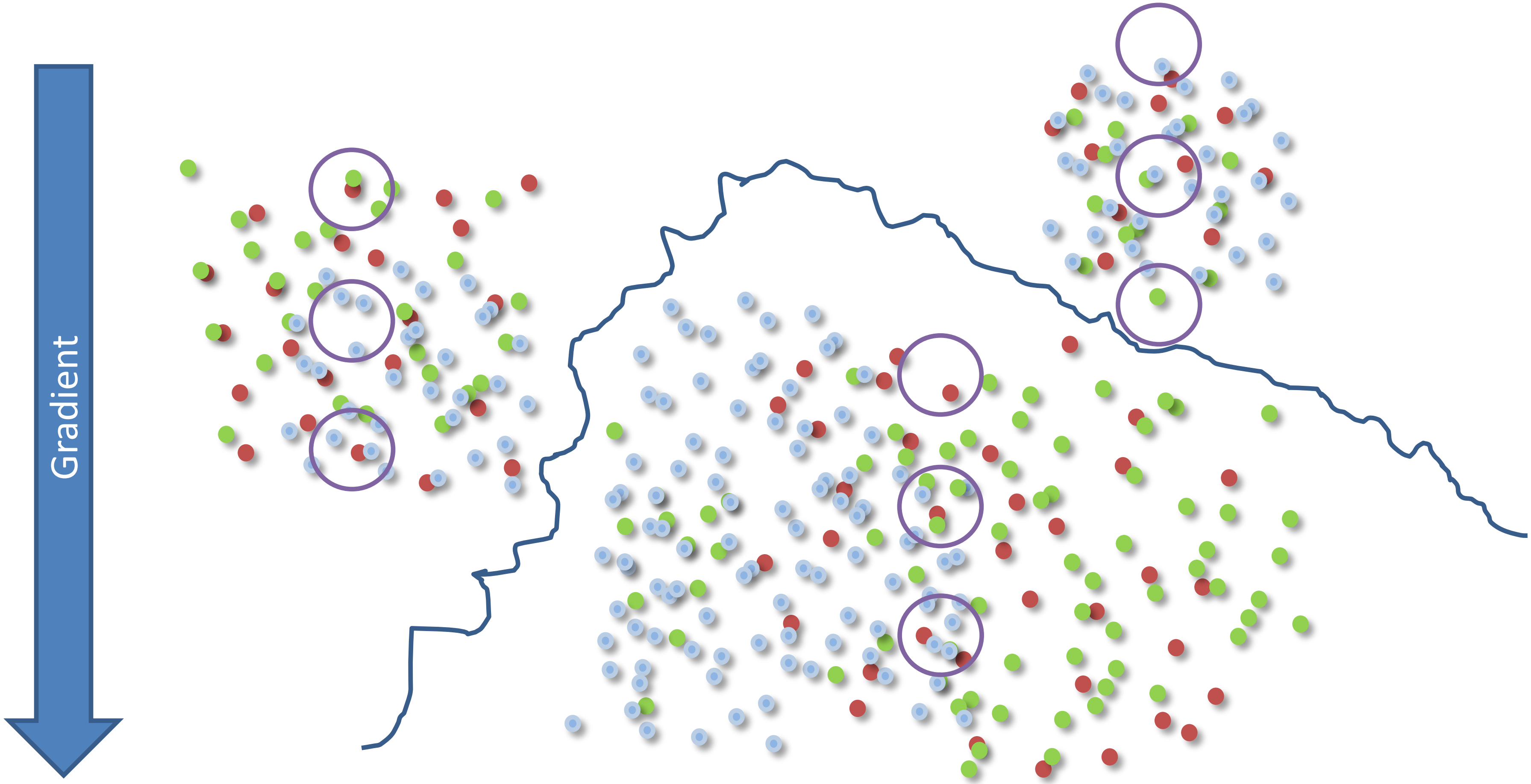
Population sampling strategies

●

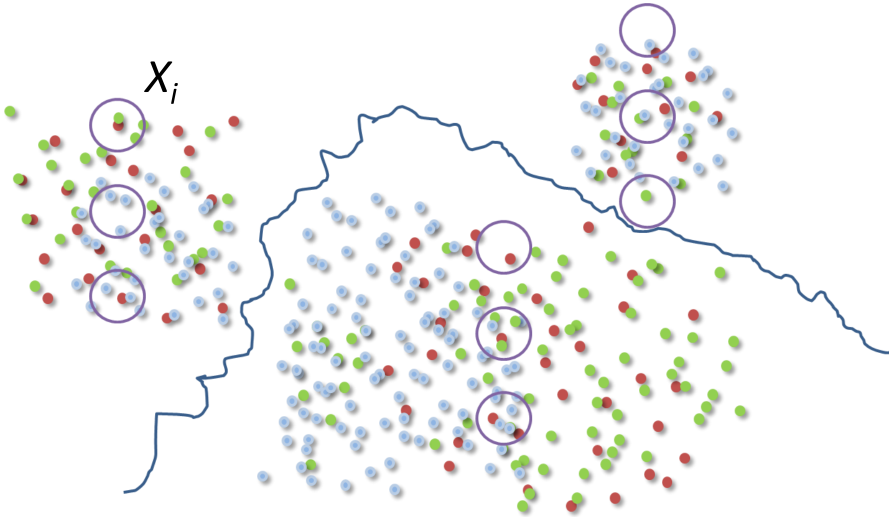
Number
Density

- Random sampling
- Stratified random sampling
- Stratified sampling
- Systematic sampling

- Objective: high accuracy, least bias, greatest precision, lowest cost

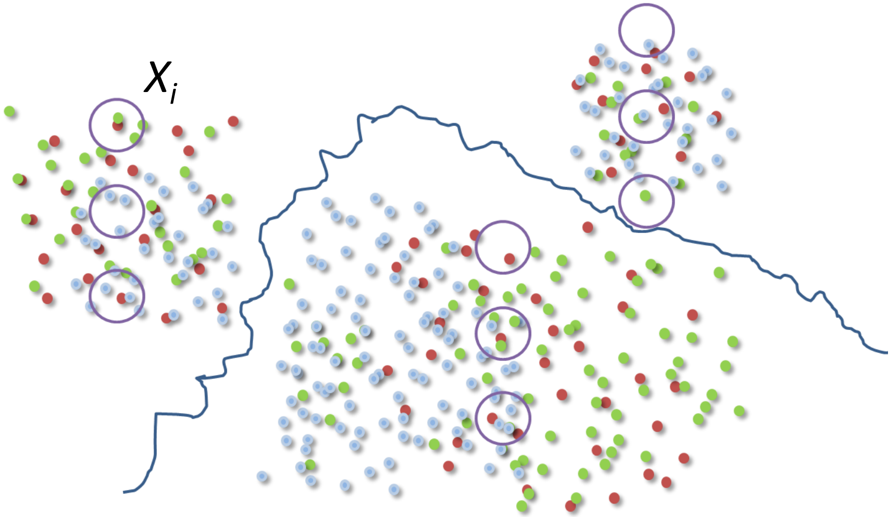


Sampling and population estimates



- Mean $$\bar{X} = \frac{\sum X_i}{n}$$
  - Population, subpopulation, strata

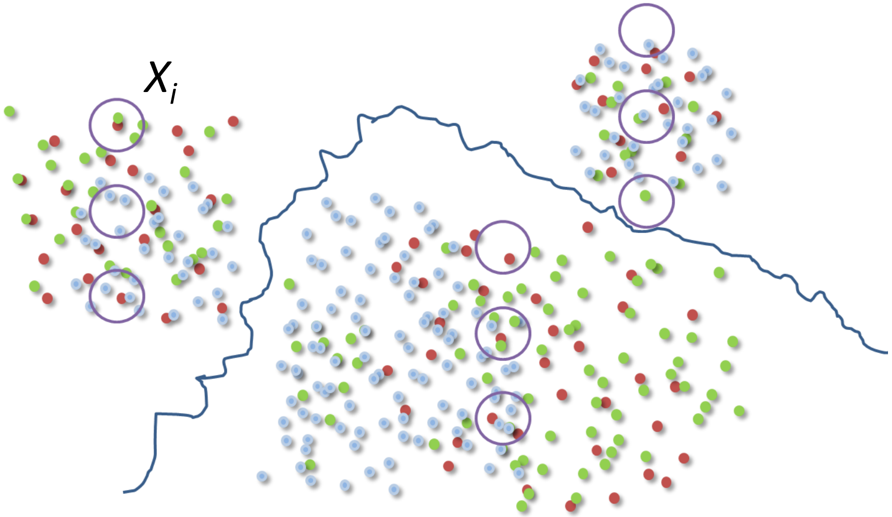
Sampling and population estimates



- Mean $$\bar{X} = \frac{\sum X_i}{n}$$

- Variance $$s^2 = \frac{\sum (X_i - \bar{X})^2}{n-1}$$

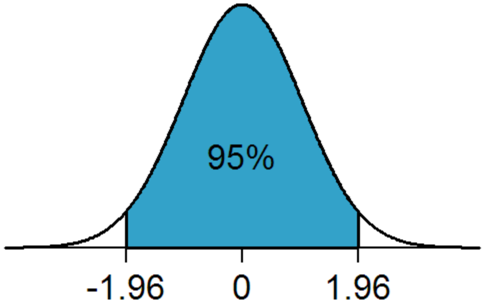
Sampling and population estimates



- Standard deviation

$$s = \sqrt{s^2} = \sqrt{\frac{\sum(X_i - \bar{X})^2}{n-1}}$$

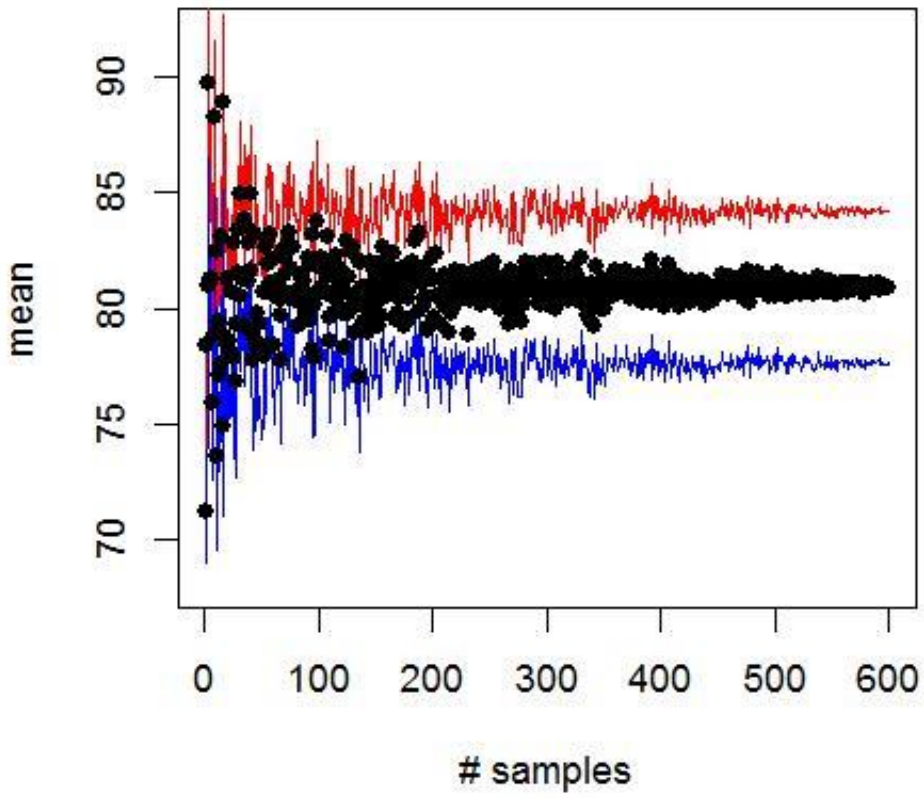
- Confidence intervals (95% confidence intervals)



$$\text{lower } CI = \bar{X} + 1.96\frac{s}{\sqrt{n}}$$

$$upper\ CI = \bar{X} + 1.96\frac{s}{\sqrt{n}}$$

Confidence intervals



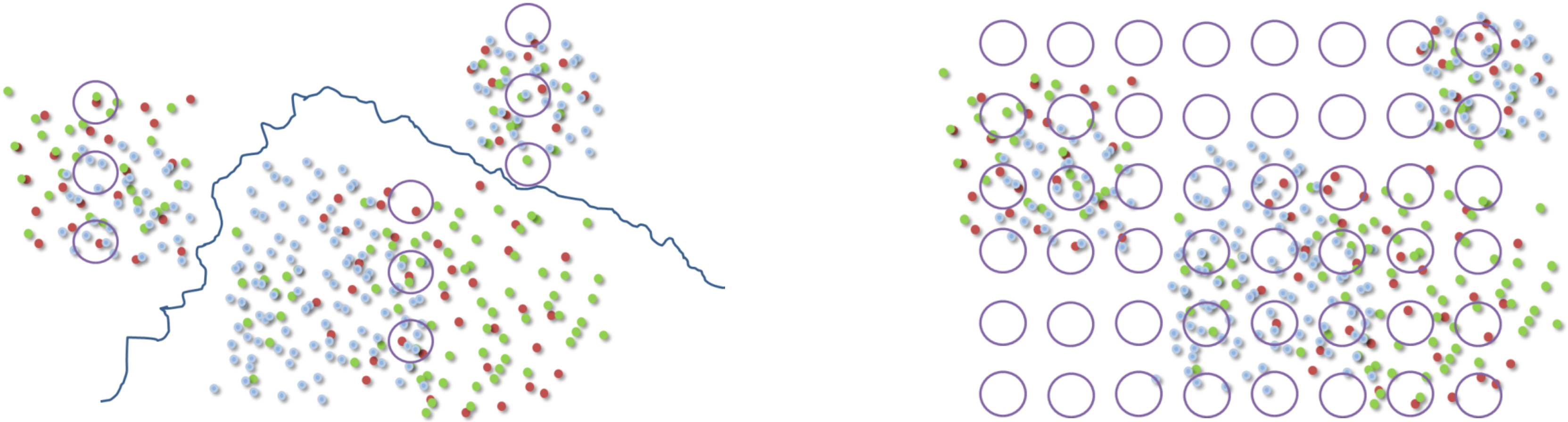
```
N <- rnorm(500,80,15)
upper <- rep(NA,length(N))
lower <- rep(NA,length(N))
nhold <- rep(NA,length(N))
shold <- rep(NA,length(N))

for(i in 1:length(N)){
  Nsample <- sample(N,i,replace = FALSE)
  n <- mean(Nsample[1:i])
  s <- sd(Nsample[1:i])
  nhold[i] <- mean(Nsample[1:i])
  shold[i] <- sd(Nsample[1:i])
  error <- qnorm(0.975)*s/sqrt(n)
  upper[i] <- n + error
  lower[i] <- n - error
}

i <- c(1:length(N))
jpeg("confidence_interval.jpg")
par(cex=1.5)
plot(i,nhold,ylim=c(68,92),ylab="mean",xlab="# samples",pch=16)
points(i,upper,type="l",col="red")
points(i,lower,type="l",col="blue")
points(i,nhold,col="black",pch=16)
dev.off()
```

$$\text{Upper } CI = \bar{X} + 1.96\frac{s}{\sqrt{n}}$$

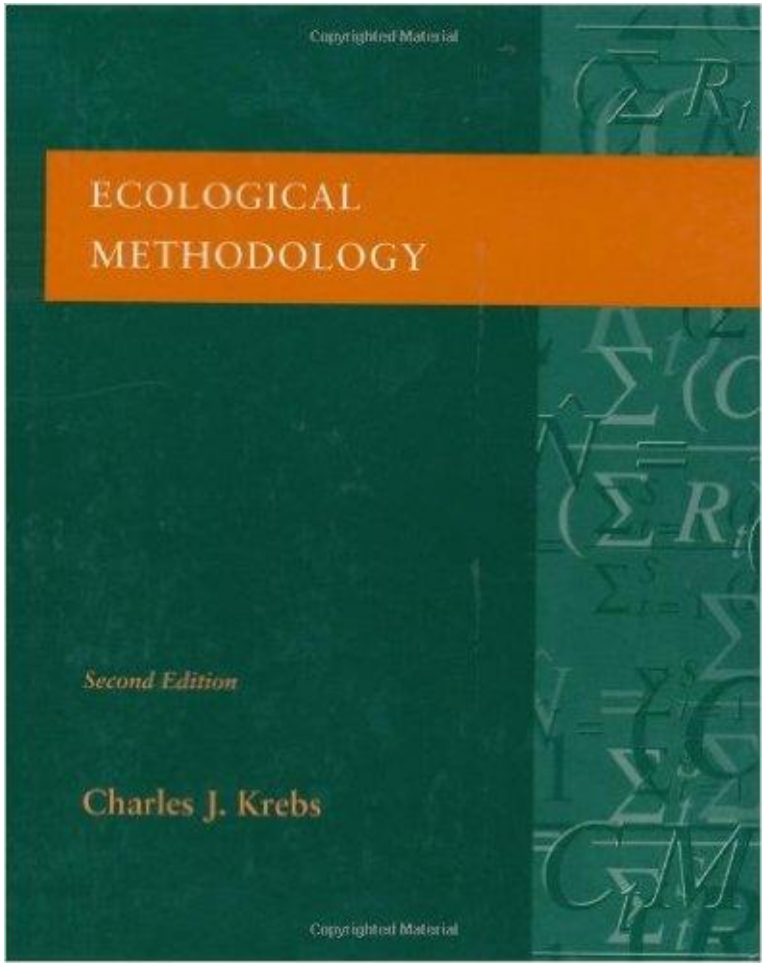
Sampling and population estimates



- Accuracy: correct mean
- Precision: small variance, small 95% confidence intervals
- Bias: least bias possible

$$\boldsymbol{s = \sqrt{s^2} = \sqrt{\frac{\sum (X_i - \bar{X})^2}{n-1}}}$$

Ecological sampling methods



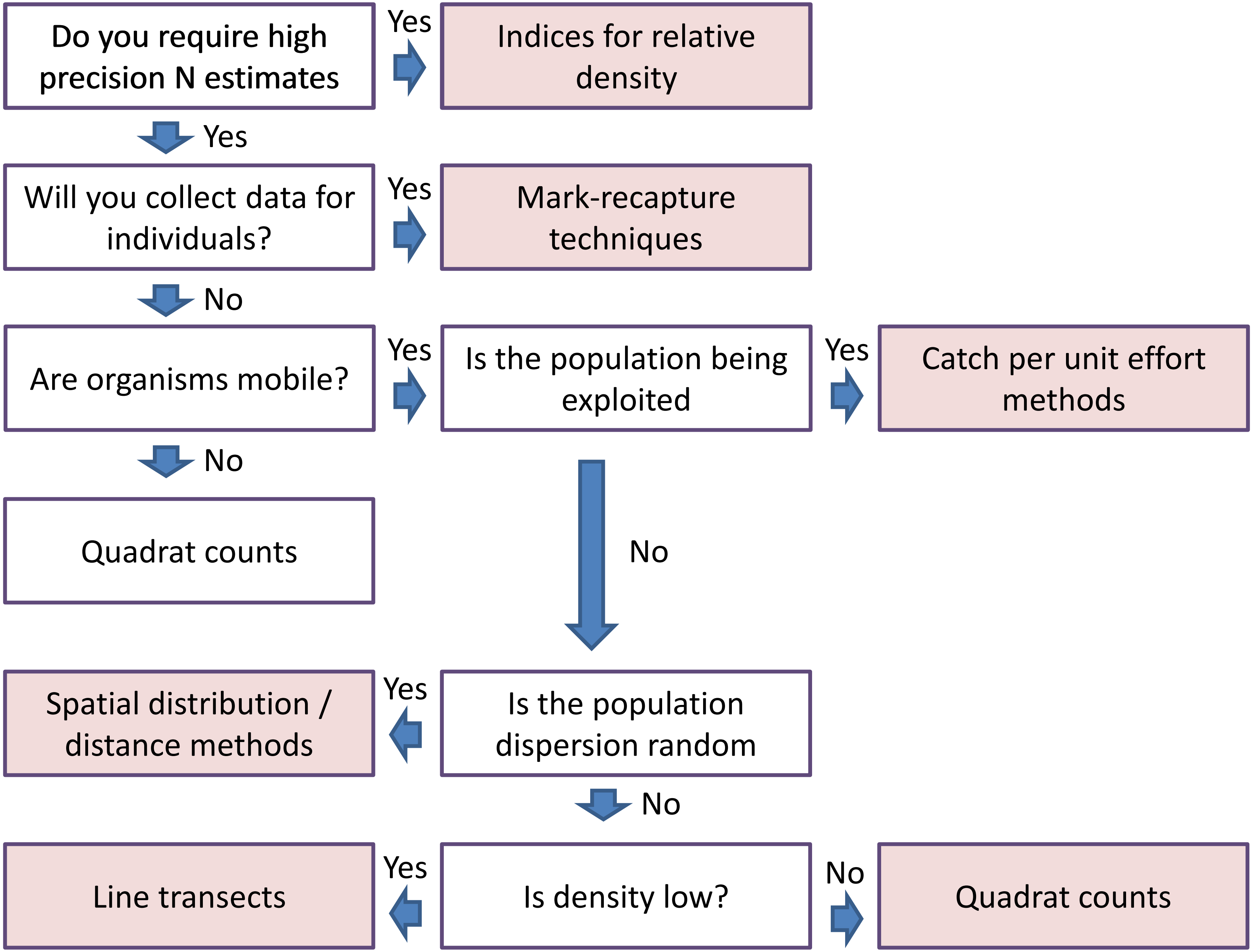
ECOLOGICAL
METHODOLOGY

Second Edition

Charles J. Krebs

UBC

https://www.zoology.ubc.ca/~krebs/ecological_rants/



Do you require high precision N estimates

Yes

Indices for relative density

Yes

Will you collect data for individuals?

Yes

Mark-recapture techniques

No

Are organisms mobile?

Yes

Is the population being exploited

Yes

Catch per unit effort methods

No

Quadrat counts

No

Spatial distribution / distance methods

Yes

Is the population dispersion random

No

Line transects

Yes

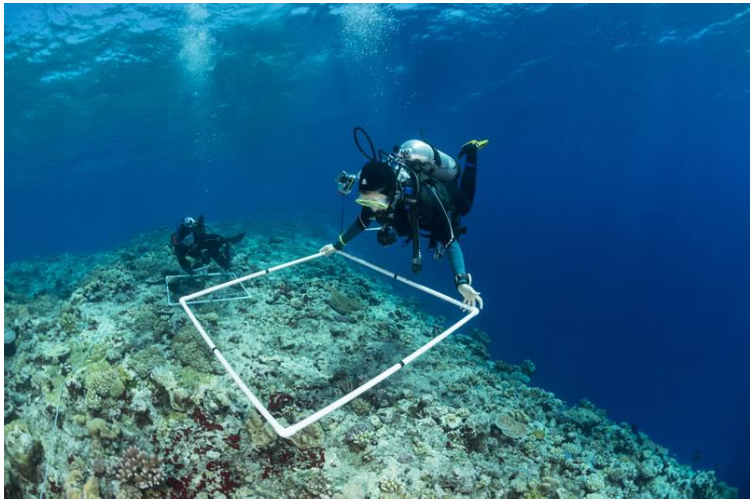
Is density low?

No

Quadrat counts

Quadrat counts

- Count plants/ animals in a known area
  - Simplest technique fore density estimation
  - Counts can be taken from units using any number of sample designs: random, stratified random, systematic..
  - Assumptions
    - All individuals in the quadrate are observed
    - Quadrat samples are representative of the study area as a whole
    - Individuals don’t move between quadrats during a sampling session

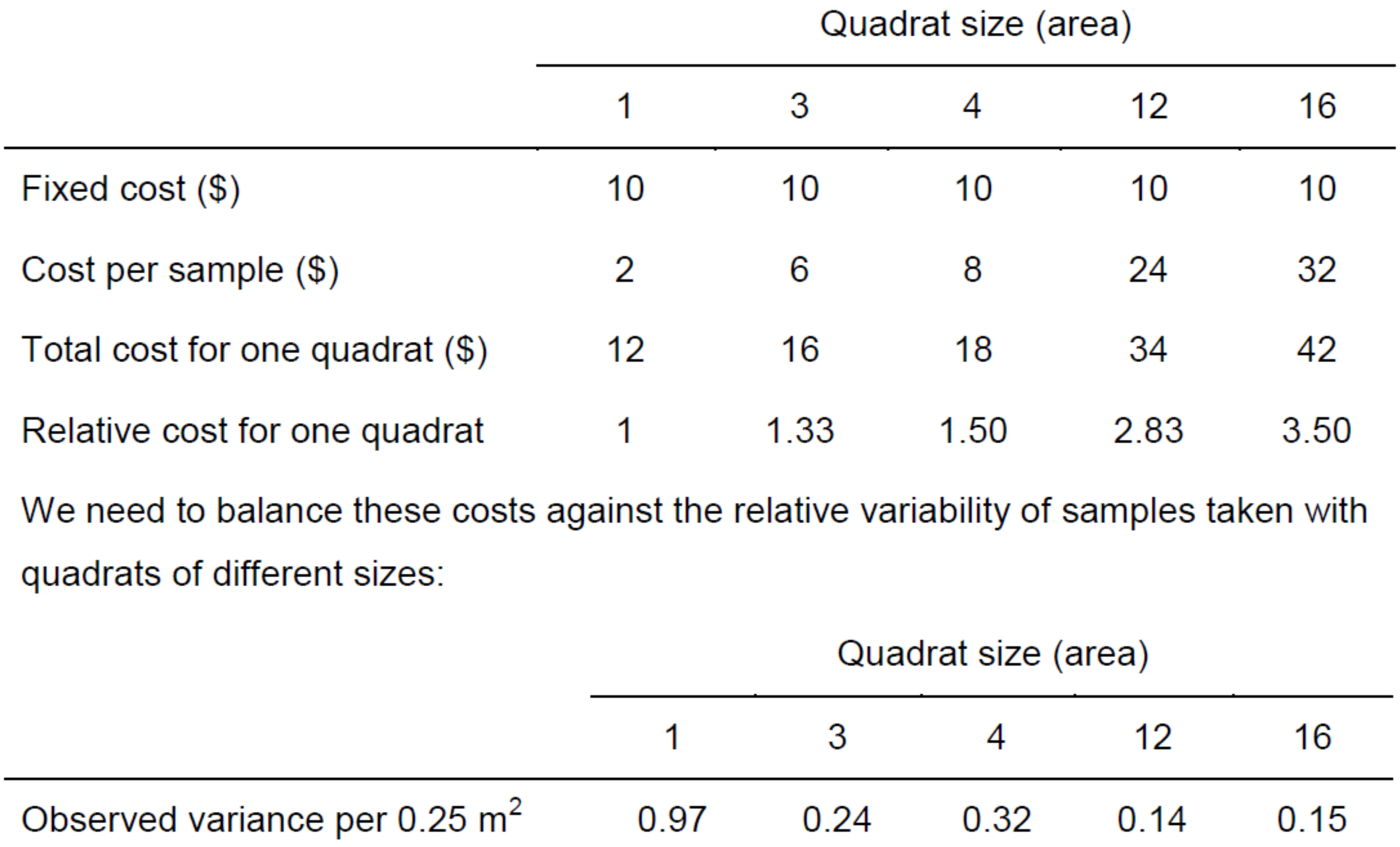


Use of quadrat counts

- Spatial considerations
  - Edge to area ratio: circle < square < rectangle
  - Edge can result in arbitrary decisions about inclusion, but difficult to traverse round edge
  - Shape dependent on sampling problem
- Size
  - Balance sample variance with cost of placeman and collection
    - Total cost = fixed costs + sampling costs
    - Minimize (Total costs)*(Observed Variance)

Optimized quadrat counts

- Wiegert's Method
  - Quadrat size that minimizes relative cost and relative variability



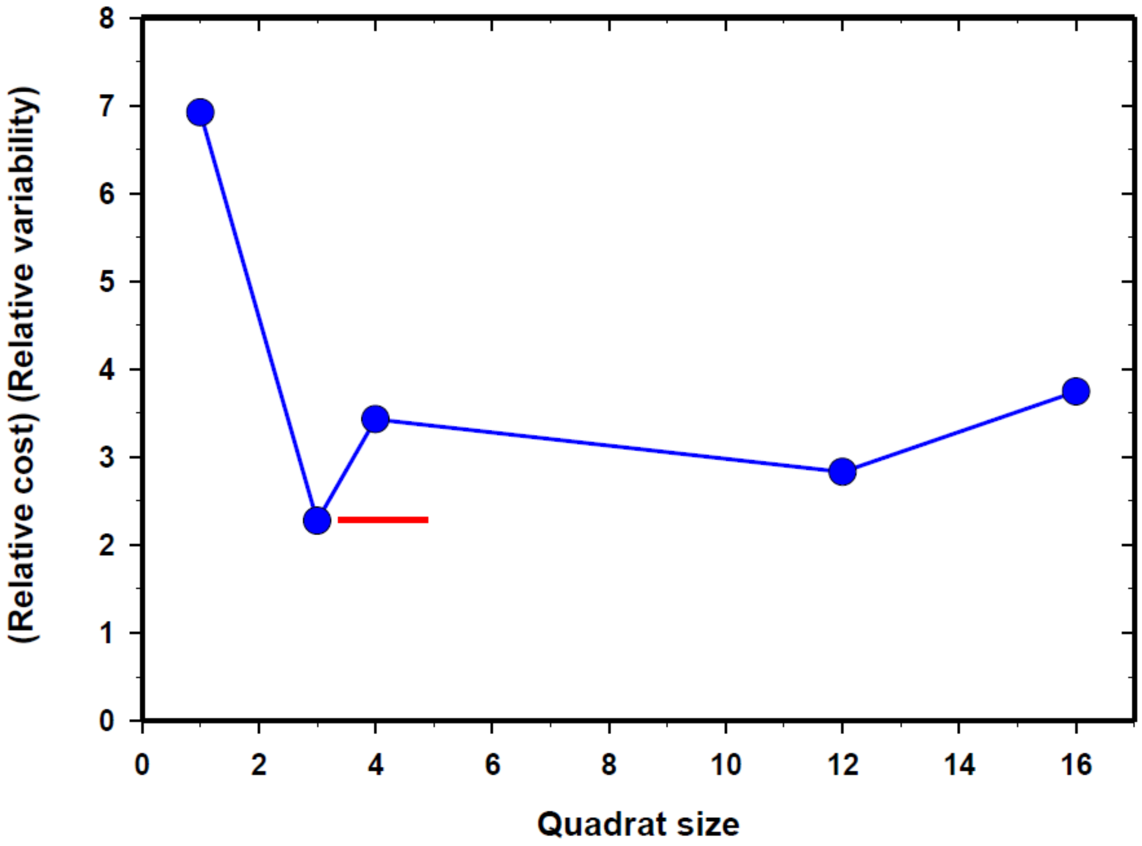
	Quadrat size (area)				
	1	3	4	12	16
Fixed cost ($)	10	10	10	10	10
Cost per sample ($)	2	6	8	24	32
Total cost for one quadrat ($)	12	16	18	34	42
Relative cost for one quadrat	1	1.33	1.50	2.83	3.50

We need to balance these costs against the relative variability of samples taken with quadrats of different sizes:

	Quadrat size (area)				
	1	3	4	12	16
Observed variance per 0.25 m^2	0.97	0.24	0.32	0.14	0.15

Optimized quadrat counts

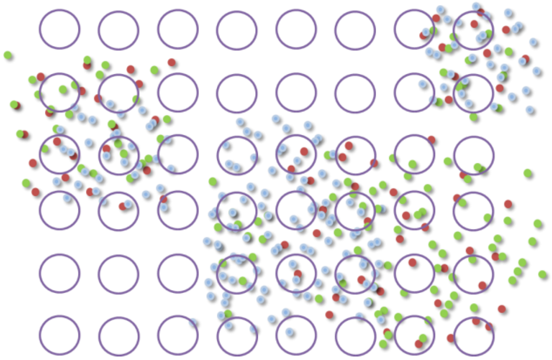
- Wiegert’s Method
  - Quadrat size that minimizes relative cost and relative variability



Quadrat counts

- Calculating abundance
  - Total/Minimum count
    - Restrict estimate to statistical population
    - Limited inference
  - Simple density estimate
    - Extrapolate estimate (n/m2) to uncounted units and/or biological population
    - Best to stratify
  - Statistical extrapolation
    - Relate distribution of counts to a statistical distribution
    - Use count distribution not continuous distribution
    - Devise statistical “model” that estimates/explains populations

Quadrat counts

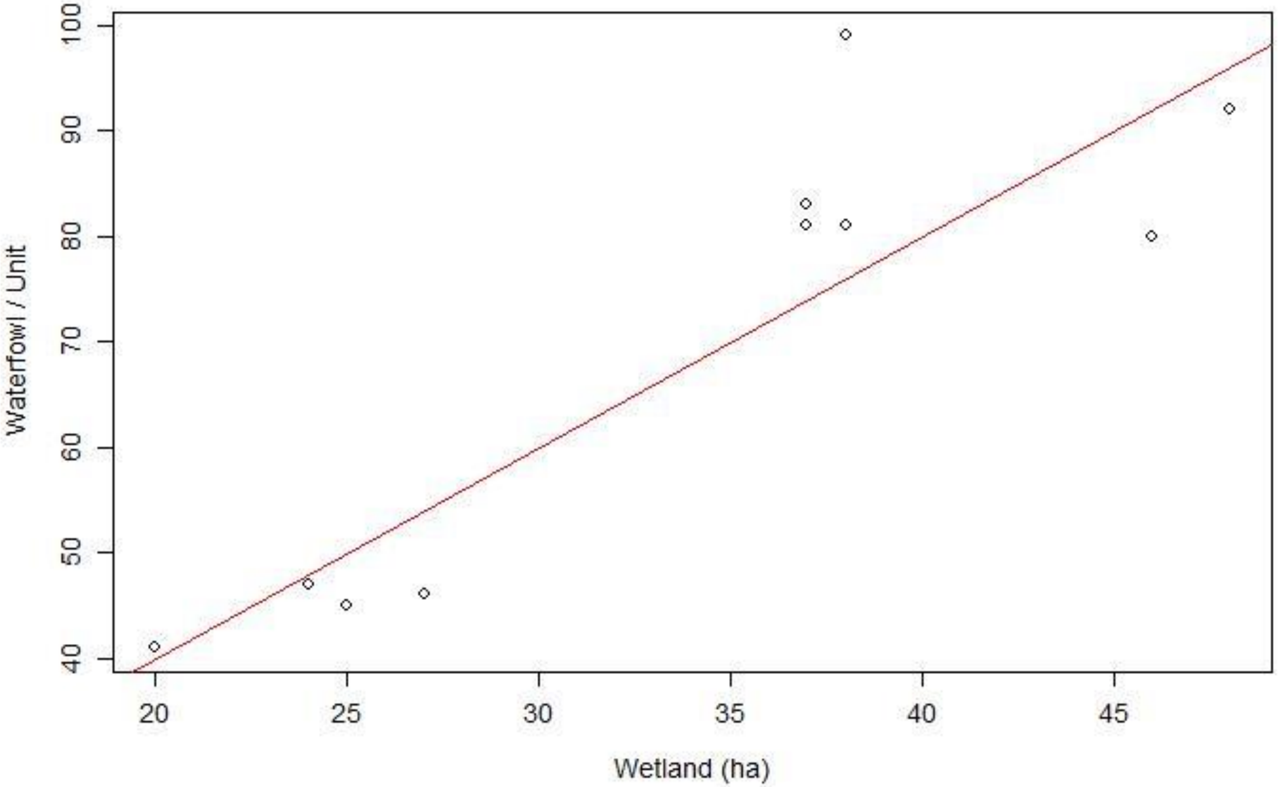


- Simple density estimates
  - (areal survey)
- Equal size sample units
  - Randomly sample n quadrates from N quadrats in statistical population
  - Mean number of animals per quadrat: $$\bar{x} = \frac{\sum x}{n}$$
  - Total number: $$\hat{X} = N\bar{x}$$
  - Variance of sample $$\hat{s}^2 = \frac{\sum x^2 - {(\sum x)^2}/{n}}{n-1}$$
  - Variance of estimate $$(Ns_{\bar{x}})^2 = \frac{N^2}{n} s^2 \left(1 - \frac{n}{N}\right)$$

Sampling without replacement

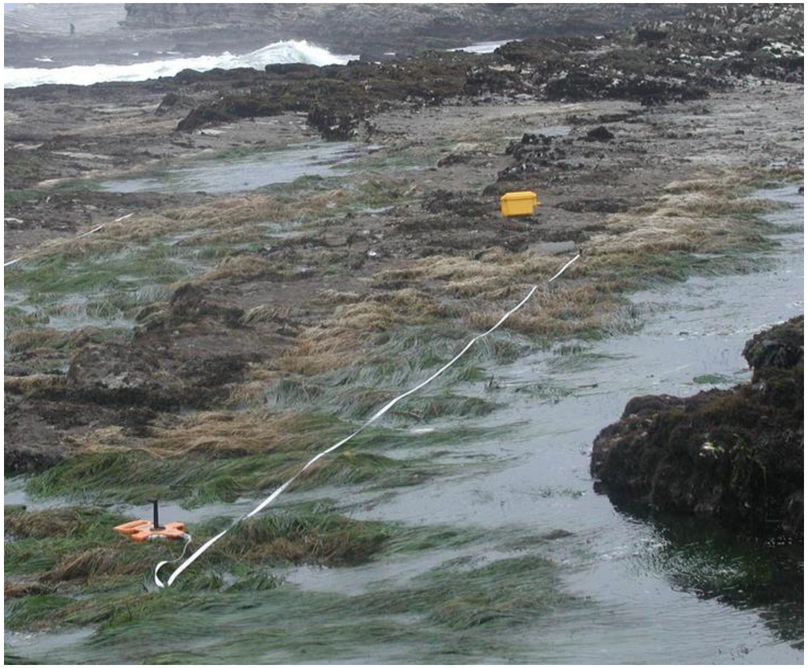
Quadrat counts

- Statistical extrapolation
  - Relate distribution of counts to a statistical distribution
  - Use count distribution not a continuous distribution
  - Devise a statistical model that estimates population size



Line transects

- Used to calculate density of animals in rectangular “quadrats”



Line transects

- Used to calculate density of animals in rectangular “quadrats”
  - If detectability 100% simple count
  - If detectability <100% then develop detection function to estimate density

$$\hat{D} = \frac{n}{2La}$$

$\hat{D}$ = density of animals per unit area
n = number of animals seen on transect
L = length of transect
a = detection constant (detection probability vs distance)

Estimators of detection distance (a)

- Hayne’s estimator

  - Assumes fixed flushing distance correction for (a)

$$\hat{D}_H = \frac{n}{2L}\left(\frac{1}{n}\sum {}^{1}\!/_{r_i}\right)$$

where $\hat{D}_H$ = Hayne's estimator of density

n = number of animals seen

L = length of transect

r_i = sighting distance to each animal i

Estimators of detection distance (a)

- Hayne’s estimator
  - Variance of Hayne’s density estimate

$$\mathrm{Var}\left(\hat{D}_H\right) = D_H^2 \left[\frac{\mathrm{var}(n)}{n^2} + \frac{\sum \left(1/r_i - R \right)^2}{R^2\, n(n-1)} \right]$$

where $\hat{D}_H$ = Hayne's estimator of density

n = number of animals seen

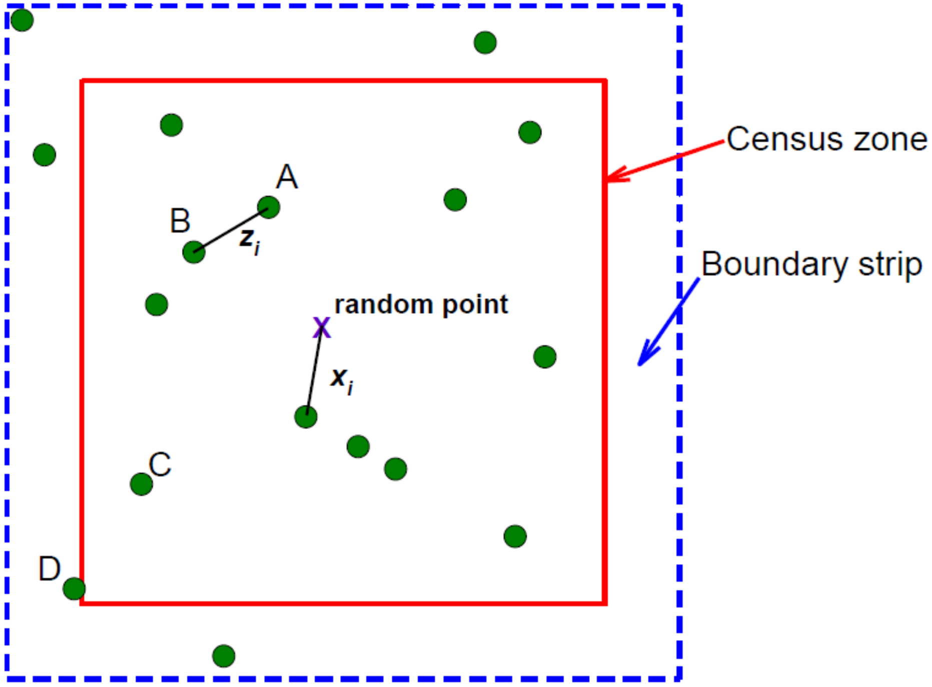
$\mathrm{var}(n)$ = variance of $n \cong n$

r_i = sighting distance for animal i

R = mean of the reciprocals of sighting distances i

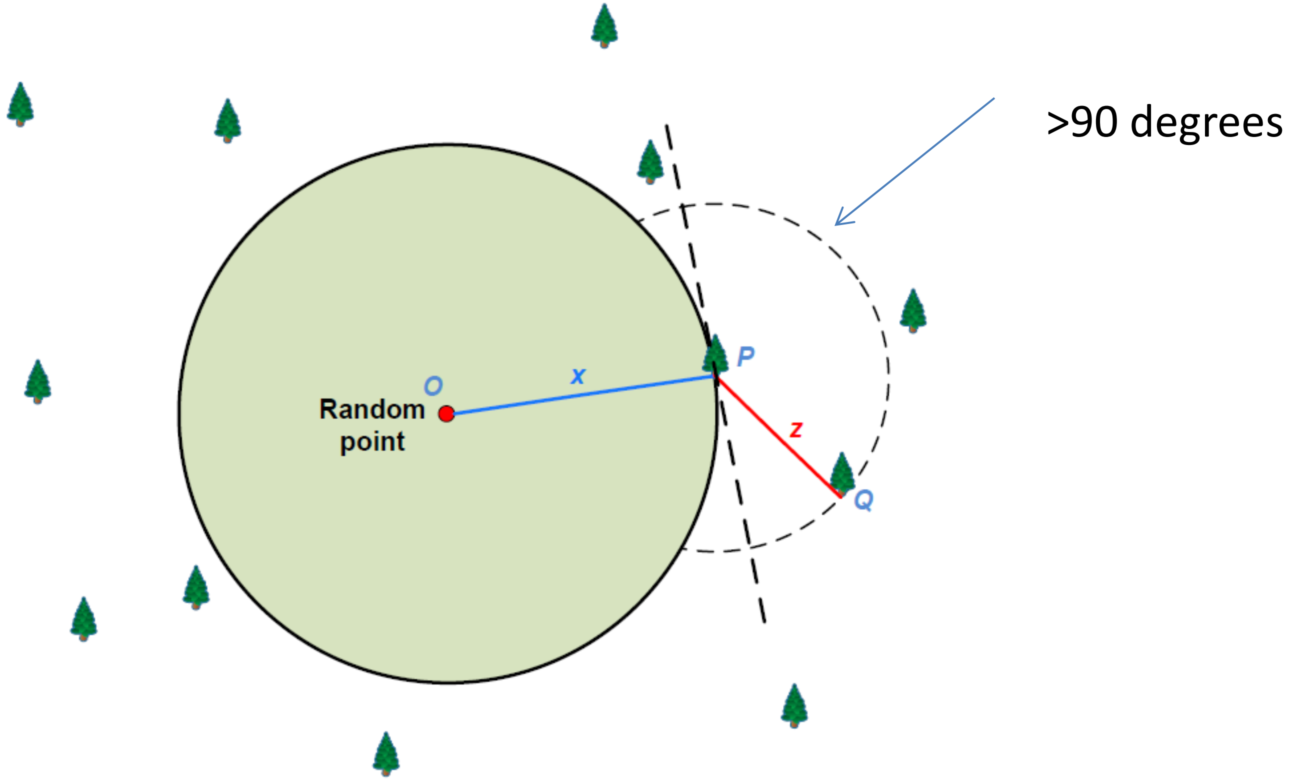
Distance methods

- Distance of a random point to the nearest organism
- Distance of a random organism to its nearest neighbour



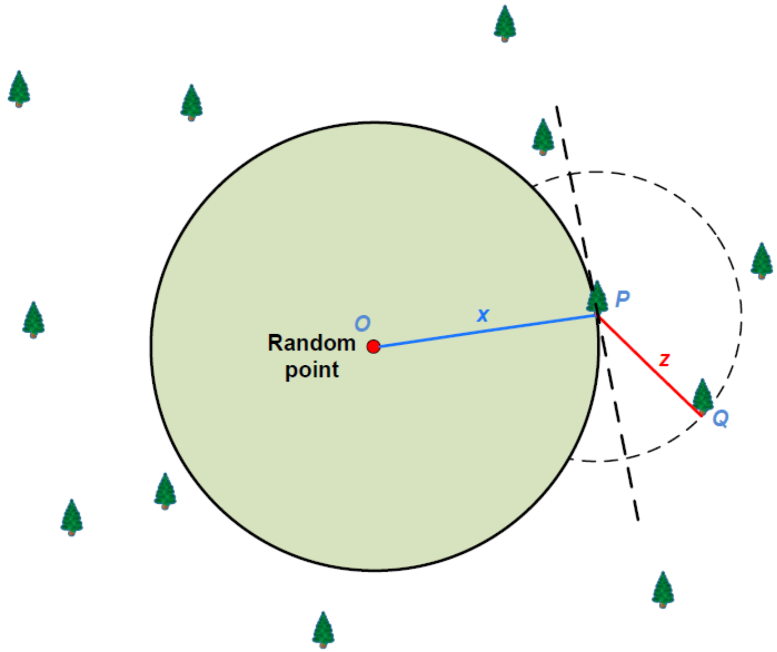
Distance methods

- T-square sampling procedure
  - Distance from random point to nearest organism
  - Distance from the organism to its nearest neighbour



Distance methods

- T-square sampling procedure



$$\hat{N}_1 = \frac{n}{\pi \sum (x_i^2)}$$

where $\hat{N}_1$ = Estimate of population density from point-to-organism data

n = Sample size

x_i = Distance from random point i to nearest organism

Distance methods

- T-square sampling procedure

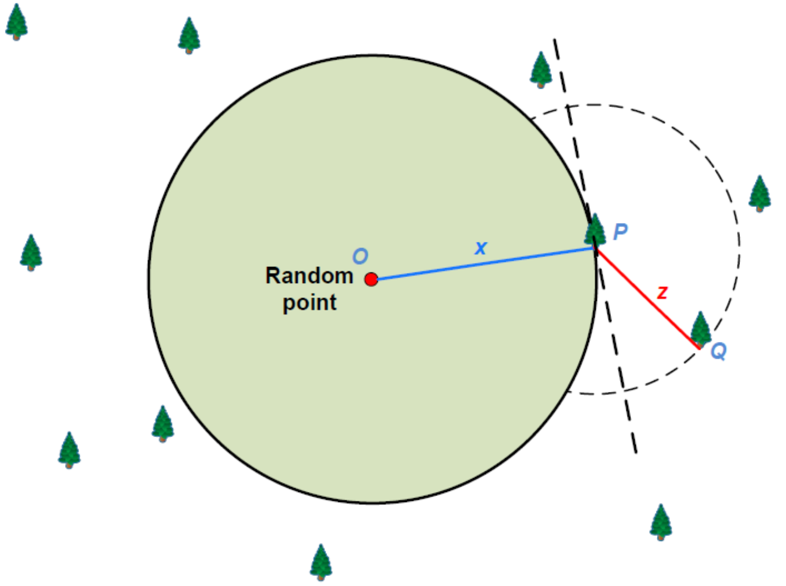
$$\hat{N}_1 = \frac{n}{\pi \sum (x_i^2)}$$

where $\hat{N}_1$ = Estimate of population density from point-to-organism data

n = Sample size

x_i = Distance from random point i to nearest organism

$$\hat{N}_2 = \frac{2n}{\pi \sum (z_i^2)}$$



Distance methods

- T-square sampling procedure
  - Compound measure using N_1, N_2

$$\hat{N}_T = \frac{n^2}{2\sum(x_i)\left[\sqrt{2}\sum(z_i)\right]}$$

$$\text{Standard error}\left(\frac{1}{\hat{N}_T}\right) = \sqrt{\frac{8(\bar{z}^2 s_x^2 + 2\,\bar{x}\,\bar{z}\,s_{xz} + \bar{x}^2 s_z^2)}{n}}$$

where $\bar{x}$ = Mean value of point-to-organism distances

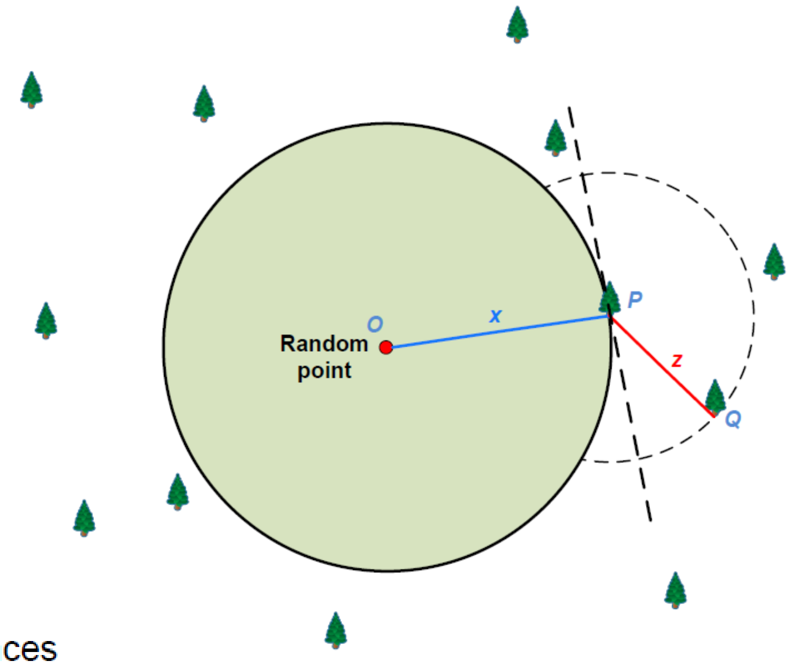
$\bar{z}$ = Mean value of T-square organism-to-neighbor distances

n = Sample size

s_x^2 .= Variance of point-to-organism distances

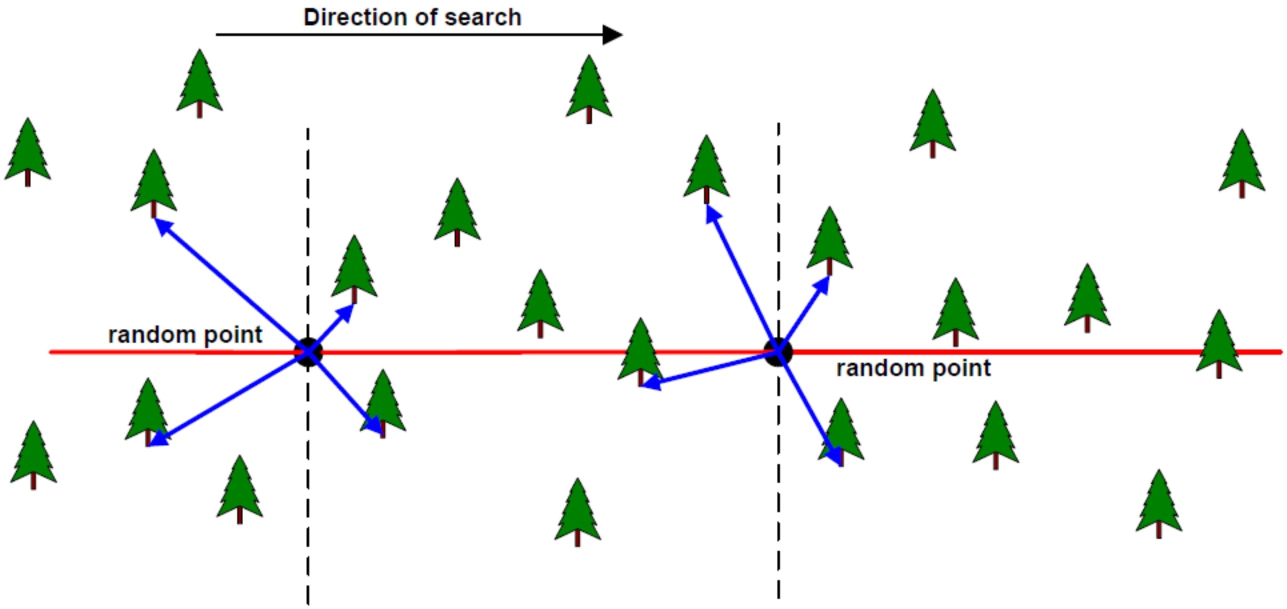
s_z^2 = variance of T-square organism-to-neighbor distances

s_{xz} = covariance of x and z distances



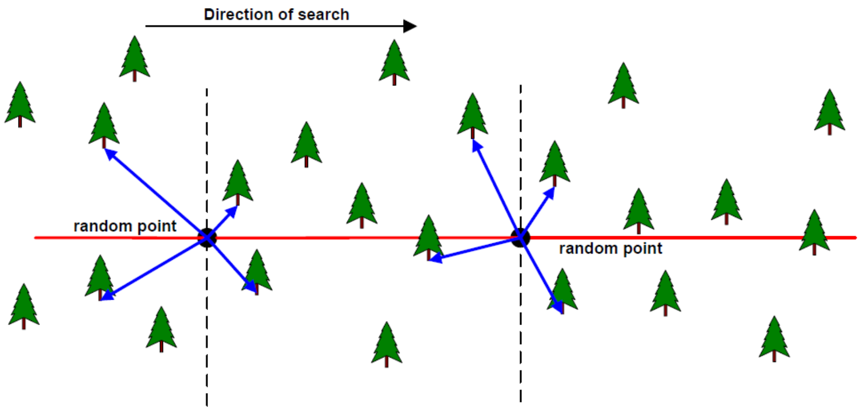
Distance methods

- Point quarter method
  - Forestry
  - Early land surveying



Distance methods

- Point quarter method



$$\hat{N}_p = \frac{4\,(4n-1)}{\pi \sum (r_{ij}^2)}$$

where $\hat{N}_p$ = Point-quarter estimate of population density

n = Number of random points

π = 3.14159

r_{ij} = Distance from random point i to the nearest organism in quadrant j (j = 1,2,3,4; i = 1, ...n)

$$\text{Variance}\,(\hat{N}_p) = \frac{\hat{N}_p^2}{4n - 2}$$

Mark Recapture methods

1. Capture and mark individuals
   - Radio transmitters, PIT tags, ear tags, physical features, genetics, etc.
2. Recapture or resight random sample of individuals during subsequent surveys
3. Calculate the proportion of new and previously captured/ sighted individuals.

Mark-Recapture Methods

Three Standard Methods

1. **Petersen Method** – closed population, single recapture event
2. **Schnabel Method** – closed population, multiple recapture events
3. **Jolly-Seber Method** – open population, multiple censusing events

  - Closed population: doesn’t change in size during study
  - Open population: population changes in size

Petersen Method

One mark and one recapture session

$$\frac{\boldsymbol{N}}{\boldsymbol{M}} = \frac{\boldsymbol{C}}{\boldsymbol{R}}$$

First sample

Second sample

Variables

M = Number of individuals marked during the first sample

C = Total number of individuals captured during the second sample

R = Number of individuals in the second sample that were marked

N = Size of the population at the time of Marking.

Petersen Method

- If the number of recaptures is less than 7 (R<7), add the value of 1 to each of the number Marked, Captured and Recaptured

$$\boldsymbol{\hat{N} = \frac{(M+1)(C+1)}{(R+1)} - 1}$$

Petersen - Confidence Intervals

How you Calculate Confidence Intervals depends on number of **R**ecaptures relative to Total **C**aptures at second marking session.

- If the proportion of recaptured individuals is greater than 10% of the total captures on the second sampling period (R/C>0.1), then use a **Binomial Confidence Interval**.

- If R/C is *less* than 10%, but the number of recaptures is greater than 50 (R>50), then use a **Normal Approximation**

- If R/C is *less* than 10% and R<50, you use a **Poisson Confidence Interval**

Petersen - Confidence Intervals

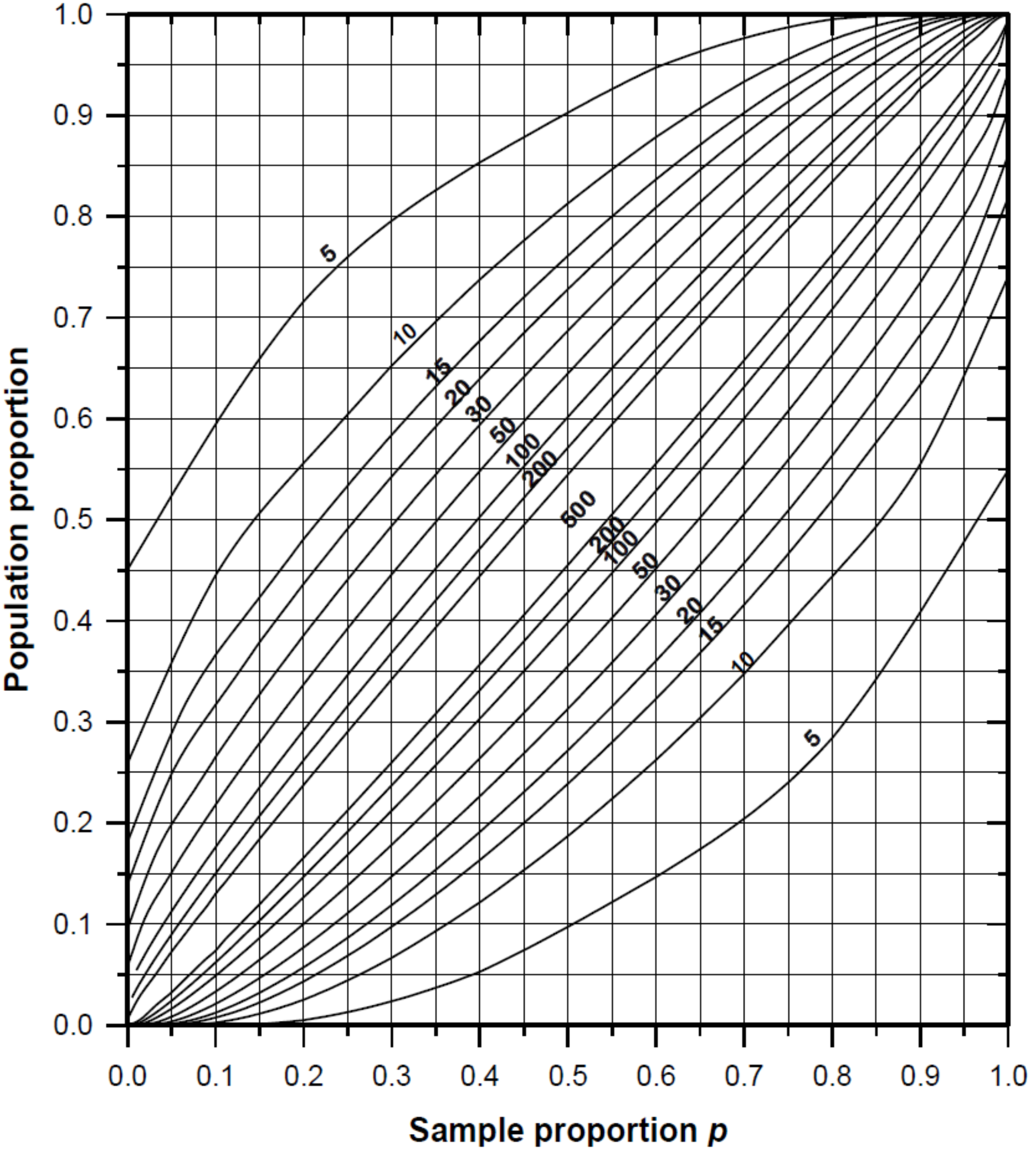
Binomial Confidence Interval

- **X-axis = Recaptures /Captures**
- **Lines –Captures**
- **Y-Axis – Upper and lower Confidence Intervals for a given R/C.**

$$\hat{N} = \frac{CM}{R}$$

$$Lower\ 95\%\ CI\ on\ \hat{N} = \frac{1}{Upper\ pop.proportion}M$$

$$Upper\ 95\%\ CI\ on\ \hat{N} = \frac{1}{Lower\ pop.proportion}M$$



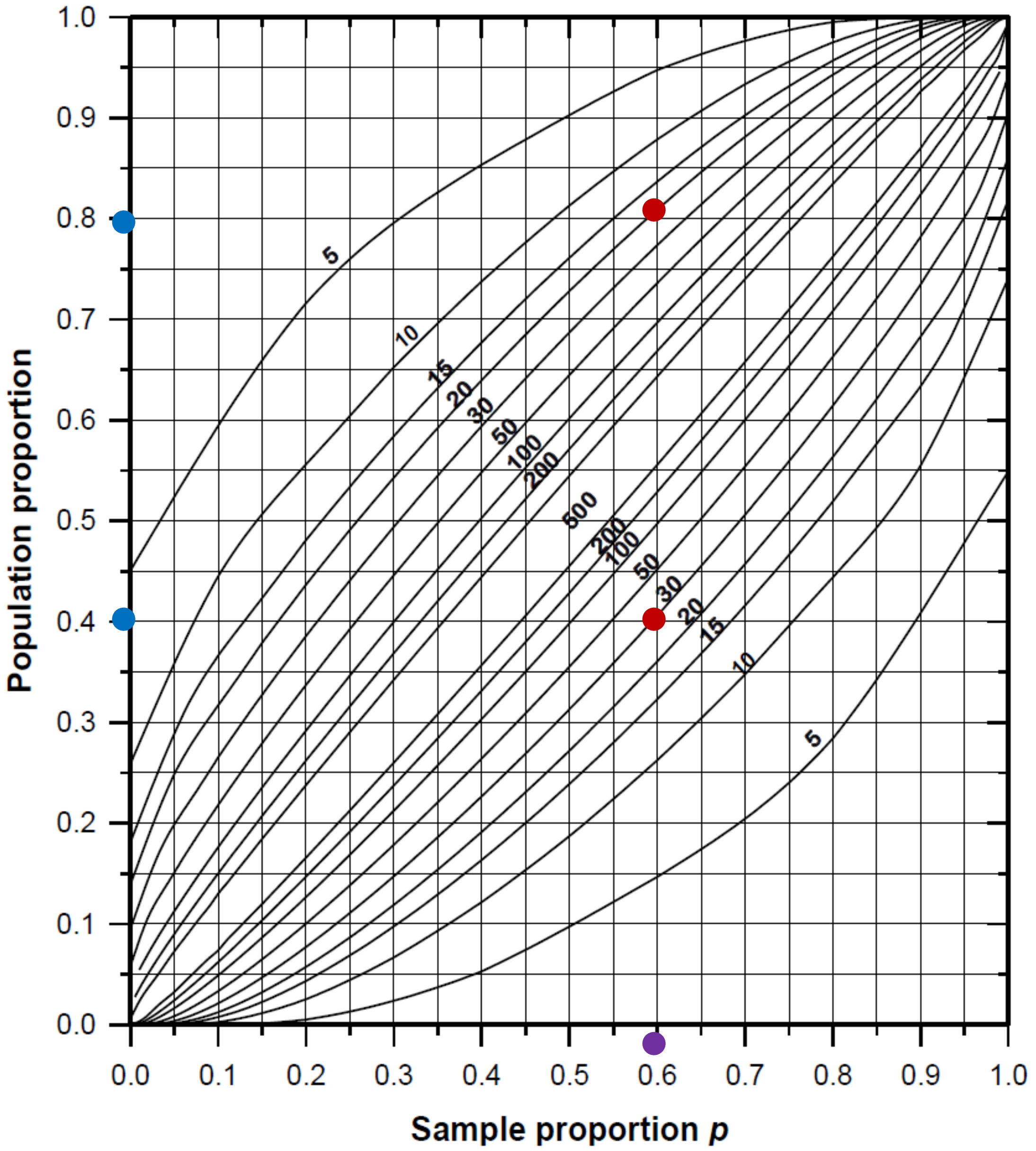
Petersen - Confidence Intervals

Binomial Confidence Interval

- M: 50 marked birds
- C: 22 captured birds
- R: 14 recaptures

- ● Sample prop. p = R/C = 14/22 = 0.60
- ● Captures = 22
- ● Lower confidence value = 0.4
- ● Upper confidence value = 0.83

- CU = (1/CV)*M
- Lower 95% CI = (1/0.4)*50 = 60
- Upper 95% CI = (1/0.83)*50 = 125



Petersen - Confidence Intervals

Poisson Confidence Interval

- **X in table corresponds to number of Recaptures in your sample (R)**
- **Sub upper and lower values into estimate of N for low recaptures to get upper and lower CI**

$$\hat{N} = \frac{(M+1)(C+1)}{(R+1)} - 1$$

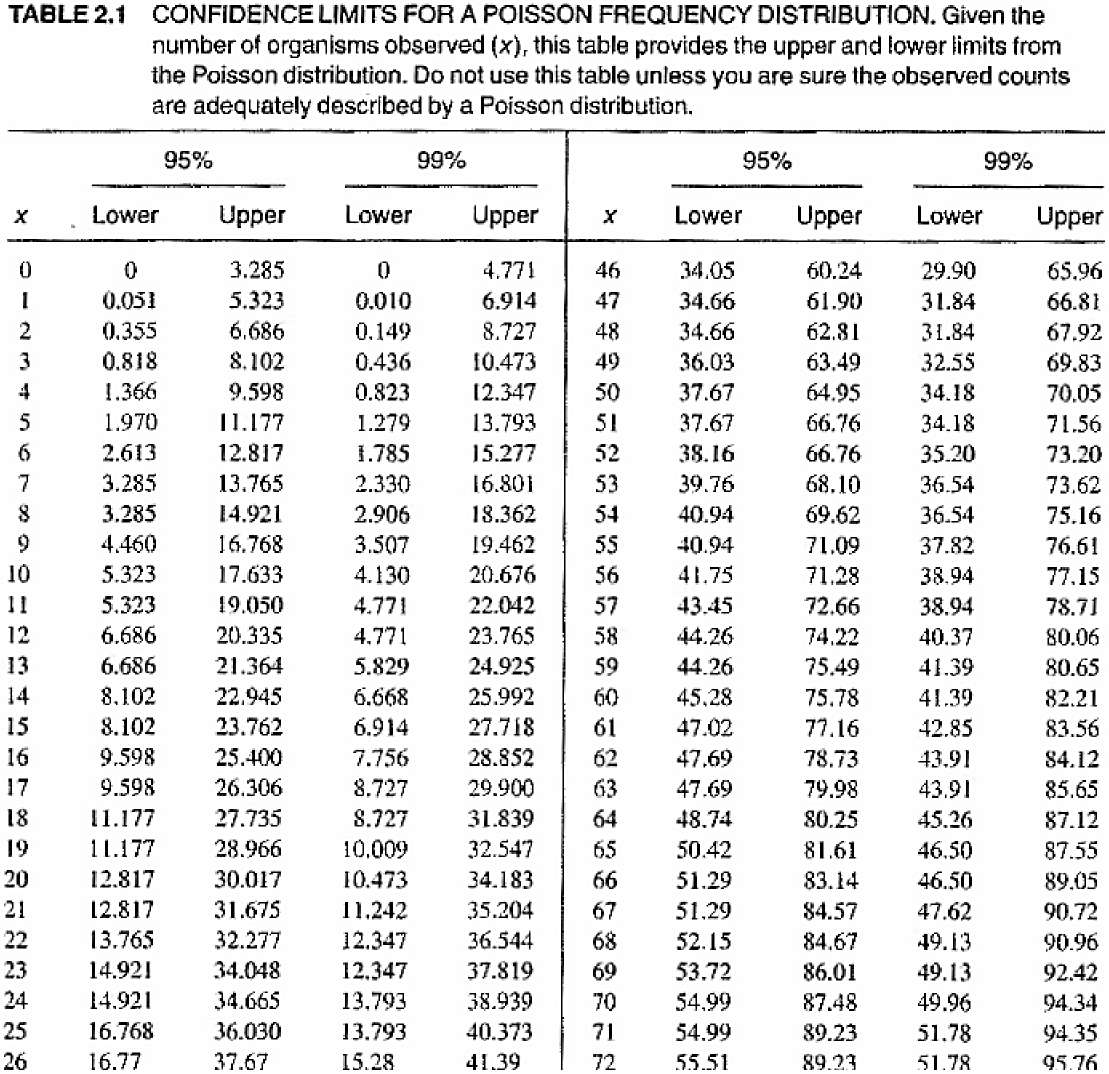
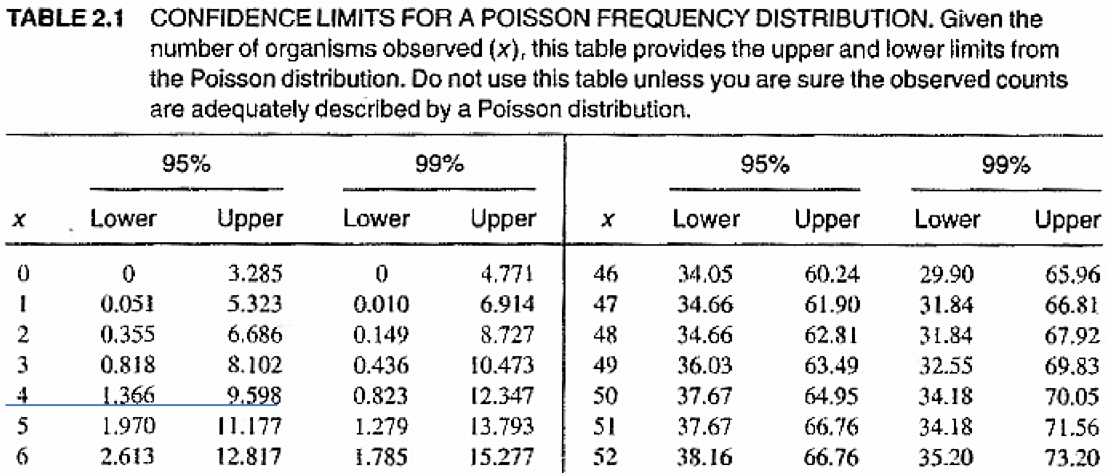


TABLE 2.1 CONFIDENCE LIMITS FOR A POISSON FREQUENCY DISTRIBUTION. Given the number of organisms observed (*x*), this table provides the upper and lower limits from the Poisson distribution. Do not use this table unless you are sure the observed counts are adequately described by a Poisson distribution.

	95%		99%			95%		99%	
x	Lower	Upper	Lower	Upper	*x*	Lower	Upper	Lower	Upper
0	0	3.285	0	4.771	46	34.05	60.24	29.90	65.96
1	0.051	5.323	0.010	6.914	47	34.66	61.90	31.84	66.81
2	0.355	6.686	0.149	8.727	48	34.66	62.81	31.84	67.92
3	0.818	8.102	0.436	10.473	49	36.03	63.49	32.55	69.83
4	1.366	9.598	0.823	12.347	50	37.67	64.95	34.18	70.05
5	1.970	11.177	1.279	13.793	51	37.67	66.76	34.18	71.56
6	2.613	12.817	1.785	15.277	52	38.16	66.76	35.20	73.20
7	3.285	13.765	2.330	16.801	53	39.76	68.10	36.54	73.62
8	3.285	14.921	2.906	18.362	54	40.94	69.62	36.54	75.16
9	4.460	16.768	3.507	19.462	55	40.94	71.09	37.82	76.61
10	5.323	17.633	4.130	20.676	56	41.75	71.28	38.94	77.15
11	5.323	19.050	4.771	22.042	57	43.45	72.66	38.94	78.71
12	6.686	20.335	4.771	23.765	58	44.26	74.22	40.37	80.06
13	6.686	21.364	5.829	24.925	59	44.26	75.49	41.39	80.65
14	8.102	22.945	6.668	25.992	60	45.28	75.78	41.39	82.21
15	8.102	23.762	6.914	27.718	61	47.02	77.16	42.85	83.56
16	9.598	25.400	7.756	28.852	62	47.69	78.73	43.91	84.12
17	9.598	26.306	8.727	29.900	63	47.69	79.98	43.91	85.65
18	11.177	27.735	8.727	31.839	64	48.74	80.25	45.26	87.12
19	11.177	28.966	10.009	32.547	65	50.42	81.61	46.50	87.55
20	12.817	30.017	10.473	34.183	66	51.29	83.14	46.50	89.05
21	12.817	31.675	11.242	35.204	67	51.29	84.57	47.62	90.72
22	13.765	32.277	12.347	36.544	68	52.15	84.67	49.13	90.96
23	14.921	34.048	12.347	37.819	69	53.72	86.01	49.13	92.42
24	14.921	34.665	13.793	38.939	70	54.99	87.48	49.96	94.34
25	16.768	36.030	13.793	40.373	71	54.99	89.23	51.78	94.35
26	16.77	37.67	15.28	41.39	72	55.51	89.23	51.78	95.76

Petersen - Confidence Intervals



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5	1.970	11.177	1.279	13.793	51	37.67	66.76	34.18	71.56
6	2.613	12.817	1.785	15.277	52	38.16	66.76	35.20	73.20

Poisson Confidence Interval

- M: 85 marked snakes
- C: 42 captured snakes
- R: 4 recaptures

- Lower confidence value = 1.366
- Upper confidence value = 9.598

$$\boldsymbol{\hat{N} = \frac{(M+1)(C+1)}{(R+1)} - 1}$$

N = (85 + 1)(42+1)/(4+1) – 1 = 739
Upper 95% CI = (85 + 1)(42+1)/(1.366+1) – 1 = 1562
Lower 95% CI = (85 + 1)(42+1)/(9.598+1) – 1 = 348

Petersen - Assumptions

Assumptions of the Petersen Method

- The Population is closed, so that N is constant
- All animals have the same chance of getting caught in the first sample
- Marking individuals does not affect their catchability
- Animals do not lose marks between the two sampling periods
- All marks are reported upon discovery in the second sample


Angelique Grava

Schnabel Method

Extension of Petersen Method with multiple marking events

- Number of Marked individuals accumulate with each time interval.

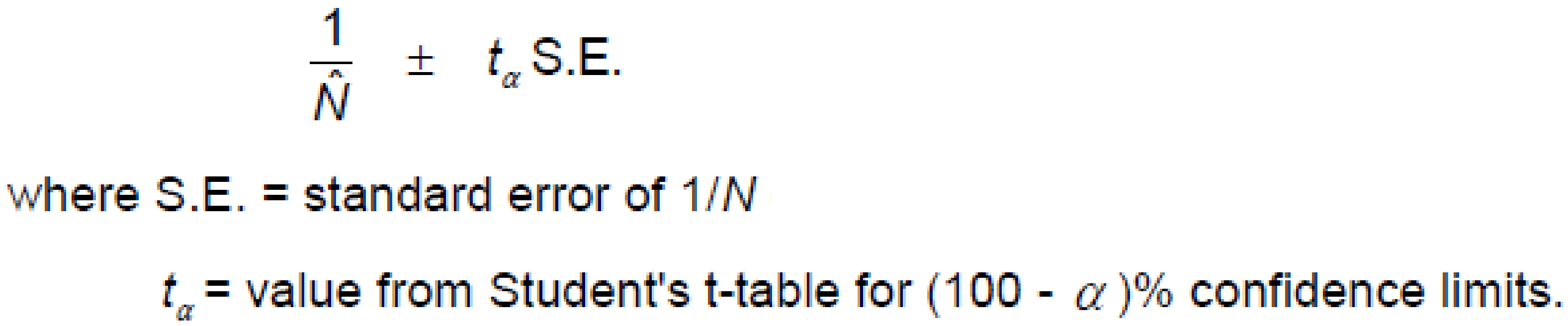
$$\hat{N} = \frac{\sum_t (C_t M_t)}{\sum_t R_t}$$

- C_t = Total number of individuals caught in sample *t*
- R_t = Number of individuals already marked when caught at sample *t*
- U_t = Number of individuals marked for first time and released in sample *t*
- M_t = The number of marked individuals in the population just before sample *t* is taken. (essentially, the cumulative number of U_t up to t-1)
  - M6 = U1 + U2 + U3 + U4 + U5 + U6

Schnabel – Confidence Intervals

If $\sum R_t$ < 50, use values from a Poisson table

If $\sum R_t$>50, calculate with a normal approximation



$$\frac{1}{\hat{N}} \pm t_\alpha \text{S.E.}$$

where S.E. = standard error of $1/N$

t_α = value from Student's t-table for (100 - α)% confidence limits.

Schnabel – Confidence Intervals

If $\sum R_t$>50, calculate with a normal approximation

$$\frac{1}{\hat{N}} \pm t_\alpha \text{S.E.}$$

where S.E. = standard error of $1/N$

t_α = value from Student's t-table for (100 - α)% confidence limits.

$$Variance\left(\frac{1}{\hat{N}}\right) = \frac{\sum R_t}{(\sum C_t M_t)^2}$$

$$Standard\ error\ of\left(\frac{1}{\hat{N}}\right) = \sqrt{Variance\left(\frac{1}{\hat{N}}\right)}$$

Vital rates

- Fundamental parameter of population change: birth rates, death rates
  - Birth rates: number of individuals born/individual
  - Death rates: number of individuals die/individual
    - Probability of survival = 1 – P(mortality)

- Why are population ecologists interested in vital rates?

Vital rate estimation

Problems

- Sample size
- Feasibility of sampling
- Hidden behavior
- Intrinsic variability
- Time frame

- Difficulty collecting data describing vital rates

Birth rates: Fecundity

- “number of female offspring produced per adult female per unit of time”

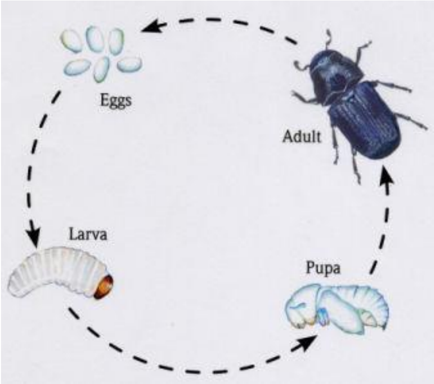
- Often generalized to the number of young produced per female per unit of time
- If interested in population productivity then must know the sex ratio of the young
- “Young” often constituted as:
  - Number of zygotes
  - Number of viable young
  - Number of individuals recruited into next time step
- Natality is synonymous with birth rate
  - Ratio of live births in area to population of area (births/1000 individuals/year)

Measuring birth rates

- Direct methods
  - Observe number of offspring at natal site
    - Some mammal and birds (eggs, litter size)
    - Link between adult and offspring (somewhat)
  - Observe number of young at breeding site
    - Weak or no link between adult and offspring
  - Placental scars from managed mammal populations

Measuring birth rates

- Indirect methods
  - Evidence of offspring at different stages



Bull trout

Upstream spawning trap

Female weight
Gonadal weight

Egg weight
GSI estimate

Redd count

Estimate fry per redd