BIOl 410 Tutorial 5

Population sampling

Quadrat sampling

- Quadrat counts
  - You want to estimate population density and size in a 1 by 1 km area
  - You sample up to 100, 10 by 10 m quadrats

```
quadrats <- round(rpois(100,8),0)
```

  - Calculate the density and total number of animals, the sample variance and the population variance estimate based on 5, 20, 50 or 100 quadrats being sampled.

$$\bar{x} = \frac{\sum x}{n} \qquad \hat{X} = N\bar{x} \qquad \hat{s}^2 = \frac{\sum x^2 - \left(\sum x\right)^2 / n}{n-1} \qquad \left(Ns_{\bar{x}}\right)^2 = \frac{N^2}{n} s^2 \left(1 - \frac{n}{N}\right)$$

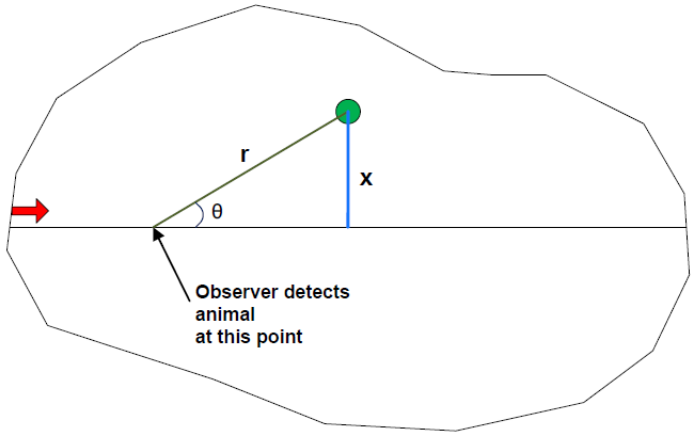
Quadrat sampling

- Useful functions

```
Mean(x[1:5])        # mean of vector
var(x[1:5])         # variance of vector
```

- How does population variance relate to sample variance?
- Plot how estimated N and population variance change as function of quadrat number

Transect sampling



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

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

1. Sighting distance (r_i)
2. Sighting angle (Θ_i)
3. Perpendicular distance (x_i)[a]

$x = r \sin(\theta)$

Transect sampling

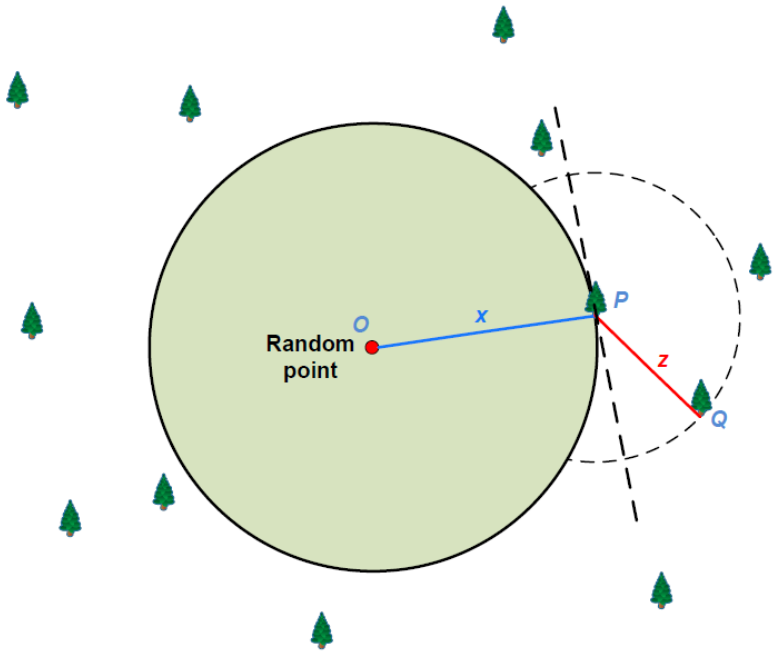
- You performed three transect sampling counts and obtained the following data from 50 m transects where the distance measured are in m

```
nt1 <- 8
nt2 <- 13
nt3 <- 4

rt1 <- c(5,2,3,6,4,4,6,2)
rt2 <- c(7,1,5,2,3,5,7,5,6,4,1,8,3)
rt3 <- c(2,4,3,7)
```

- Using Hayne's estimator calculate the estimated population density for each transect and for the population as a whole
- Assuming the habitat range of the population is 3.78 square km, what is the absolute population number

Distance metrics



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

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 metrics

- You are sampling mushroom density using distance metrics and obtain the following data (in m) based on random point sampling

```
rx <- c(2,15,7,5,21,3,7,1,6,14)
```

- Estimate what the density of mushrooms in the forest

Mark Recapture

- You are using mark (paint spot) and recapture methods to estimate the density of a freshwater snail. You obtain the following data from a single mark, recapture iteration.

```
mark      <- 264
capture   <- 86
recapture <- 16
```

- Using the Petersen method calculate population size and the 95% CI.

Mark recapture

Binomial Confidence Interval

- p= Recaptures /Captures
- Lines –Captures

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

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

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