

POPULATION ESTIMATION USING MARK-RECAPTURE METHODS

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PURPOSE

We will estimate population size using capture-recapture methods that differ in their ability to model natural populations.

DESCRIPTION

Capture-recapture methods sample and mark individuals from a population and then resample the population to determine the proportion of marked individuals present. From this information, total population size is estimated.

THEORY

A variety of methods exist to estimate population size from capture-recapture methodology. We will use a simple, somewhat unrealistic method and a more sophisticated method that takes into account aspects of population dynamics.

1. *Lincoln-Peterson method*- computed by the simple relationship:

Total population = (size of the first sample x size of the second sample) / number of marked individuals recaptured in the second sample.

This method assumes no immigration, emigration, mortality or natality (a closed population), so it is applicable only to single, short-term mark-recapture projects. However, all methods make some assumptions, such as 1) random population sampling, 2) fates of individuals and age classes are independent and 3) there is no loss of markers.

2. *Jolly-Seber method*- used for multiple mark-recapture studies of open populations. This method has wide utility in longer-term studies because it incorporates the realistic assumptions that individuals enter and leave the population. Computation involves construction of a data matrix of sampling intervals and individuals captured. The tedious computations of this and other sophisticated methods may be accomplished using the free MARK software or by using a spreadsheet. Data gathered are entered into a matrix, which is symbolized as follows:

C_i - the number of individuals captured in sample i (i goes from 1 to n) that are marked and unmarked.

R_{hi} - recaptures of marked individuals in sample i that were most recently captured in sample h (h goes from 1 to $n - 1$, with $h < i$ (e.g. if an individual was caught in samples 1 and 2, it is recorded at R_{12} . If the same individual is again recaptured at sample 5, it is recorded at R_{25}).

F_i - the number of marked individuals released from sample i ($= C_i$).

The form of the matrix is:

	h							
i	C_i	1	2	3	4	5	6	F_i
1	C_1							F_1
2	C_2	R_{12}						F_2
3	C_3	R_{13}	R_{23}					F_3
4	C_4	R_{14}	R_{24}	R_{34}				F_4
5	C_5	R_{15}	R_{25}	R_{35}	R_{45}			F_5
6	C_6	R_{16}	R_{26}	R_{36}	R_{46}	R_{56}		F_6
7	C_7	R_{17}	R_{27}	R_{37}	R_{47}	R_{57}	R_{67}	F_7

Sums from the matrix are computed as:

$R_{\cdot i}$ - sum of marked individuals in sample i.

U_i - number of marked individuals not caught in sample i but caught subsequently, so present at time i.

V_i - number of individuals released in F_i that are caught subsequently, and therefore present at time i + 1.

Additional symbols are:

N_i - number in the population at time i.

M_i - number of marked individuals present in the population at time i.

a_i - proportion of marked individuals in the population.

s_i - probability of survival of individuals from time i to i + 1.

B_i - number recruited into the population from i to i + 1.

Computations based on these data are as follows:

$$1. a_i = R_{\cdot i} / C_i$$

$$2. M_i = (F_i U_i / V_i) + R_{\cdot i} \quad (= 0 \text{ for } M_1 \text{ and cannot be estimated for the last sample; similarly, } N_i \text{ cannot be estimated at these times and } a_i = 0 \text{ for } a_1)$$

$$3. N_i = M_i / a_i$$

$$4. s_i = M_{i+1} / (M_i - R_{\cdot i} + F_i)$$

$$5. B_i = N_{i+1} - s_i(N_i - C_i + F_i)$$

METHODS

Experiment I (Lincoln-Peterson method):

We will use beans as our experimental population.

1. Add a large handful of white beans to a 500 ml beaker.
2. **Sample 1:** remove small handful of beans and mark them with a felt marker. Count and record the number of beans in the sample. Return the marked beans to the beaker and thoroughly mix them with the remaining beans.
3. **Sample 2:** remove a second small handful of beans about the same size as the first handful. Count the total number of beans removed and also the number of beans in the sample that are marked.
4. Insert the data into the Lincoln-Peterson formula and compute an estimate of population size.
5. Count the actual number of beans in the beaker and compute the percent error of the estimate.

Experiment II (Jolly-Seber method):

A. Use the following example, solved for $i = 4$ and $i = 5$, to assist in making computations:

i	C_i	h						F_i
		1	2	3	4	5	6	
1	73							73
2	81	8						81
3	89	6	7					89
4	88	4	6	6				87
5	92	5	3	4	7			90
6	96	2	5	5	4	6		96
7	98	3	4	4	4	5	7	98

i = 4

$$C_4 = 88$$

$$F_4 = 87$$

$$R_4 = 4 + 6 + 6 = 16$$

$$U_4 = 5 + 2 + 3 + 3 + 5 + 4 + 4 + 5 + 4 = 35$$

$$V_4 = 7 + 4 + 4 = 15$$

$$a_4 = R_4 / C_4 = 16 / 88 = 0.182$$

$$M_4 = (F_4 U_4 / V_4) + R_4 = [(87 \cdot 35) / 15] + 16 = 219$$

$$N_4 = M_4 / a_4 = 219 / 0.182 = 1203$$

i = 5

$$C_5 = 92$$

$$F_5 = 90$$

$$R_5 = 5 + 3 + 4 + 7 = 19$$

$$U_5 = 2 + 3 + 5 + 4 + 5 + 4 + 4 + 4 = 31$$

$$V_5 = 6 + 5 = 11$$

$$a_5 = R_5 / C_5 = 19 / 92 = 0.207$$

$$M_5 = (F_5 U_5 / V_5) + R_{.5} = [(90 \cdot 31) / 11] + 19 = 272$$

$$N_5 = M_5 / a_5 = 272 / 0.207 = 1314$$

$$s_4 = M_5 / (M_4 - R_{.4} + F_4) = 272 / (219 - 16 + 87) = 0.938$$

$$B_4 = N_5 - s_4(N_4 - C_4 + F_4) = 1314 - 0.938(1203 - 88 + 87) = 186$$

B. Follow the above example in making computations with real data. The data were collected during a 1992-3 netting and banding study on the Bridled White-eye- a tropical island bird that has among the highest population densities of any bird species:

During four sampling periods (i goes from 1 to 4) the total birds netted (C_i) were 12, 32, 16 and 38, respectively. The number of banded birds released from the samples (F_i) were 12, 32, 16 and 37, respectively (in the last sample, one bird escaped before banding). Two individuals captured in sample 1 were recaptured in sample 2. One bird captured in sample 1 was recaptured in sample 4, 2 captured in sample 2 were recaptured in sample 3, and one captured in sample 2 was recaptured in sample 4. Two birds captured in sample 3 were recaptured in sample 4 (R_{hi}).

Compute all of the parameters in the example above for the banding data.

C. Create a multiple mark-recapture simulation using white beans. Fill a 500 ml beaker with beans and do the following:

1. **Sample 1:** Withdraw a handful of beans, count them and mark each with a separate number. Return the beans to the beaker and thoroughly mix them.
2. **Sample 2:** Withdraw a second handful of beans from the beaker, count the total beans in the handful, record the number of recaptures and return the beans to the sample.
3. Remove a handful of beans from the beaker and place them aside. Take a new handful of beans, count them and place them into the beaker. Mix well.
4. **Sample 3:** Withdraw a handful of beans from the beaker, count the total beans in the handful and count the recaptures from samples 1 and 2. Return them to the beaker and mix well.
5. **Samples 4 – 7:** Repeat the above process until the beaker has been samples seven times.

ANALYSIS

Experiment I

1. Insert the data into the Lincoln-Peterson formula and compute an estimate of population size.
2. Count the actual number of beans in the beaker and compute the percent error of the estimate.

Experiment II

B. Compute all of the parameters in the example above for the banding data.

C.

1. Create a data matrix and compute all of the parameters in the above example for samples 2 through 7. Compute average values for each parameter.

2. Determine the actual population by directly counting the beans in the beaker. Compare your population estimates as well as your estimates for recruitment and loss from the population.
3. Compute percent errors in your estimates.

INTERPRETATION

1. Create relevant hypotheses that you test for Experiments I and II. Develop a third hypothesis that predicts the relative effectiveness of the two mark-recapture methods examined.
2. Make sure to report all your data in tables in the *Results* section of your lab report. In the *Analysis* portion of the *Results*, report how close your estimates were to the actual values. Also report the percent error in estimates.
3. In the *Conclusions*, evaluate your hypotheses. Support or reject (not prove or disprove) your hypotheses based solely on your data.
4. Discuss in your *Conclusions* the role of random chance in producing the error you observe in your estimates. Did experimental error play any role in the observed discrepancy between estimates and actual values? What might it be?
5. Discuss the relative strengths and weaknesses of using closed vs. open methods in estimating populations.
6. How might the populations estimates be converted to estimates of population densities?