

Name: \_\_\_\_\_

Period: \_\_\_\_\_

## Mark and Recapture Lab

In these techniques, a sample of organisms, usually mobile animals, is captured from the population whose density we wish to estimate and an identifying mark is applied to them. In practice, these marks can be of many types, including radio collars in large mammals, leg bands in birds, fin clipping in fish, etc. The marked animals are released back into the original population, and after a period of time a second sample is captured. The size of the population is related to the fraction of individuals in the second sample which carry marks.

Slightly different mark-recapture techniques must be applied to populations that are **open** (meaning that individuals may migrate into and out of the population, be born, or die) or **closed** (where the population does not change size during the study period). In this example, we will examine the use of the Petersen technique, which is the simplest mark-recapture technique and is used to study closed populations.

In the Petersen method, the size of the population at the time of marking  $N$  is related to three variables:

$$N = C * M / R$$

where:         $M$  = number of individuals marked in the first sample  
                  $C$  = total number of individuals captured in the second sample  
                  $R$  = number of individuals in the second sample which are marked

To illustrate this, do the following:

### Part 1

1. Grab several handfuls of beans (at least 100) and place them into a paper bag.
2. Mark 10 of the beans with a wax pencil so that you can clearly identify them as being "marked". This is your initial marked sample, so  $M = 10$ .
3. Shake the bag and then withdraw 10 beans. This is your second sample, so  $C = 10$ .
4. Count the number of beans in the sample that are marked ( $= R$ ) and record your answer in Table 1. Replace your beans into the bag.
5. Estimate the size of your bean population  $N$  by dividing  $M * C$  by the number of marked beans in your sample.
6. Repeat steps 3 through 5 nine more times and average the population estimates you obtained in each trial to get an overall population size estimate.

Name: \_\_\_\_\_

Period: \_\_\_\_\_

**TABLE 1: Petersen mark-recapture estimates for bean “population”**

	C = 10 M = 10	
Trial 1	# of marked beans in sample (R)	Population size estimate (= 100/R)
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
Average estimated pop size	-----	

Name: \_\_\_\_\_

Period: \_\_\_\_\_

**Part 2**

Repeat part 1 with the exception of taking 20 beans from the bag with each sample instead of 10. Thus, C for each pop. size estimate here will be 20 instead of 10.

	C = 20 M = 10	
Trial 2	# of marked beans in sample (R)	Population size estimate (= 200/R)
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
Average estimated pop size	-----	

**Part 3**

Name: \_\_\_\_\_

Period: \_\_\_\_\_

Repeat part 2 after taking 10 unmarked beans from the bag and adding marks to them. In this set of estimates,  $M = 20$  and  $C = 20$ .

	$C = 20$ $M = 20$	
Trial 3	# of marked beans in sample (R)	Population size estimate ( = $400/R$ )
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		
Average estimated pop size	-----	

Name: \_\_\_\_\_

Period: \_\_\_\_\_

**Part 4**

Count the beans in your bag to determine the actual bean population size.

Total Beans: \_\_\_\_\_

**Questions:**

1. How did your various average estimated population sizes compare to the actual size?
2. Which combination of C and M gave you the best estimate?
3. Which combination of C and M gave you the worst estimate?
4. If you were trying to estimate the population density of a real species why might you have to sacrifice some accuracy in your estimation?