



# Lecture 2

## How many are there? Estimating abundance

WILD3810 (Spring 2020)

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# Readings:



Mills 54-63

Powell & Gale 169-173; 177-180

# Abundance

the number of individual organisms in a population at a particular time

Also referred to as **population size**

# Why measure abundance?

Abundance is the central *state variable* of a population

How many are there?

- Setting harvest limits
- Maintaining viable populations of threatened/endangered species
- Monitoring non-native/invasive species

# Estimating abundance

# Why not just count every individual?

Sometimes we can (*census*)

But usually:

1) Not practical

- Area too big

2) Not every individual detected

- Elusive

# Estimation methods

# Q1: Abundance or index?



# Indices

We don't always need to know *exactly* how many individuals there are

Sometimes we just want to know the **relative** change in population size over time (or space).

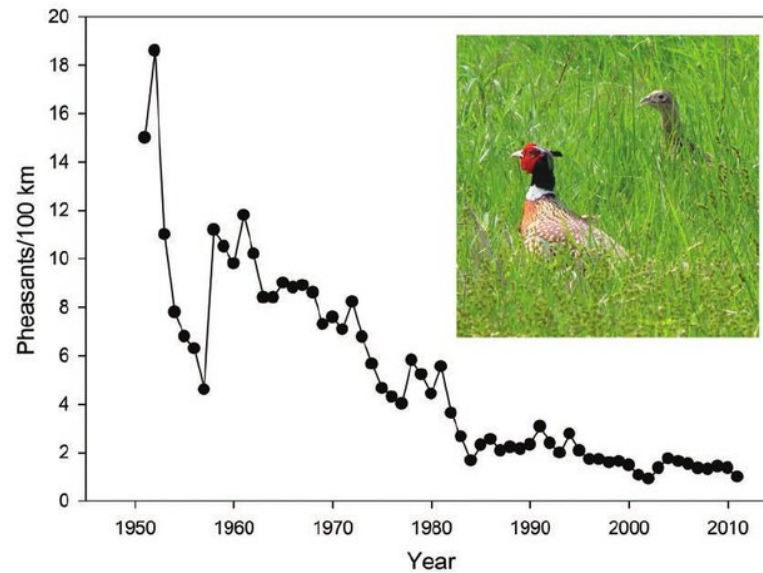
In this case, we can use an **index**

counts  $C$  that are correlated with the actual number of individuals  $N$

# Indices

## Example

### Rural Mail Carrier Survey



# Indices

## Problems

1) What if the relationship between  $N$  and  $C$  is not linear? <sup>2</sup>

# Indices

## Problems

- 1) What if the relationship between  $N$  and  $C$  is not linear?
- 2) What if the observation process changes? <sup>3</sup>

# Indices

## Problems

- 1) What if the relationship between  $N$  and  $C$  is not linear?
- 2) What if the observation process changes?

Without standardized survey protocols, it is impossible to distinguish between changes in abundance and changes in the observation process

# Estimates

# Estimates

Estimates attempt to *correct* for sample area and imperfect detection to estimate  $N$  from  $C$

$$\hat{N} = \frac{C}{P_{area} \hat{P}_d}$$

$P_{area}$  is the proportion of the study area sampled by our surveys

Q2: Is  $\hat{P}_d = 1$ ?



# Census

If  $\hat{P}_d = 1$ , we detect every individual in our sampling area

When counts are equal to the true number of individuals, this is referred to as a **census**

# Census

## Excercise

- 1) Divide into groups of (about) 3
- 2) Remove all of the beans from the cup and count
- 3) Record how many beans are in the cup ( $N$ )
- 4) Return all of the beans to the cup

# Complete vs. sample plot census

## Complete census

count of every individual in the population (usually not possible)

$$C = N$$

## Sample plot census

count of individuals within sample plot(s)

# Sample plot census

$$\hat{N} = \frac{C}{P_{area}}$$

## Example

- $C = 23$
- $P_{area} = 0.1$
- $\hat{N} = 23/0.1 = 230$

# Sample plot census

## Exercise

- 1) Divide back into your groups
- 2) Place your empty cup on the scale and press 'Tare'
- 3) Remove a portion of the beans from the first cup and place them in the empty cup; record the weight
- 4) Count and record the number of beans you removed
- 5) Estimate  $\hat{N}$  using: <sup>1</sup>

# Imperfect detection

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# Imperfect detection

Usually,  $\hat{P}_d < 1$  (even for plants!)

Need to estimate  $\hat{P}_d$ , the probability of detecting an individual that is present in the populations

**Many** methods for doing so<sup>5</sup>

# Q3: Capture or count?



# Capture or count?

The major divide in the methods to estimate  $\hat{P}_d$  is whether you are dealing with individually identifiable individuals or not.

## Mark-recapture

- Individual ID known (physical or natural marks)
- Harder to collect
- (often) requires physical handling
- More information

## Counts

- Individual ID not known
- Easy to collect
- Minimally invasive
- Less information

# Capture-mark-recapture (CMR)

CMR includes a wide variety of related techniques and models

Traditionally, CMR referred to methods of capturing, marking, and then recapturing individuals at some point in the future

This results in a **capture-history** for each individual <sup>6</sup>:

Individual 1: 101101

Individual 2: 011001

# Capture-mark-recapture

From capture-histories, we can estimate:

- abundance
- detection probability
- survival
- movement
- recruitment
- individual growth
- populations trends

# Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures <sup>7</sup>



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# Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures<sup>8</sup>

# Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures<sup>9</sup>

# Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures<sup>10</sup>

# Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures

*What ties all of these methods together is that we have individual-level capture-histories*



# Capture-mark-recapture

## Exercise

- 1) Divide into groups your groups
- 2) Record how many beans you removed in the previous exercise (call this  $n_1$ )
- 3) Count the same number of black-eyed peas and put them back in the original cup (these are your marked individuals)
- 4) Cover and shake/stir the cup

# Lincoln-Peterson (LP) model

LP is one of the first and most basic **closed** CMR models

*Closed* population models:

the number of individuals in the population does not change between sampling occasions. No births, no deaths, no movement in or out

How can we make this assumption? Usually by conducting sampling within a short <sup>11</sup> period of time

Key questions for determining whether population is closed:

- When are the birth pulses? Do they happen a specific time of year (colonial birds) or continuously (humans)

# Lincoln-Peterson model

## Basic logic

On the first occasion, we capture  $n_1$  individuals

What proportion of the total number of individuals is  $n_1$ ?

$$p = \frac{n_1}{N}$$

If we knew  $p$ , we could estimate  $N$  as  $\frac{n_1}{p}$

## Example

If  $p$  is 35% and  $N = 100$ ,  $n_1$  should be approximately 35 individuals.

# Lincoln-Peterson model

## Basic logic

# Lincoln-Peterson model

## Basic logic

On the first occasion, we capture  $n_1$  individuals

On the second occasion, we capture  $n_2$  individuals

- $m_2$  of those individuals were captured and marked on the first occasion

# Lincoln-Peterson model

## Basic logic

# Lincoln-Peterson model

## Basic logic

Lincoln & Peterson realized that:

$$\frac{m_2}{n_2} = \frac{n_1}{N}$$

We can rearrange that to solve for  $N$ :

$$N = \frac{n_1 n_2}{m_2}$$

# Lincoln-Peterson model

## Basic logic



# Lincoln-Peterson model

## Exercise

- 1) Take a second handful of beans from the cup
- 2) Count and record the total number of beans (this is  $n_2$ )
- 3) Count and record the number of black-eyed peas in the sample (this is  $m_2$ )
- 4) Estimate  $\hat{N}$  using the formula above<sup>12</sup>

# Uncertainty

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# Lincoln-Peterson model

It is very unlikely that  $\hat{N} = N$

But, with large sample sizes, LP is **unbiased**<sup>13</sup>:

■ on average  $\hat{N}$  will be equal to  $N$

# Lincoln-Peterson

For any given estimate,  $\hat{N}$  will not exactly equal  $N$

The difference between  $N$  and  $\hat{N}$  occurs because we have to **sample** the true population

In any given sample, we might get a few more marked individuals than expected, or a few less (flipping a coin)

# Measuring uncertainty

All estimated parameters require information about *how certain* we are in our estimate

We **cannot** make inferences about population parameters without providing information to interpret how confident we are in those estimates!

## Example

We do a CMR study of two populations and estimate  $\hat{N}_1 = 142$  and  $\hat{N}_2 = 160$

Is  $N_1 < N_2$ ?

# Measuring uncertainty

Uncertainty measures *on average* how far off our estimate is from the true value

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Uncertainty measures *on average* how far off our estimate is from the true value

We measure spread as the **variance** of the samples<sup>14</sup>

We don't know the true value but statisticians have developed ways to approximate how far we are from the true value using only our data

# Uncertainty of Lincoln-Peterson estimator

Variance of the LP estimator can be calculated as:

$$\text{var}(\hat{N}) = \frac{(n_1 + 1)(n_2 + 1)(n_1 - m_2)(n_2 - m_2)}{(m_2 + 1)^2(m_2 + 2)}$$



# Assumptions of Lincoln-Peterson

All models have assumptions

Just as it's important to report variance, it's important to know the assumptions of our model and to make those assumptions clear

If we violate the assumptions, we can get the wrong answer!

# Assumptions of Lincoln-Peterson

The assumptions of LP are:

- 1) the population is closed between samples
- 2) the marking of an animal does not effect  $p$
- 3) marks are not lost between capture occasions
- 4) each sample of the population is a random sample of the population

What effects would violating these assumptions have on estimates of  $N$ ?

# Assumptions of Lincoln-Peterson

## 1) The population is closed between samples

- Violation of the assumption means that  $N$  either decreases (animals die/leave) or increases (animals are born/enter) between samples
- Can bias  $\hat{N}$  high or low
- Address by sampling over a short period

# Assumptions of Lincoln-Peterson

2) The marking of an animal does not effect  $p$

- What happens if animals that are trapped on occasion one are less likely to be trapped later because they figure out that trapping is unpleasant?

$$\frac{m_2}{n_2} < \frac{n_1}{N}$$

- $\hat{N}$  will be too high
- Addressed by using less invasive trapping methods or through more advanced statistical methods

# Assumptions of Lincoln-Peterson

## 3) Marks are not lost between capture occasions

- If marks are lost, individuals that should be in  $m_2$  will be recorded as unmarked
- $m_2$  will be too low and  $\hat{N}$  will be too high
- Addressed by double marking or looking for physical evidence of tag loss

# Assumptions of Lincoln-Peterson

4) Each sample of the population is a random sample of the population

- What happens if our sampling only detects  $\frac{1}{2}$  of the population? What happens if we only sample is really good habitat?
- Addressed by random sampling