Estimating Population Size using Mark-Recapture techniques

Why use capture methods?

- Allows for estimation of density

- Allows for estimation of birth and mortality rates

- More practical method for small, fast, hard to spot species

There are variety of models for mark-recapture studies that attempt to account for different assumptions of the base model. These deal with:

- Capture rates
- Individual variation
- Post-trap response
- Time

General Mark-Recapture methods:

- Population sampled 2 or more times
- Captured individuals marked and released in first session
- Additional session(s) to follow, in some cases new unmarked individuals marked
- Capture can be physically trapped, photographs, DNA samples, etc

Lincoln-Petersen method:

- Population sampled 2 times (1 recapture event)
- Captured individuals marked and released in first session
- Closed population
- Probability of catching individuals equal in both session
- Marks not lost, gained, or overlooked
- Marks needn't be unique to individuals

Lincoln-Petersen method:

Remember our general model for abundance estimates:

Estimate of abundance = Count / estimated probability of detection

N-hat = n_1 / (m_2 / n_2) or N-hat = n_1 * n_2 / m_2

n_1 = # captured and marked in 1st session

n_2 = Total # captures in 2nd session

m_2 = # of marked animals captured in 2nd session

Lincoln-Petersen method:

Chapman modified this original formula to account for bias due to small samples:

$$\text{N-hat} = (n_1 + 1)/ (m_2 + 1) / (n_2 + 1)$$

or $$\text{N-hat} = (n_1 + 1) * (n_2 + 1) / (m_2 + 1)$$

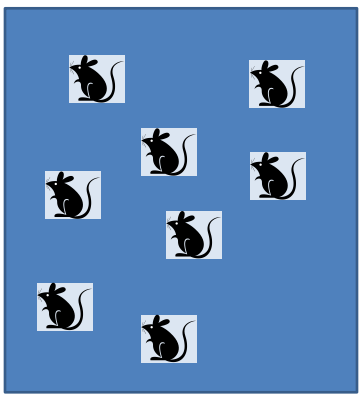
n_1 = # captured and marked in 1st session

n_2 = Total # captures in 2nd session

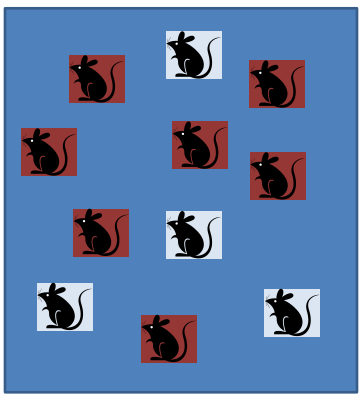
m_2 = # of marked animals captured in 2nd session

Lincoln-Petersen method:

Session 1



Session 2



= marked individual

= unmarked individual

Marks can be unique patterns on individuals capture in images. An example of this is Calambokidis & Barlows study of Humpback Whales

Box 4.4 An example of abundance estimation using the LP method and noninvasive sampling

Eastern North Pacific humpback whales can be uniquely (and noninvasively) identified from natural markings including pigmentation, scars, and ridging of the flukes. Population closure over 1–3 years can be assumed because the whales have high site fidelity to distinct feeding aggregations off the coast of California, Oregon, and Washington before migrating to wintering grounds off Baja California, mainland Mexico, and Central America. Some humpback whale data and abundance estimates are shown below. Many animals were captured (photographed) several times in a year, so the number of photographs is much greater than the number of uniquely identified whales (n_1 and n_2; Calambokidis & Barlow 2004).

Years for n_1 and n_2	Number of identification photographs in first year	n_1	Number of identification photographs in 2nd year	n_2	m_2	$\hat{N}$	95% Confidence interval around $\hat{N}$
1991 and 1992	668	269	1023	398	188	569	537–601
1992 and 1993	1023	398	512	254	173	584	547–620
1993and 1994	512	254	402	244	108	572	512–633
1994 and 1995	402	244	661	331	100	804	704–904
1995 and 1996	661	331	564	331	144	759	690–829

n_1, The number of individuals identified in photographs in the first year; n_2, the number of individuals identified in photographs in the second year; m_2, the number of individuals in the second year that had been identified in the first year.

Closed models w/ >1 recapture periods:

- Population sampled 2 times (1 recapture event)
- Captured individuals marked and released in first session
- Closed population
- Probability of catching individuals equal within a sampling period but can vary between sampling periods
- Marks not lost, gained, or overlooked
- For some models/purposes Marks need must be unique to individuals, unique encounter histories created
- Calculation intensive, use programs such as CAPTURE or Program MARK for analyses

Different models address different sources of variation in capture probabilities:

- **M_0 = Equal Catchability Model (null model)** -- Assumes every animal in the population has the same p-hat for each sampling period in the study.
- **M_h = The Heterogeneity Model** -- Assumes that each animal has a unique p-hat that remains constant over all trapping occasions. Furthermore, capture probabilities are assumed to be a random sample of all individuals in the population.
- **M_b = The Trap Response Model** -- Adjusts for a change in capture probabilities caused by a response to trapping. An assumption of the M_b model is that the initial p-hat for all animals is the same (equal catchability).

Different models address different sources of variation in capture probabilities:

- **M_{bh} = The Heterogeneity and Trap Response Model**-- Based on the assumption that each animal has its own unique pair of potential capture probabilities, p_j and c_j (j = 1, ..., N animals in the population), where p_j is the initial capture probability and c_j is the recapture probability.
- **M_t = The Time Variation (Schnabel) Model** -- Based on the assumption that every individual in the population has the same p-hat for a given sampling occasion, but capture probabilities can vary at each sampling time.
- **Other Time-Dependent Models: M_{th}, M_{tb},** and **M_{tbh}** (various combinations of the above models).

Open Models:

- **Cormack-Jolly-Seber models** (based on k>2) in **Program MARK.**

- Combination of open and closed models (Pollock's Robust Design) in **Program MARK**