

# Basic overview/features of CMR for paleobiology

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# THE ESSENCE OF CAPTURE RECAPTURE APPROACHES

Day 1: caught 10 rats, put tags on them

Day 2: caught rats in the same place. 2 had your tags, but 8 didn't

What is the capture probability?

$2/10=0.2$

How many rats are there in that "place?"

50



*"Careful—it might be a trap!"*

$$\frac{\text{marked Day 2}}{\text{total for Day 2}} = \frac{\text{marked Day 1}}{\text{Estimated Total}}$$

The **Lincoln–Petersen method** (Petersen–Lincoln index)

# THE DATA

Taxon	Time intervals							
	1	2	3	4	5	6	7	8
A	0	0	1	1	0	0	1	0
B	0	1	0	0	0	0	0	0
C	0	0	0	0	0	1	1	1
D	1	0	1	1	0	1	0	0
E	0	0	0	1	0	0	1	1
F	0	1	0	0	1	1	0	1
G	0	0	0	1	0	1	1	0
H	0	0	0	0	0	1	1	0
I	0	0	1	0	1	1	0	1
J	1	0	0	0	0	0	0	0
K	0	0	0	0	1	0	1	1
L	0	0	1	1	0	0	0	0
M	0	1	0	1	1	0	0	0
N	1	1	0	0	1	0	1	0
O	0	0	0	1	0	1	1	1
P	0	0	1	0	0	0	0	0
Q	0	0	0	0	0	0	1	0
R	0	0	1	0	1	1	0	1
S	0	0	0	0	1	0	0	1
T	0	0	0	1	0	0	0	0

**Liow L.H. & Nichols, J.D. 2010** Estimating rates and probabilities of origination and extinction using taxonomic occurrence data: Capture-recapture approaches. In Quantitative Paleobiology Short Course. Eds. Alroy J. & Hunt G. Paleontological Society pp. 81-94

## DETECTION HISTORIES

Time interval	1	2	3	4	5	6	7	8
L	0	1	1	0	0	0	0	0
M	0	1	0	1	1	0	0	0

### Encounter/detection histories

- Series of ones and zeros
- Ones are taken as true presences
- Two types of zeros
  - Not sampled
  - Not sampled or truly absent

		Time intervals							
Taxon		1	2	3	4	5	6	7	8
		0	0	1	1	0	0	1	0
A		0	0	1	1	0	0	1	0
B		0	1	0	0	0	0	0	0
C		0	0	0	0	0	1	1	1
D		1	0	1	1	0	1	0	0
E		0	0	0	1	0	0	1	1
F		0	1	0	0	1	1	0	1
G		0	0	0	0	0	1	1	0
H		0	0	0	0	0	1	1	0
I		0	0	0	0	0	0	0	0
J		0	0	0	0	1	0	1	1
K		0	0	1	1	0	0	0	0
L		0	1	0	1	1	0	0	0
M		0	1	0	0	1	0	1	0
N		0	0	0	1	0	1	1	1
O		0	0	1	0	0	0	0	0
P		0	0	0	0	0	0	1	0
Q		0	0	1	0	1	1	0	1
R		0	0	0	0	1	0	0	1
S		0	0	0	1	0	0	0	1
T		0	0	0	1	0	0	0	0

Detection  
probability

$$\hat{p}_6 = 5 / 10 = 0.5$$

Estimated  
no. taxa

$$\hat{S}_6 = s_6 / \hat{p}_6 = 8 / 0.5 = 16$$

Taxon	Time intervals							
	1	2	3	4	5	6	7	8
A	0	0	1	1	0	0	1	0
B	0	1	0	0	0	0	0	0
C	0	0	0	0	0	1	1	1
D	1	0	1	1	0	1	0	0
E	0	0	0	1	0	0	1	1
						1	0	1
						1	1	0
						1	1	0
I	0	0	1	0	1	1	0	1
J	1	0	0	0	0	0	0	0
K	0	0	0	0	1	0	1	1
L	0	0	1	1	0	0	0	0
M	0	1	0	1	1	0	0	0
N	1	1	0	0	1	0	1	0
O	0	0	0	1	0	1	1	1
P	0	0	1	0	0	0	0	0
Q	0	0	0	0	0	0	1	0
R	0	0	1	0	1	1	0	1
S	0	0	0	0	1	0	0	1
T	0	0	0	1	0	0	0	0

		Time intervals							
Taxon		1	2	3	4	5	6	7	8
Extinction probability	A	0	0	1	1	0	0	1	0
	B	0	1	0	0	0	0	0	0
	C	0	0	0	0	0	1	1	1
	D	1	0	1	1	0	1	0	0
				0	1	0	0	1	1
				0	0	1	1	0	1
				0	1	0	1	1	0
				0	0	0	1	1	0
				1	0	1	1	0	1
				0	0	0	0	0	0
				0	0	1	0	1	1
				1	1	0	0	0	0
				0	1	1	0	0	0
				0	0	1	0	1	0
				0	1	0	1	1	1
	P	0	0	1	0	0	0	0	0
	Q	0	0	0	0	0	0	1	0
	R	0	0	1	0	1	1	0	1
	S	0	0	0	0	1	0	0	1
	T	0	0	0	1	0	0	0	0

Extinction  
probability

Time intervals								
Taxon	1	2	3	4	5	6	7	8
A	0	0	1	1	0	0	1	0
B	0	1	0	0	0	0	0	0
C	0	0	0	0	0	1	1	1
D	1	0	1	1	0	1	0	0
$\hat{\varepsilon}_5 = 1 - (\hat{M}'_6 / s_5)$ $= 1 - (\frac{m'_6}{\hat{p}_6})$ $= 1 - (\frac{3/0.5}{16})$			0	1	0	0	1	1
			0	0	1	1	0	1
			0	1	0	1	1	0
			0	0	0	1	1	0
			1	0	1	1	0	1
			0	0	0	0	0	0
			0	0	1	0	1	1
			1	1	0	0	0	0
			0	1	1	0	0	0
			0	0	1	0	1	0
P	0	0	1	0	0	0	0	0
Q	0	0	0	0	0	0	1	0
R	0	0	1	0	1	1	0	1
S	0	0	0	0	1	0	0	1
T	0	0	0	1	0	0	0	0



Time intervals

Extinction  
probability

Taxon	1	2	3	4	5	6	7	8
A	0	0	1	1	0	0	1	0
B	0	1	0	0	0	0	0	0
C	0	0	0	0	0	1	1	1
D	1	0	1	1	0	1	0	0
E	0	0	1	1	0	0	1	1
F	0	0	0	0	1	1	0	1
G	0	1	0	1	0	1	1	0
H	0	0	0	0	0	1	1	0
I	1	0	0	0	1	1	0	1
J	0	0	0	0	0	0	0	0
K	0	0	1	0	1	0	1	1
L	1	1	0	0	0	0	0	0
M	0	1	1	0	1	0	0	0
N	0	0	0	0	1	0	1	0
O	0	1	0	0	0	1	1	1
P	0	0	1	0	0	0	0	0
Q	0	0	0	0	0	0	1	0
R	0	0	1	0	1	1	0	1
S	0	0	0	0	1	0	0	1
T	0	0	0	1	0	0	0	0

Alive in T 5 and 6

Alive in T5

Survival  
Probability  
From T5 to T6

$$\hat{\epsilon}_5 = 1 - (\hat{M}'_6 / s_5)$$
$$= 1 - (m'_6 / \hat{p}_6)$$
$$= 1 - \left( \frac{3 / 0.5}{16} \right)$$

# Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
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**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

Pr(eh = 0 0 1 0 1 1 0 0 | initial encounter in interval 3) =

**CJS model**

## Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
--	--	--	--------------	--------------	--------------	--------------	--------------	--

**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

$\Pr(\text{eh} = 0\ 0\ 1\ 0\ 1\ 1\ 0\ 0 \mid \text{initial encounter in interval } 3) =$

$$(1-\epsilon_3)(1-p_4)(1-\epsilon_4)p_5(1-\epsilon_5)p_6 [\epsilon_6 + (1-\epsilon_6)(1-p_7)\{\epsilon_7 + (1-\epsilon_7)(1-p_8)\}]$$

## Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
--	--	--	--------------	--------------	--------------	--------------	--------------	--

**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

$\Pr(\text{eh} = 0\ 0\ 1\ 0\ 1\ 1\ 0\ 0 \mid \text{initial encounter in interval } 3) =$

$$(1-\epsilon_3)(1-p_4) (1-\epsilon_4)p_5 (1-\epsilon_5)p_6 [\epsilon_6 + (1-\epsilon_6)(1-p_7)\{\epsilon_7+(1-\epsilon_7)(1-p_8)\}]$$

## Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
--	--	--	--------------	--------------	--------------	--------------	--------------	--

**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

$\Pr(\text{eh} = 0\ 0\ 1\ 0\ 1\ 1\ 0\ 0 \mid \text{initial encounter in interval } 3) =$

$$(1-\epsilon_3)(1-p_4) (1-\epsilon_4)p_5 (1-\epsilon_5)p_6 [\epsilon_5 + (1-\epsilon_6)(1-p_7)\{\epsilon_7+(1-\epsilon_7)(1-p_8)\}]$$

## Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
--	--	--	--------------	--------------	--------------	--------------	--------------	--

**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

Pr(eh = 0 0 1 0 1 1 0 0 | initial encounter in interval 3) =

$$+ (1-\epsilon_6)(1-p_7)\{\epsilon_7+(1-\epsilon_7)(1-p_8)\}$$

## Representing detection/encounter histories

1	2	3	4	5	6	7	8
0	0	1	0	1	1	0	0
			$p_4$	$p_5$	$p_6$	$p_7$	$p_8$

**Detection probabilities**

			$\epsilon_3$	$\epsilon_4$	$\epsilon_5$	$\epsilon_6$	$\epsilon_7$	
--	--	--	--------------	--------------	--------------	--------------	--------------	--

**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

$\Pr(\text{eh} = 0\ 0\ 1\ 0\ 1\ 1\ 0\ 0 \mid \text{initial encounter in interval } 3) =$

$(1-\epsilon_3)(1-p_4) (1-\epsilon_4)p_5 (1-\epsilon_5)p_6 [\epsilon_6 + (1-\epsilon_6)(1-p_7)\{\epsilon_7+(1-\epsilon_7)(1-p_8)\}]$

"sampling" and vital parameters are both explicit! (closer to generating process of the data)

## We have detection histories – now what?

$\Pr(eh = 0\ 0\ 1\ 0\ 1\ 1\ 0\ 0) =$

$(1-\epsilon_3)(1-p_4) (1-\epsilon_4)p_5 (1-\epsilon_5)p_6 [\epsilon_6 + (1-\epsilon_6)(1-p_7)\{\epsilon_7+(1-\epsilon_7)(1-p_8)\}]= H1$

Likelihood (parameters | data) =  $H_1^{\text{No. cases}}$   $H_2^{\text{No. cases}}$   $H_x^{\text{No. cases}}$

0001010010	10
0010001101	3
	4
0101010100	18
1001000000	2
0001010111	1
	3
0011101000	No. cases



## Likelihood of Detection histories

1. Estimate parameters (by maximizing the likelihood)
2. Estimate uncertainty in parameters
3. Compare models
  - e.g. same or different  $p$ 's or  $\epsilon$ 's
  - e.g. with or without covariates (important factors that you think might influence  $p$  and  $\epsilon$ )
    - i. Akaike Information Criteria, AIC
    - ii. classical hypothesis testing
    - iii. extendable to Bayesian approaches
4. Good statistical properties

## Assumptions of the CJS model

- 1. After initial encounters, detection/encounter probabilities are equal for all taxa in the data/group of interest**
- 2. After initial encounters, extinction probabilities for all taxa are equal**
- 3. Sampling intervals are short relative to the time over which extinction is to be estimated**
- 4. The fate of each taxon (with respect to extinction and encounter) is independent of the fate of every other taxon**

## Assumptions of the CJS model

1. After initial encounters, detection/encounter probabilities are equal for all taxa in the data/group of interest
  - Taxon specific covariates
2. After initial encounters, extinction probabilities for all taxa are equal
3. Sampling intervals are short relative to the time over which extinction is to be estimated
4. The fate of each taxon (with respect to extinction and encounter) is independent of the fate of every other taxon

## Assumptions of the CJS model

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## Assumptions of the CJS model

1. After initial encounters, detection/encounter probabilities are equal for all taxa in the data/group of interest
2. After initial encounters, extinction probabilities for all taxa are equal
3. **Sampling intervals are short relative to the time over which extinction is to be estimated**
  - **Simulations show that this is not a big problem; other models (e.g. robust design models, never applied in paleo) tackle this head-on**
4. The fate of each taxon (with respect to extinction and encounter) is independent of the fate of every other taxon

## Assumptions of the CJS model

1. After initial encounters, detection/encounter probabilities are equal for all taxa in the data/group of interest
2. After initial encounters, extinction probabilities for all taxa are equal
3. Sampling intervals are short relative to the time over which extinction is to be estimated
4. **The fate of each taxon (with respect to extinction and encounter) is independent of the fate of every other taxon**
  - **Corrections for over-dispersion**
  - **Co-occurrence analyses**

## Covariate modeling

- A way to include factors or variables that may be important in explaining variation in the parameters (e.g. extinction, sampling) you are interested in
- Allows us to compare models with different [or no] covariates (Model Comparison and Selection)
- models to compare
  - $\epsilon(\text{constant})p(\text{time-varying})$
  - $\epsilon(\text{time-varying})p(\text{sea-levels})$

## Covariate modeling via link functions

$$\text{logit}(\varepsilon_{i,t}) = \log\left(\frac{\varepsilon_{i,t}}{1 - \varepsilon_{i,t}}\right) = \beta_0 + \beta_1 x_i + \beta_2 y_t$$

Taxon specific covariates

- size
- minerology
- taxonomic group



## Covariate modeling via link functions

$$\text{logit}(\varepsilon_{i,t}) = \log\left(\frac{\varepsilon_{i,t}}{1 - \varepsilon_{i,t}}\right) = \beta_0 + \beta_1 x_i + \beta_2 y_t$$

Time specific covariates

- Duration of bin
- Sea-level
- Temperature

## Covariate modeling via link functions

$$\text{logit}(\varepsilon_{i,t}) = \log\left(\frac{\varepsilon_{i,t}}{1 - \varepsilon_{i,t}}\right) = \boxed{\beta_0} + \boxed{\beta_1}x_i + \boxed{\beta_2}y_t$$

$$\varepsilon_{i,t} = \frac{e^{\boxed{\beta_0} + \boxed{\beta_1}x_i + \boxed{\beta_2}y_t}}{1 + e^{\boxed{\beta_0} + \boxed{\beta_1}x_i + \boxed{\beta_2}y_t}}$$

# Why Capture-Mark-Recapture (CMR) ?

- Detection probability
- Separating between
  - probability of detection (given presence)
  - probability of the parameters in question  
(e.g. survivorship, origination, occupancy, immigration)  
and derived parameters such as species richness/diversity

The probability of detection or sampling is sometimes only a nuisance but sometimes interesting in itself.

- Covariates can be EASILY included in models for both vital parameters and sampling/detection estimates.
- Covariates can be modeled at a variety of levels (e.g. group factors, individual traits, temporal characteristics)

# Chapters in MARK book most relevant (if not using MARK)

- Chapter 1 (introduction)
- Chapter 4 (dipper example, but skip the MARK specific bits)
- Chapter 5 (goodness of fit –not covered in lectures but important)
- Chapter 6 (more on covariates and link functions)
- Chapter 11 (individual covariates)
- Chapter 12 (Pradel) and 13 (JS models in general)

<http://www.phidot.org/software/mark/docs/book/>