Basic overview/features of CMR for paleobiology

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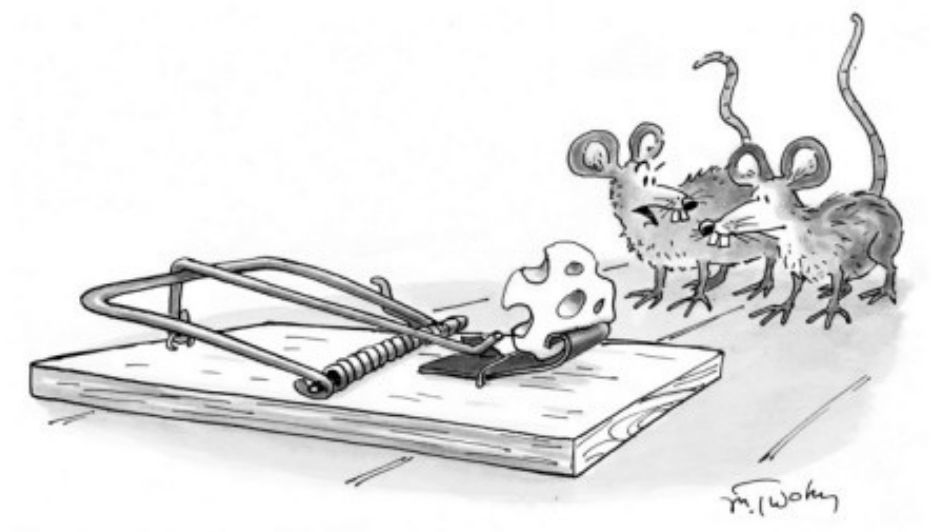
THE ESSENCE OF CAPTURE RECAPTURE APPROACHES



"Careful—it might be a trap!"

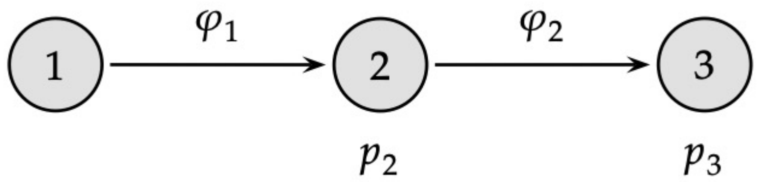
$$\frac{marked\ Day\ 2}{total\ for\ Day2} = \frac{marked\ Day1}{Estimated\ Total}$$

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

Encounter history

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

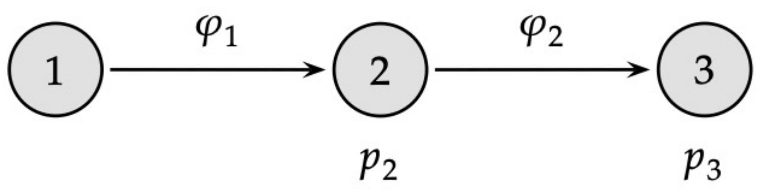
Encounter history



encounter history	*probability of encounter history*
111	$\varphi_1 p_2 \varphi_2 p_3$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

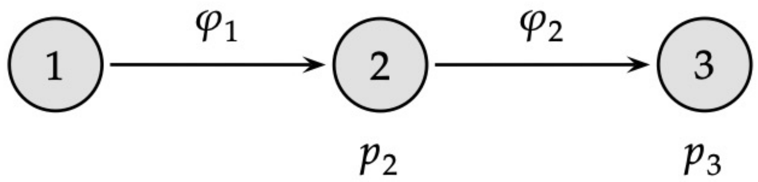
Encounter history



encounter history	*probability of encounter history*
111	$\varphi_1 p_2 \varphi_2 p_3$
110	$\varphi_1 p_2 \left[\varphi_2(1-p_3)+(1-\varphi_2)\right]$ $= \varphi_1 p_2 (1-\varphi_2 p_3)$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

Encounter history

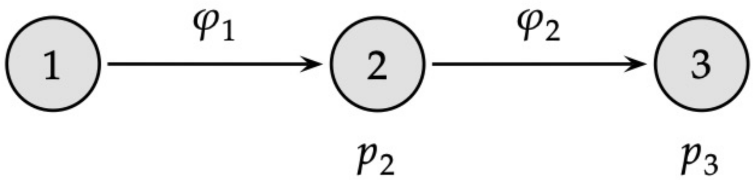


encounter history	*probability of encounter history*
111	$\varphi_1 p_2 \varphi_2 p_3$
110	$\varphi_1 p_2 \left[\varphi_2(1-p_3) + (1-\varphi_2)\right] = \varphi_1 p_2 (1-\varphi_2 p_3)$
101	$\varphi_1 \left(1-p_2\right) \varphi_2 p_3$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

Trilobite taxa

Encounter history

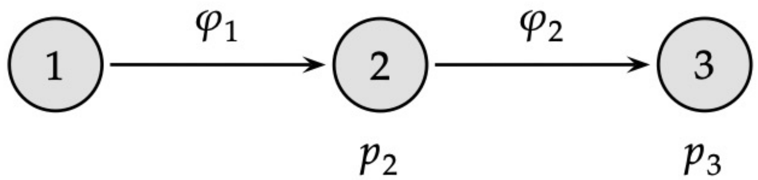


encounter history	*probability of encounter history*
111	$\varphi_1 p_2 \varphi_2 p_3$
110	$\varphi_1 p_2 \left[\varphi_2(1-p_3)+(1-\varphi_2)\right] = \varphi_1 p_2 (1-\varphi_2 p_3)$
101	$\varphi_1 \left(1-p_2\right) \varphi_2 p_3$
100	$\left(1-\varphi_1\right)+\varphi_1(1-p_2)(1-\varphi_2)+\varphi_1(1-p_2)\varphi_2(1-p_3) = 1-\varphi_1 p_2-\varphi_1(1-p_2)\varphi_2 p_3$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

Trilobite taxa

Encounter history

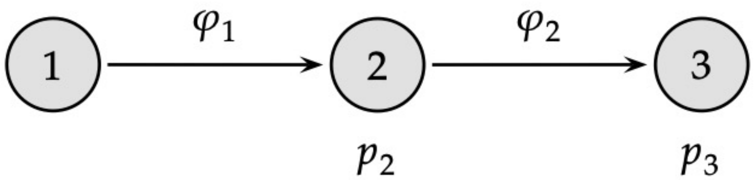


	encounter history	*probability of encounter history*
Trilobite taxon A	111	$\varphi_1 p_2 \varphi_2 p_3$
Trilobite taxon B	110	$\varphi_1 p_2 \left[\varphi_2(1-p_3)+(1-\varphi_2)\right]$ $= \varphi_1 p_2(1-\varphi_2 p_3)$
Trilobite taxon C	101	$\varphi_1 \left(1-p_2\right) \varphi_2 p_3$
Trilobite taxon D	100	$\left(1-\varphi_1\right)+\varphi_1(1-p_2)(1-\varphi_2)+\varphi_1(1-p_2)\varphi_2(1-p_3)$ $= 1-\varphi_1 p_2-\varphi_1(1-p_2)\varphi_2 p_3$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

Trilobite taxa

Encounter history



	encounter history	*probability of encounter history*
A, X, P	111	$\varphi_1 p_2 \varphi_2 p_3$
B, E	110	$\varphi_1 p_2 \left[\varphi_2(1-p_3)+(1-\varphi_2)\right] = \varphi_1 p_2 (1-\varphi_2 p_3)$
C, Q R, T, S, X, Z	101	$\varphi_1 \left(1-p_2\right) \varphi_2 p_3$
D, G H, J, K, Y	100	$\left(1-\varphi_1\right)+\varphi_1(1-p_2)(1-\varphi_2)+\varphi_1(1-p_2)\varphi_2(1-p_3) = 1-\varphi_1 p_2-\varphi_1(1-p_2)\varphi_2 p_3$

http://www.phidot.org/software/mark/docs/book/pdf/chap1.pdf

THE DATA

Taxon	1	2	3	4	5	6	7	8
	Time intervals							
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

DECTECTION 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
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
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	1	0
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	1	0
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	0	1
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	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

Detection probability

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

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
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

Estimated no. taxa

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

Extinction probability

$$\hat{\varepsilon}_5 = 1 - (\hat{M}_6^{'} / s_5)$$

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
			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

Time intervals

Extinction probability

$$\hat{\varepsilon}_5 = 1 - (\hat{M}'_6 / s_5)$$

$$= 1 - (\frac{m'_6 / \hat{p}_6}{s_5})$$

$$= 1 - (\frac{3 / 0.5}{\boxed{16}})$$

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
			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

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
			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

$$\hat{\varepsilon}_5 = 1 - (\hat{M}'_6 / s_5)$$

$$= 1 - \left(\frac{m'_6 / \hat{p}_6}{s_5}\right)$$

$$= 1 - \left(\frac{3 / 0.5}{16}\right)$$

Alive in T 5 and 6

Alive in T5

Survival Probability From T5 to T6

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**

			ε_3	ε_4	ε_5	ε_6	ε_7		**Extinction probabilities**

eh = 0 0 1 0 1 1 0 0

CJS model

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

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**

			ε_3	ε_4	ε_5	ε_6	ε_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) =

$(1-\varepsilon_3)(1-p_4)\ (1-\varepsilon_4)p_5\ (1-\varepsilon_5)p_6\ [\varepsilon_6 + (1-\varepsilon_6)(1-p_7)\{\varepsilon_7+(1-\varepsilon_7)(1-p_8)\}]$

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**

			ε_3	ε_4	ε_5	ε_6	ε_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) =

$(1-\varepsilon_3)(1-p_4)\ (1-\varepsilon_4)p_5\ (1-\varepsilon_5)p_6\ [\varepsilon_6 + (1-\varepsilon_6)(1-p_7)\{\varepsilon_7+(1-\varepsilon_7)(1-p_8)\}]$

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

			ε_3	ε_4	ε_5	ε_6	ε_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) =

$(1-\varepsilon_3)(1-p_4)\ (1-\varepsilon_4)p_5\ (1-\varepsilon_5)p_6\ [\varepsilon_6 + (1-\varepsilon_6)(1-p_7)\{\varepsilon_7+(1-\varepsilon_7)(1-p_8)\}]$

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**

			ε_3	ε_4	ε_5	ε_6	ε_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) =

$$+ (1-\varepsilon_6)(1-p_7)\{\varepsilon_7+(1-\varepsilon_7)(1-p_8)\}]$$

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**

			ε_3	ε_4	ε_5	ε_6	ε_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) =

$(1-\varepsilon_3)(1-p_4)\ (1-\varepsilon_4)p_5\,(1-\varepsilon_5)p_6\ [\varepsilon_6 + (1-\varepsilon_6)(1-p_7)\{\varepsilon_7+(1-\varepsilon_7)(1-p_8)\}]$

"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) =

$(1-\varepsilon 3)(1-p4)\ (1-\varepsilon 4)p5\ (1-\varepsilon 5)p6\ \ [\varepsilon 6 + (1-\varepsilon 6)(1-p7)\{\varepsilon 7+(1-\varepsilon 7)(1-p8)\}] = H1$

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

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

Maximum likelihood estimation

- statistical approach for estimating the parameters of a model
- parameters are chosen to maximize the likelihood for the assumed model given the data

So do to MLE, we have to

- assume a model (e.g. data generating process) for the data in questions
- derive the likelihood function for our data, given our assumed model

- The event of falling right
- The event of falling left
- The falling : call it y

- There are only two discrete values for y, 1 or 0 (right and left)

- What’s the probability of fall left? Or right?

https://towardsdatascience.com/maximum-likelihood-the-easy-way-1f14c0e2a5ce/

The Data

I	y	what
1	0	L
2	1	R
3	1	R
4	0	L
5	0	L
6	1	R
7	1	R
8	1	R
9	0	L
10	0	L

Probability mass function (PMF) for Bernoulli: $p^{y_i}(1 - p)^{1-y_i}$

$y_i = 0$ Negative outcome - falling left

$y_i = 1$ Positive outcome - falling right

PMF Example

if $y_i = 1$, and p = 0.5

$p^{y_i}(1 - p)^{1-y_i}$

$0.5^1(1 - 0.5)^{1-1} = 0.5$

The likelihood function is the joint probability distribution (multiplication) of the PMFs for each observation. We are simply multiplying all the PMFs together

$$p^{y_1}(1 - p)^{1-y_1} \cdot p^{y_2}(1 - p)^{1-y_2} \ldots \cdot p^{y_n}(1 - p)^{1-y_n}$$

joint probability distribution

https://towardsdatascience.com/maximum-likelihood-the-easy-way-1f14c0e2a5ce/

$$L(\theta) = \prod_{i=1}^{n} p^{y_i}(1 - p)^{1-y_i}$$

likelihood function

We want to maximize this function. Rather than doing calculus to figure this out, let's play around with different values of p to see how it affects the likelihood. You can try it out using this workbook (tab: fair_coin).

p=0.3

i	y	p(y)	PMF(y)
1	0	0.3	0.7
2	0	0.3	0.7
3	0	0.3	0.7
4	1	0.3	0.3
5	1	0.3	0.3
6	0	0.3	0.7
7	1	0.3	0.3
8	1	0.3	0.3
9	1	0.3	0.3
10	0	0.3	0.7
		L=	0.0004

p=0.5

i	y	p(y)	PMF(y)
1	0	0.5	0.5
2	0	0.5	0.5
3	0	0.5	0.5
4	1	0.5	0.5
5	1	0.5	0.5
6	0	0.5	0.5
7	1	0.5	0.5
8	1	0.5	0.5
9	1	0.5	0.5
10	0	0.5	0.5
		L=	0.0010

p=0.7

i	y	p(y)	PMF(y)
1	0	0.7	0.3
2	0	0.7	0.3
3	0	0.7	0.3
4	1	0.7	0.7
5	1	0.7	0.7
6	0	0.7	0.3
7	1	0.7	0.7
8	1	0.7	0.7
9	1	0.7	0.7
10	0	0.7	0.3
		L=	0.0004

https://towardsdatascience.com/maximum-likelihood-the-easy-way-1f14c0e2a5ce/

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 ε's**
   - **e.g. with or without covariates (important factors that you think might influence p and ε)**
     1. **Akaike Information Criteria, AIC**
     2. **classical hypothesis testing**
     3. **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**
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1. After initial encounters, detection/encounter probabilities are equal for all taxa in the data/group of interest

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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**
    - **ε(constant)p(time-varying)**
    - **ε(time-varying)p(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

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

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

"Some simple rules of thumb are often useful in assessing the relative merits of models in the set: Models having $\Delta i \leq 2$ have substantial support (evidence), those in which $4 \leq \Delta i \leq 7$ have considerably less support, and models having $\Delta i > 10$ have essentially no support." Burnham & Anderson 2004 – see dAIC

$$\Delta_i(AIC) = AIC_i - min(AIC)$$

$$L \propto exp\left(-\tfrac{1}{2}\Delta_i(AIC)\right)$$

$$AIC = -2\ln(L) + 2k$$

$$w_i(AIC) = \frac{exp\left(-\frac{1}{2}\Delta_i(AIC)\right)}{\sum_{k=1}^{K} exp\left(-\frac{1}{2}\Delta_k(AIC)\right)}$$

	Model	Npar (k)	Rank	logLik (L)	AIC	AICc	dAIC	AICwt
Model A	p~1 phi~1	2	2	-333	670	671	0	0.79
Model B	p~1 phi~t	7	7	-330	673	676	2.9	0.19
Model C	p~t phi~1	7	7	-332	678	678	7.6	0.02
Model D	p~t phi~t	12	12	-328	681	688	10.1	0.00

Model selection is cool, but don’t stop there

Look at your parameter estimates and check if they make sense!

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/

Some newer fossil papers using CMR (but oldies are goodies too)

- Schachat et al. **2021.** A Cretaceous peak in family-level insect diversity estimated with mark–recapture methodology. Proceedings of the Royal Society, B 286:20192054.
- Monarrez et al. **2021** Mass extinctions alter extinction and origination dynamics with respect to body size Proceedings of the Royal Society, B https://doi.org/10.1098/rspb.2021.1681
- Cohen et al. **2022** Plio-Pleistocene environmental variability in Africa and its implications for mammalian evolution, PNAS 119 (16) e2107393119
- Wilson et al. **2024**. Unveiling the underlying drivers of Phanerozoic marine diversification. Proceedings of the Royal Society, B 291: 20240165
- Leventhal S, Samuels-Fair M. **2025** Larval brooding correlated with high early origination rates in cheilostome Bryozoa. *Paleobiology*. 51(2):261-267