

# A bit of everything related to CMR in paleo

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2.9.2024 (Tuesday)



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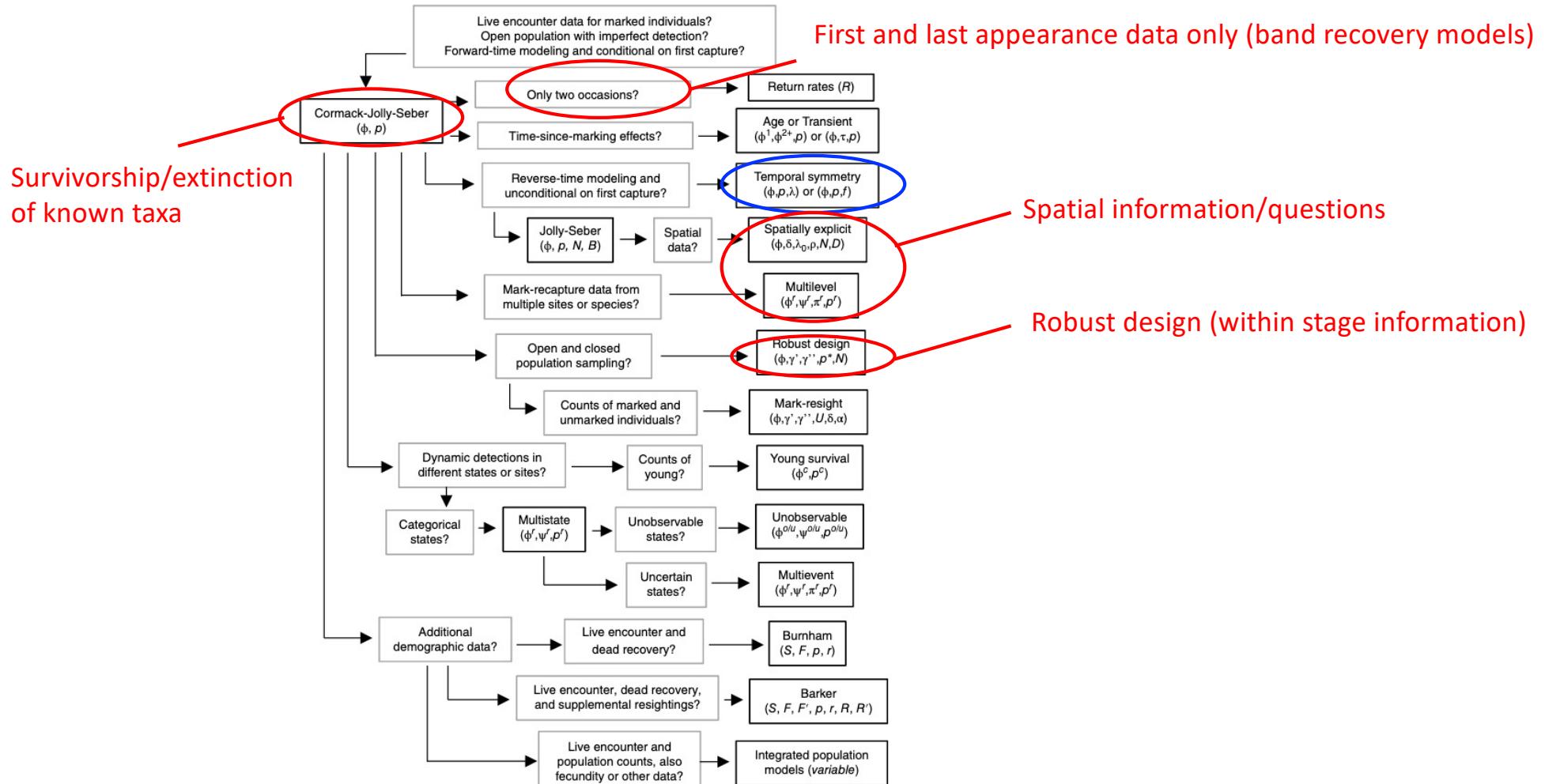


# Summary

$p \neq 1$

Two types of zeros

# Many models: few explored in paleo



<https://bksandercock.files.wordpress.com/2020/11/sandercock2020popcolpractice.pdf>

MARK is the “main” software and easy to read reference (but you must “translate”)

The screenshot shows a web browser displaying the official documentation for the MARK software. The URL in the address bar is [www.phidot.org/software/mark/docs/book/](http://www.phidot.org/software/mark/docs/book/). The page features a blue header with the text "program MARK" and "'A Gentle Introduction'". Below the header is a green navigation bar with links to "Home", "About", "Download", "Support Forum", and "Training". A large image of the book "Program MARK: A gentle introduction" (version 1.2) is prominently displayed. To the right of the book image is the "Overview" section, which contains text about the software's purpose and requirements. On the left side of the main content area, there is a sidebar titled "Book chapters & data files" with a dropdown menu labeled "Select chapter". Below this is a section titled "Thoughts for the day..." containing a quote by Gary White.

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

Gary White

# Self learning material and software

Gary White MARK

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

(great if you are windows user, a bit more involved if you us Mac) great to pair with Rmark (Jeff Laake)

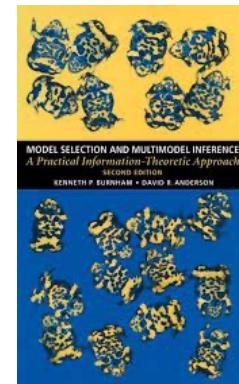
Gary White MARK book

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

Michael Conroy lecture notes (bare bones description of models; useful for Mark/Rmark code and data)  
<https://sites.google.com/site/cmrssoftware/>

Burnham and Anderson 2022:

**Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach**



# R packages for CMR

- [RMark](#) (runs MARK from R, works best with Windows)
- [serc](#) and [openCR](#)
- [Marked](#) (some overlap with openCR and MARK but this doesn't have Pradel models)
- [R2ucare](#) (for goodness of fit tests and simulations for CMR)
- [mra](#), [Rcapture](#), [BaSTA](#)

# Other languages for capture recapture

Python <https://www.python.org/>

- <https://austinrochford.com/posts/2018-01-31-capture-recapture.html>
- [https://pyro.ai/examples/capture\\_recapture.html](https://pyro.ai/examples/capture_recapture.html)

Stan <https://mc-stan.org/>

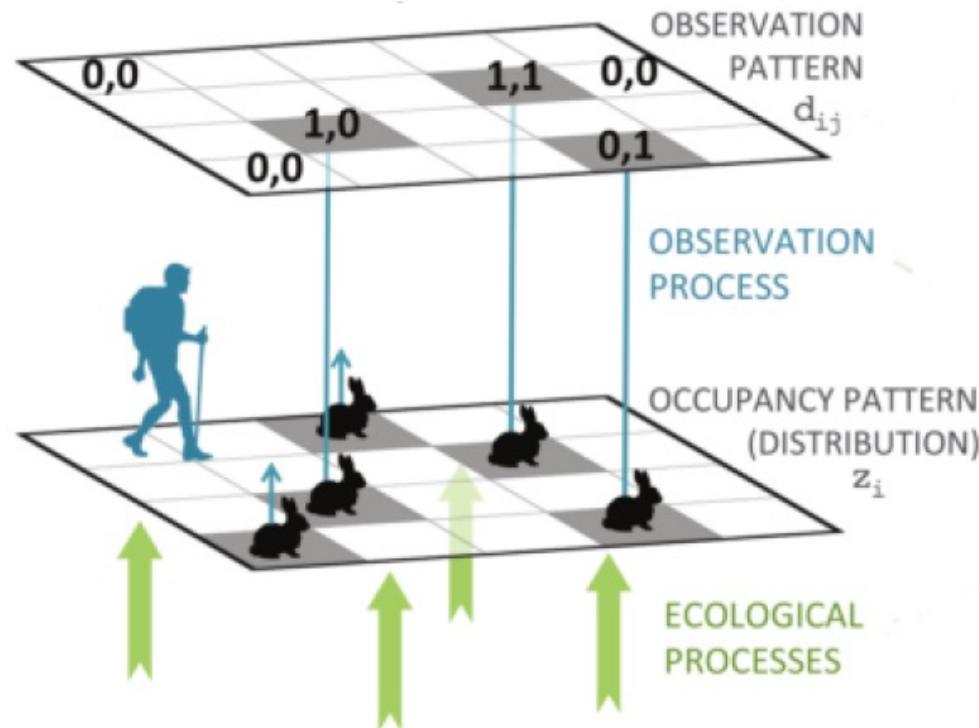
- <https://mc-stan.org/docs/stan-users-guide/latent-discrete.html#mark-recapture-models>

BUGS, JAGS

<https://bccs.org.my/tut/bayes-with-jags-a-tutorial-for-wildlife-researchers/abundance-from-capture-recapture-data/basic-spatial-capture-recapture-models/>

<https://esajournals.onlinelibrary.wiley.com/doi/full/10.1002/ecs2.3810>

# Site-occupancy modeling in statistical ecology

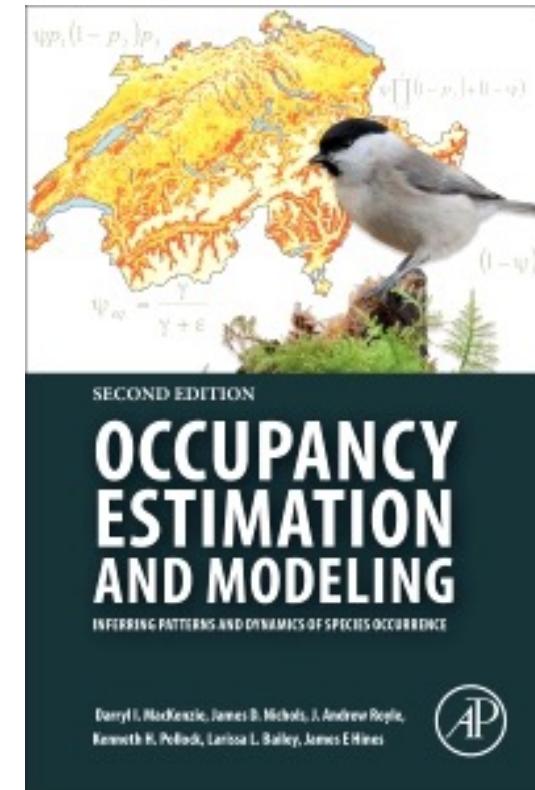


Not to be confused with

Foote, M. et al. (2007) Rise and fall of species occupancy in Cenozoic fossil molluscs. *Science* (80-). 318, 1131–11341

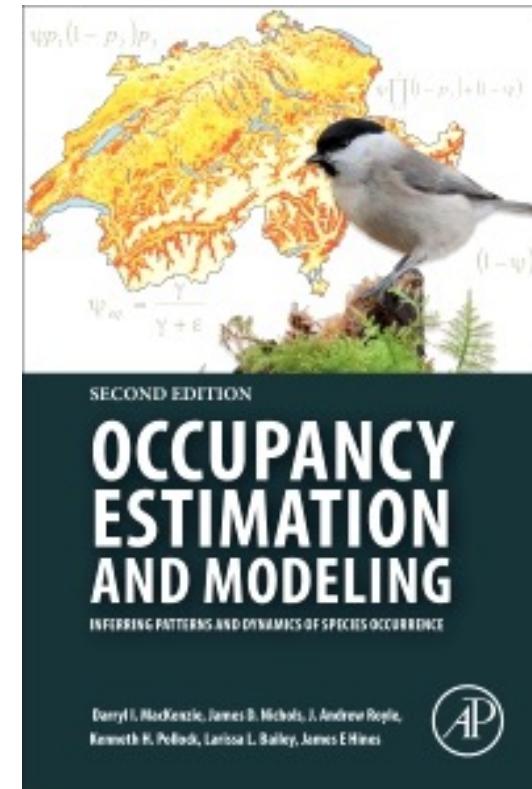
Foote, M. (2016) On the measurement of occupancy in ecology and paleontology. *Am. Nat.* 42, 707–729

# (Site)-Occupancy modeling

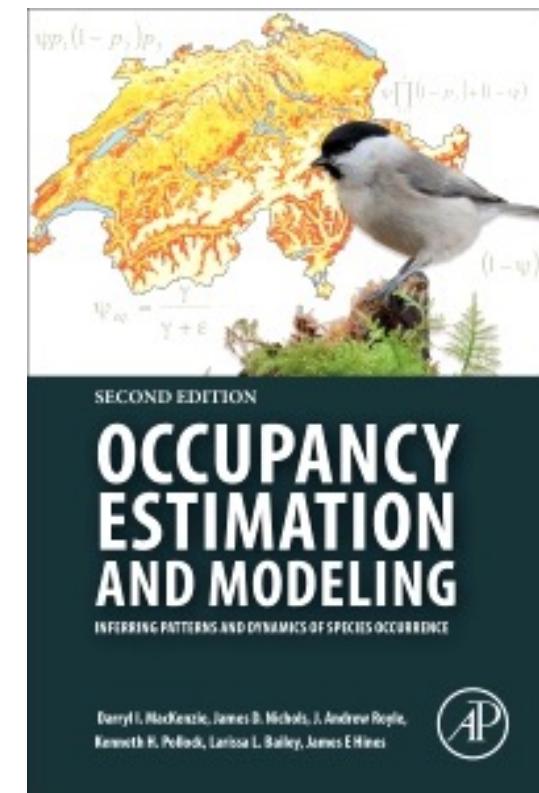
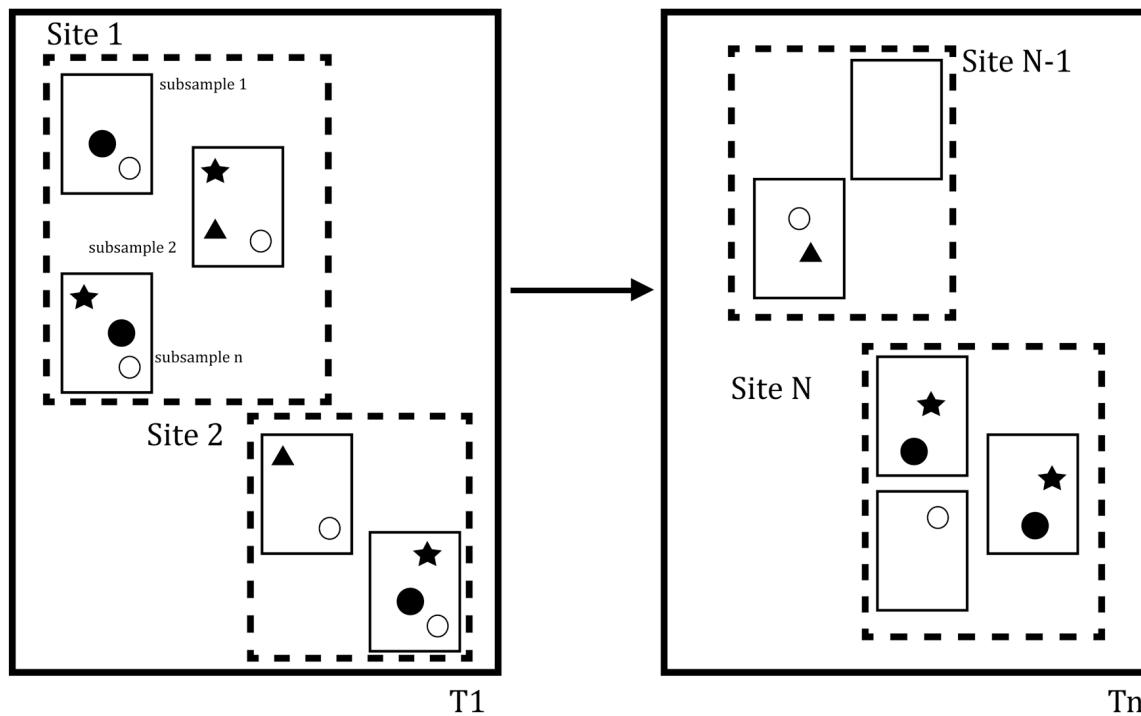


# Occupancy modeling in paleo

- Liow, L.H. (2013) Simultaneous estimation of occupancy and detection probabilities: an illustration using Cincinnatian brachiopods. *Paleobiology* 39, 193–213
- Lawing, A. Michelle, et al. (2021). Occupancy models reveal regional differences in detectability and improve relative abundance estimations in fossil pollen assemblages. *Quaternary Science Reviews* 253: 106747.  
<https://doi.org/10.1016/j.quascirev.2020.106747>
- Reitan, T., Ergon, T., & Liow, L. H. (2022). Relative species abundance and population densities of the past: Developing multispecies occupancy models for fossil data. *Paleobiology*, 1-16.  
doi:10.1017/pab.2022.17
- Reitan, T., E. D. Martino, and L. H. Liow. (2024). Estimating relative species abundance using fossil data identified to different taxonomic levels. *Ecography* 2024:e06866.

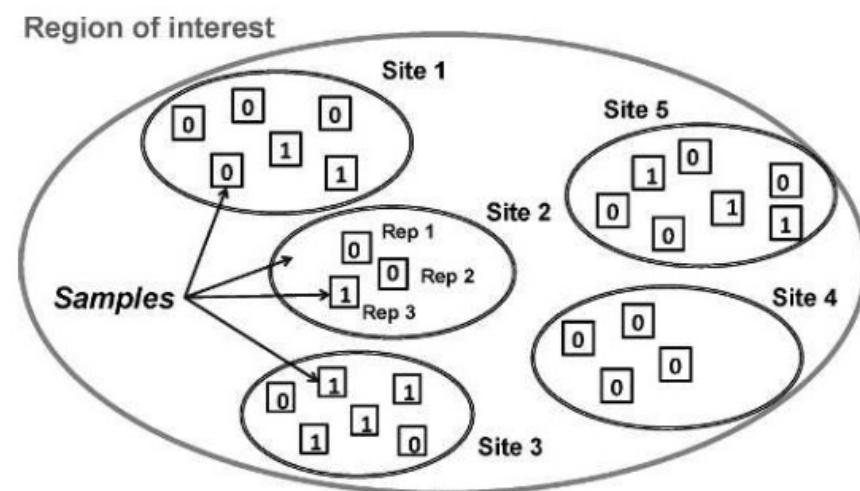


# Occupancy modeling in paleo



$$Pr(h = 1010) = \varphi(1 - p)^2 p^2$$

$$Pr(h = 0000) = ? ? ? ?$$



$$Pr(h=1010)=\varphi(1-p)^2p^2$$

$$Pr(h=0000)=(1-\varphi)+\varphi(1-p)^4$$

$$\begin{aligned}L(\varphi,p|h_1,h_2,\dots\;h_s) = &\prod_{i=1}^s \Pr(h_i)\\&(1-\varphi)+\varphi(1-p)\end{aligned}$$

$$\prod_{i=1}^s \Pr(h_i)$$

# R package occupancy modeling

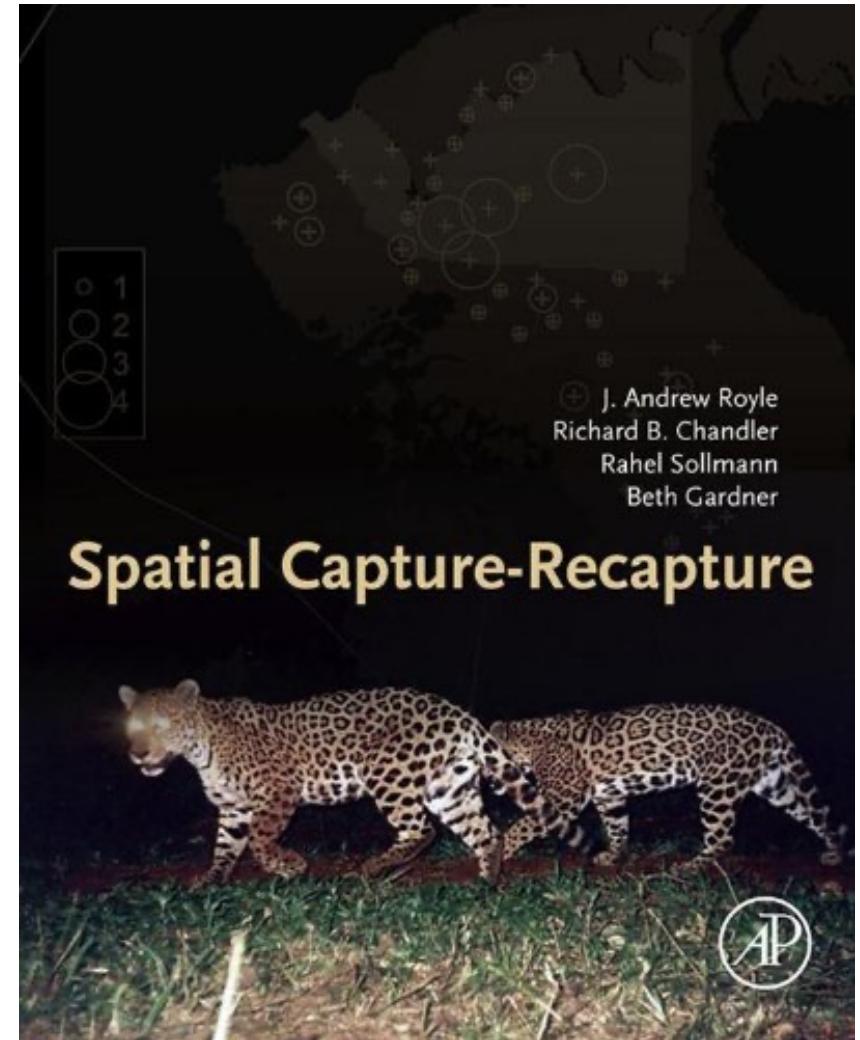
- openCR, serc
- unmarked

# Some resources for occupancy modeling

- <https://kevintshoemaker.github.io/NRES-746/Occupancy.html>
- <https://science.uct.ac.za/seec/stats-toolbox-seminars-spatial-and-species-distribution-toolboxes/single-season-occupancy-models-using-bayesian-approach>

# Spatial capture recapture

- Combining the best of capture recapture and occupancy
- Also implemented in serc, openCR, unmarked



Brief comparisons of CMR with other approaches (paleo context)

## HISTORY OF ESTIMATION TAXONOMIC RICHNESS AND DIVERSIFICATION RATES

Nichols & Pollock 1983 Estimating taxonomic diversity, extinction rates, and speciation rates from fossil data using capture-recapture models. *Paleobiology* 9, 150–163

Foote & Raup 1996 Fossil preservation and the stratigraphic ranges of taxa. *Paleobiology*

Foote 1999/2001 (Boundary crossers method)

Alroy et al. 2001 (sampling standardization)

Connolly and Miller papers 2001-2 using CMR (Connolly is an ecologist)

Foote 2003 (few people use this) – CMR-like, but accounts for origination and extinction within time interval (but see robust design)

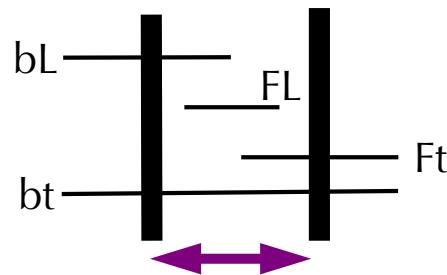
(2009) My own first capture recapture paleo-paper – I met Nichols in 2006; short course paper with Nichols

Silvestro, Schintzler & Liow Syst bio 2014 Pyrate model paper (not the software)

Warnock et al. 2020 RevBayes (starting from birth death models but dropping the “relationships”)

# Comparisons with other approaches

Foote's per capita origination and extinction rates (boundary crossers)



- Easy to use
- Lose information of “singletons” (FL class information not used)
- Hard to compare different models

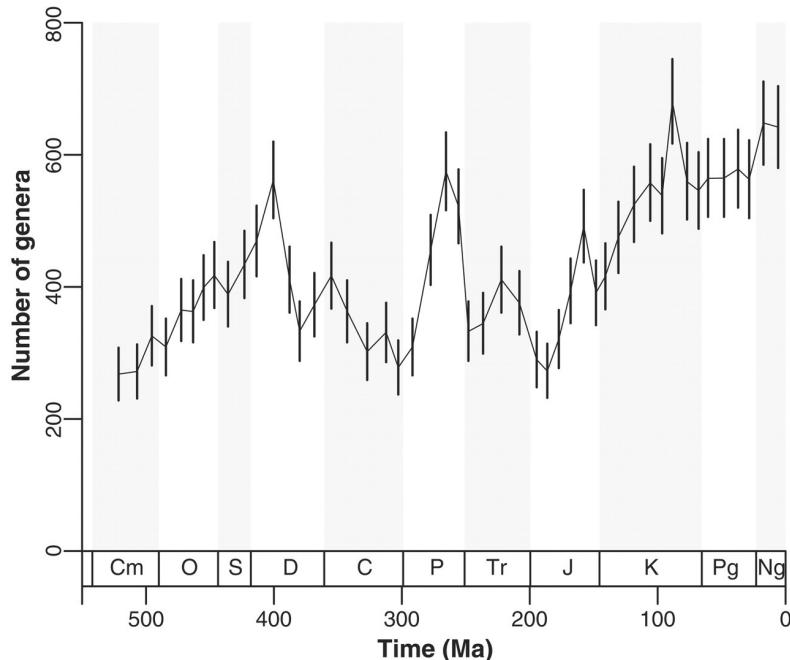
$$\hat{p} = \ln\left(\frac{N_t}{N_{bt}}\right) / \Delta t$$

$$\hat{q} = \ln\left(\frac{N_b}{N_{bt}}\right) / \Delta t$$

Foote, M. 2000. Origination and extinction components of taxonomic diversity: general problems. *Paleobiology* 26:74-102.

# Comparisons with other approaches

Sampling standardization approaches (including SQS)



- Easy to use
- Assume that even sample or quorums will allow unbiased relative change to be estimated
- Ad hoc rather than modelling approach (preservation is not modelled although it is part of the process)
- Hard to compare different models

# Comparisons with other approaches

CMR-like approaches in paleo independently developed

Foote 2003 Journal of Geology

- Some hard, some easy to use, not easy to understand

Alroy “three-timer” and related methods

- Hard to compare different models
- (very) Special cases of CMR

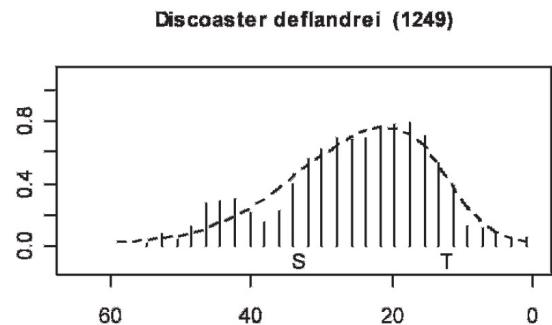
# Comparisons with other approaches

PyRate (Silvestro et al. Sys Bio 2014)

Key preservation assumption (different) is the shape of species observations (beta distribution based on “hat”)

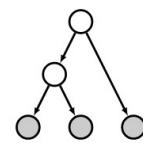
Smooths out temporal information

Conditioned on at least one observation per taxon (like the CMR models conditioned on first observation)



RevBayes

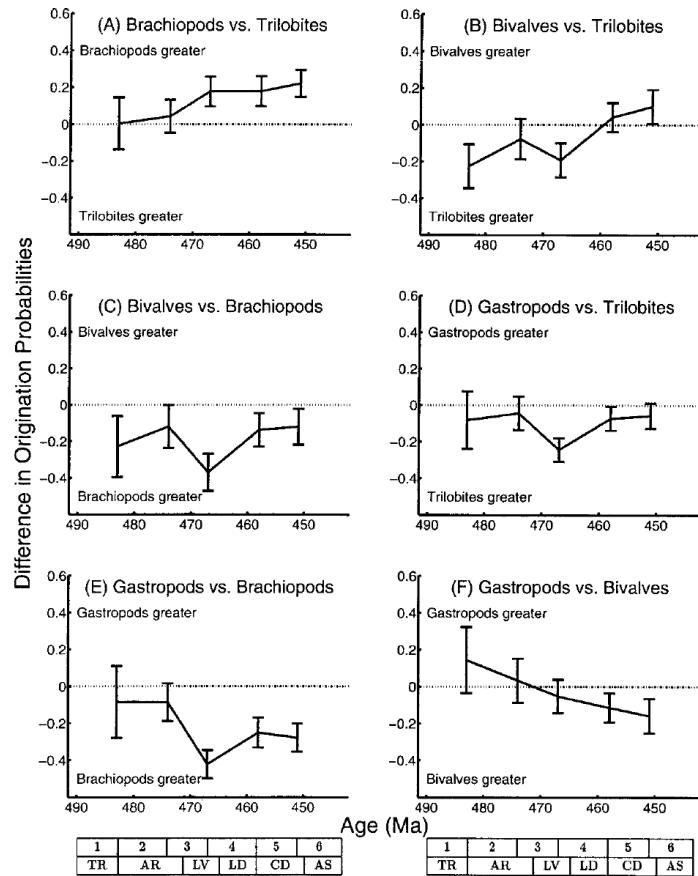
[https://revbayes.github.io/tutorials/fbd\\_range/](https://revbayes.github.io/tutorials/fbd_range/)



RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language

# Some paleo papers using CMR



E 4. Model-averaged estimates of between-class differences in genus origination probabilities over time ob-



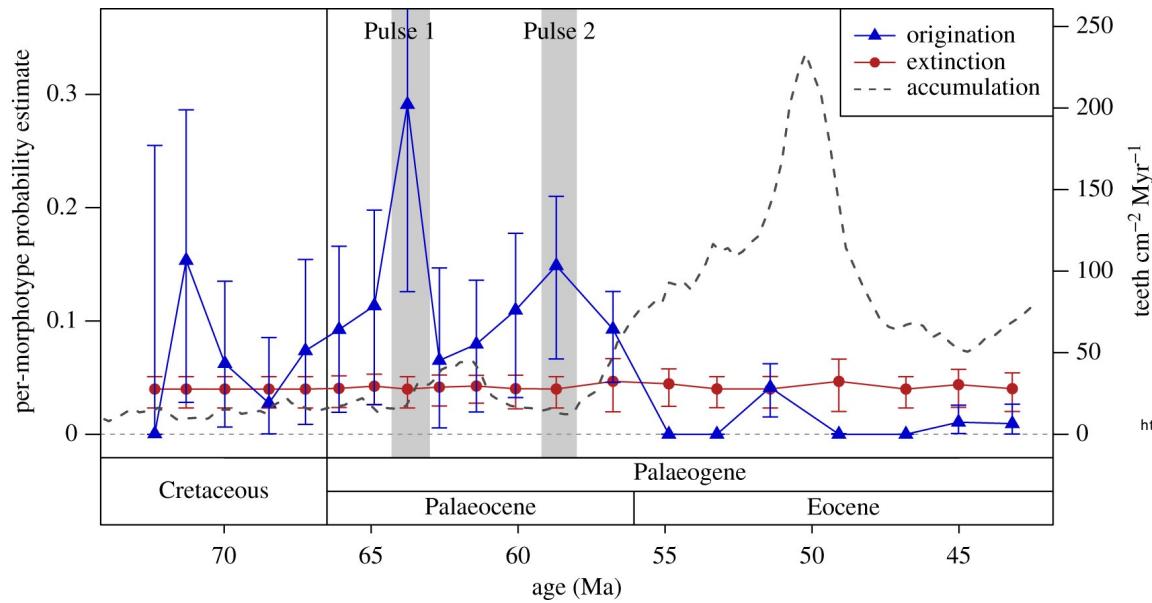
Nichols, J.D. and Pollock, K.H. (1983) Estimating taxonomic diversity, extinction rates, and speciation rates from fossil data using capture-recapture models. *Paleobiology* 9, 150–163

Connolly, S.R. and Miller, A.I. (2001) Joint estimation of sampling and turnover rates from fossil databases: Capture-Mark-Recapture methods revisited. *Paleobiology* 27, 751–767

Connolly, S.R. and Miller, A.I. (2001) Global Ordovician faunal transitions in the marine benthos: proximate causes. *Paleobiology* 27, 779–795

Connolly, S.R. and Miller, A.I. (2002) Global Ordovician faunal transitions in the marine benthos: ultimate causes. *Paleobiology* 28, 26–40

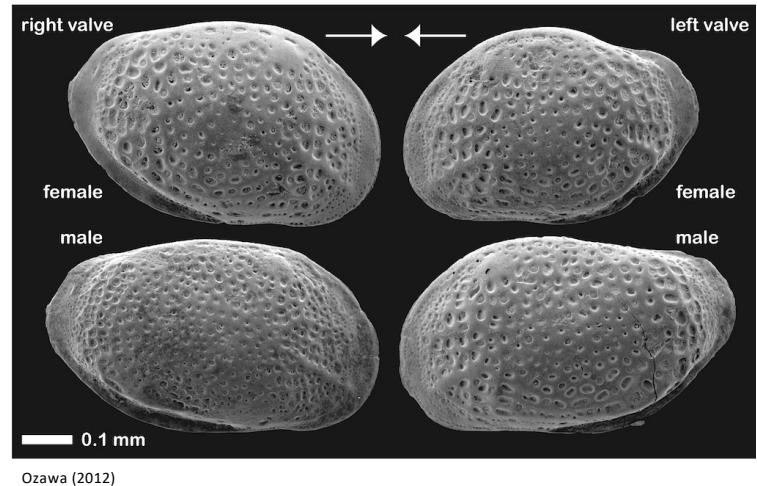
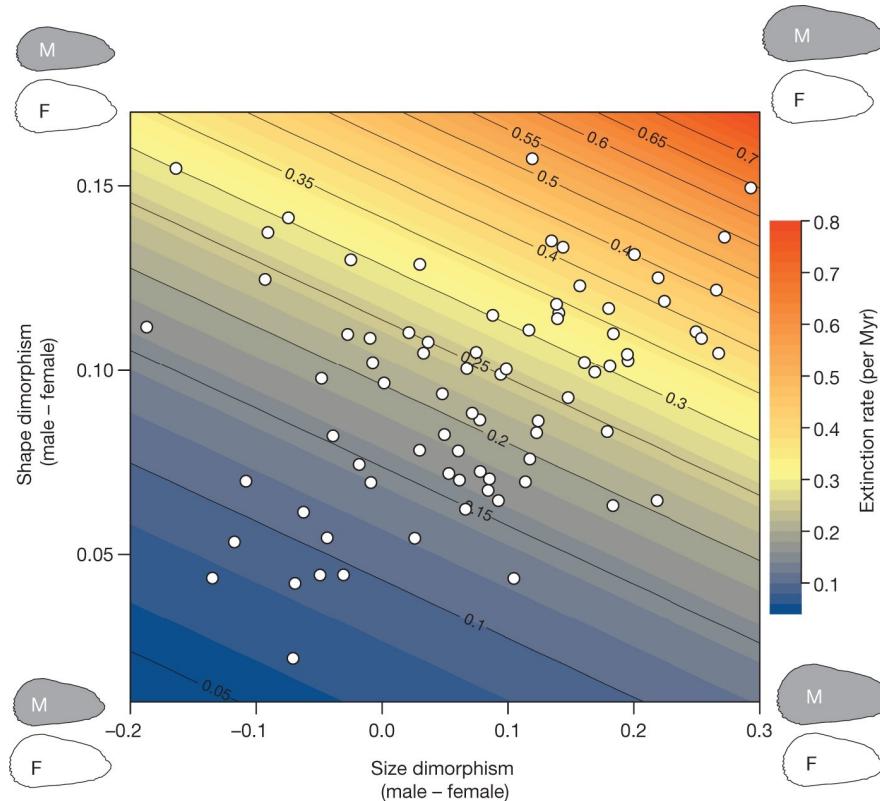
# Some paleo papers using CMR



<https://news.harvard.edu/gazette/story/2018/11/tiny-teeth-tell-the-story-of-two-fish-species-rapid-evolution/>

Sibert, E. et al. (2018) Two pulses of morphological diversification in Pacific pelagic fishes following the Cretaceous - Palaeogene mass extinction. *Proc. R. Soc. B-BIOLOGICAL Sci.* 285,

# Some paleo papers using CMR



Martins, M.J.F. et al. (2018) High male sexual investment as a driver of extinction in fossil ostracods. *Nature*

# Some paleo papers using CMR

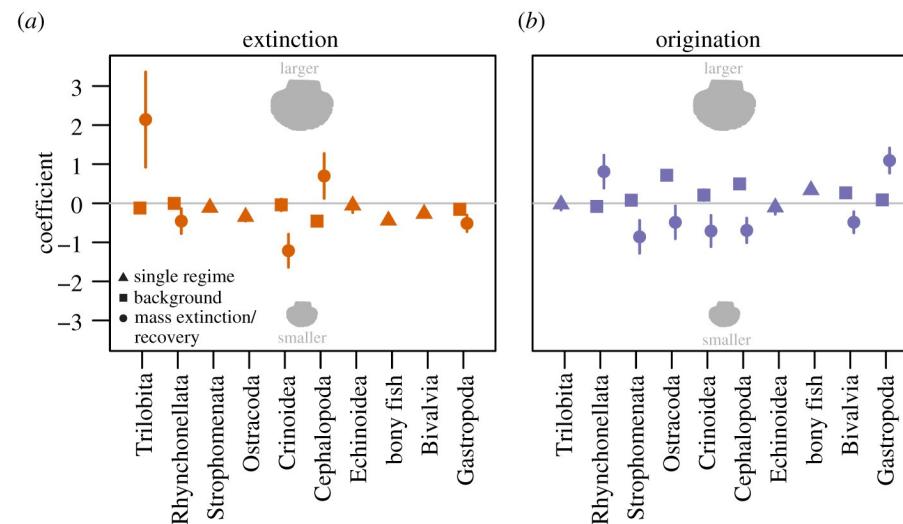
Payne, J., & Heim, N. (2020). Body size, sampling completeness, and extinction risk in the marine fossil record. *Paleobiology*, 46(1), 23-40. doi:10.1017/pab.2019.43

Pedro M. Monarrez, Noel A. Heim and Jonathan L. Payne 2021

[Mass extinctions alter extinction and origination dynamics with respect to body size](#)

Proc B

“CMR analysis of the fossil record reveals a  
bias against the sampling of smaller-bodied  
genera within classes”



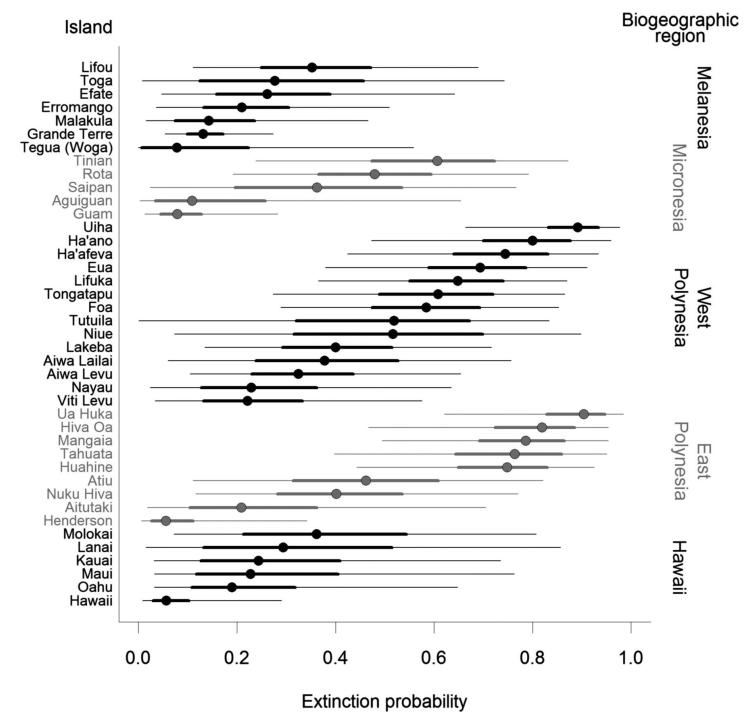
# Some paleo papers using CMR

## Magnitude and variation of prehistoric bird extinctions in the Pacific 2013

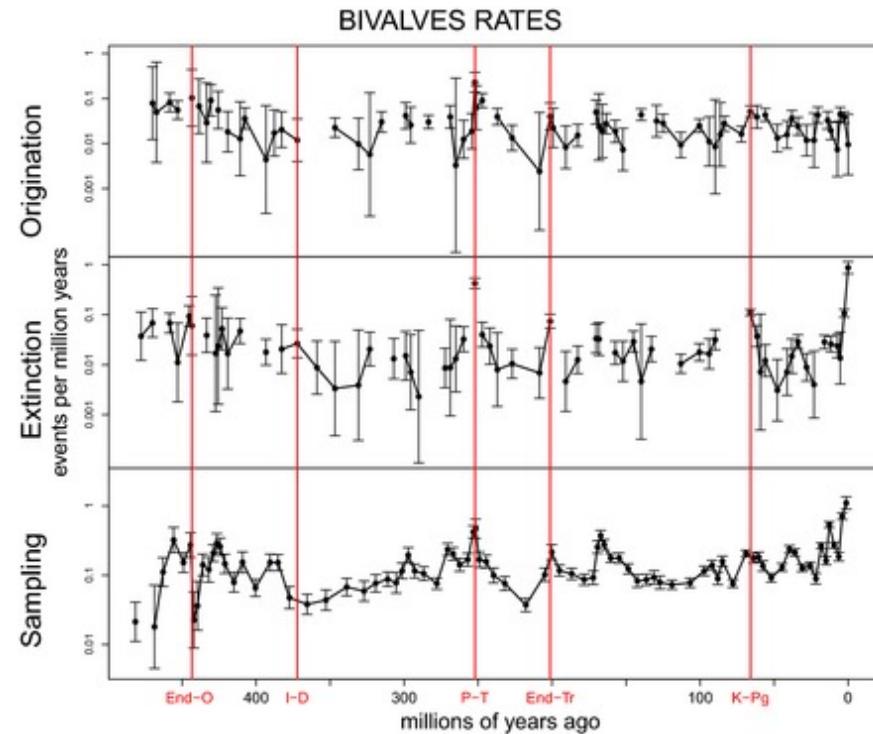
Richard P. Duncan [richard.duncan@canberra.edu.au](mailto:richard.duncan@canberra.edu.au), Alison G. Boyer, and Tim M. Blackburn

PNAS

“We use a Bayesian mark-recapture approach to model gaps in the fossil record and to quantify losses of nonpasserine landbirds on 41 Pacific islands.”



# Some paleo papers using CMR



Liow, L.H. et al. (2015) Ecological interactions on macroevolutionary time scales: clams and brachiopods are more than ships that pass in the night. *Ecol. Lett.* 18, 1030–1039