

A bit of everything related to CMR in paleo

Lee Hsiang Liow

Natural History Museum, University of Oslo, Norway

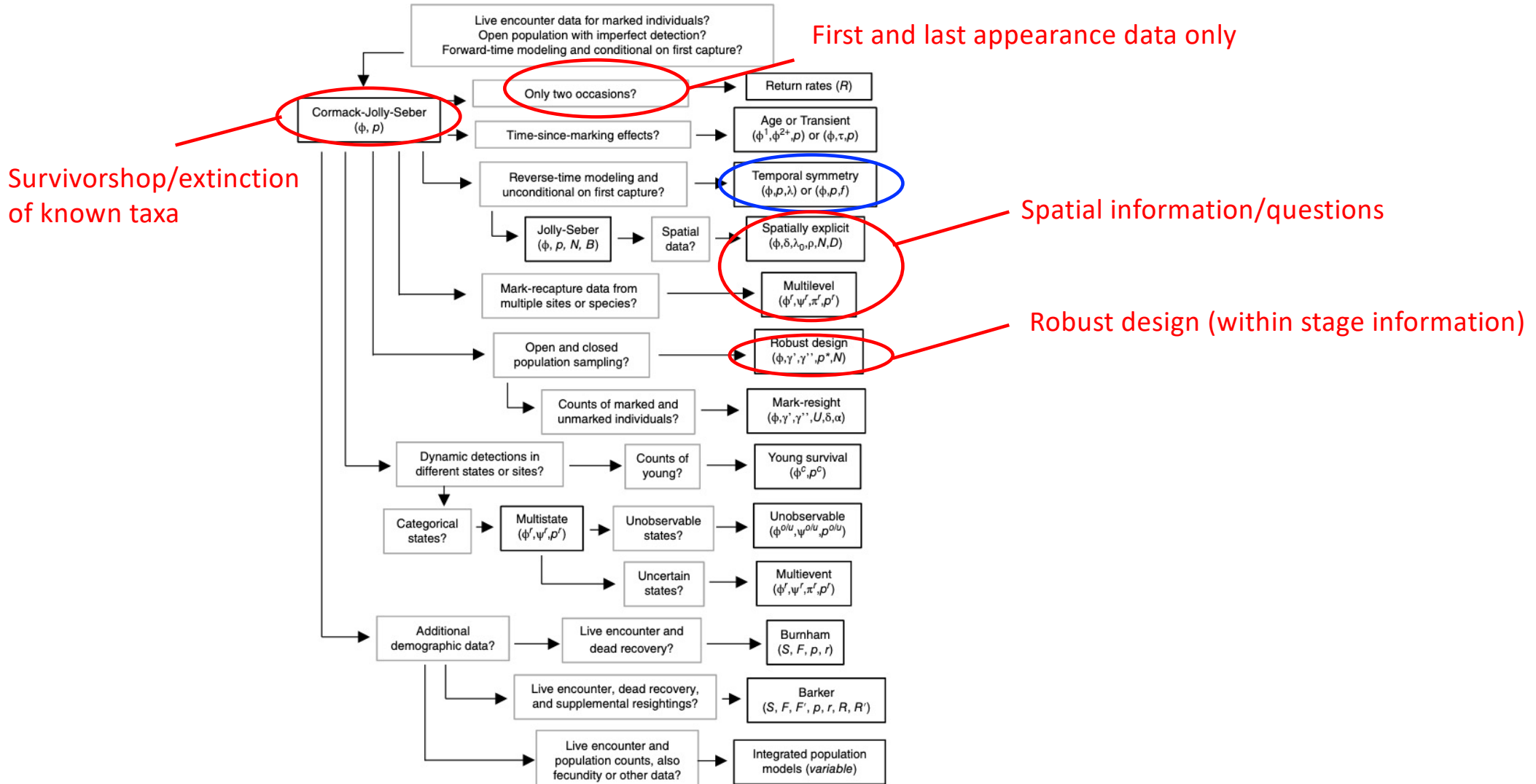
2.9.2022



Friedrich-Alexander-Universität
Erlangen-Nürnberg



Many models: few explored in paleo



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

A screenshot of a web browser displaying the 'program MARK' website. The browser's address bar shows 'www.phidot.org/software/mark/docs/book/'. The website has a blue header with 'program MARK' in white and 'A Gentle Introduction' below it. A green navigation bar contains links: Home, About, Download, Support Forum, and Training. On the left, there is a book cover image for 'Program MARK' with the subtitle 'A Gentle Introduction' and the author 'e.g. cooch & g.c. white (eds)'. Below the cover is a 'Book chapters & data files' section with a 'Select chapter' dropdown menu. Further down is a 'Thoughts for the day...' section with a quote: 'Debugging is twice as hard as writing the code in the first place. Therefore, if you write the code as cleverly as possible, you are, by definition, not smart enough to debug it'. The main content area on the right has an 'Overview' section with text about the program's development and purpose, and an 'About the book...' section with information about the book's format and availability. A 'Note' at the bottom of the 'About the book...' section mentions the book's size and pricing.

<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)

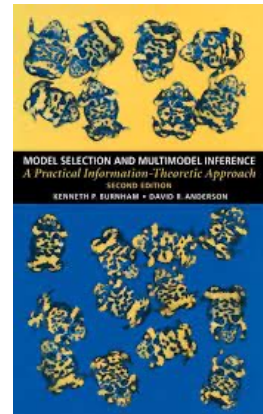
Gary White MARK book

<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/cmrsoftware/>

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](#)
- [unmarked](#): occupancy modeling (a related approach used in ecology, but also paleoecology NOT the same as Foote's occupancy definition)

Other languages

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

- <https://austinrochford.com/posts/2018-01-31-capture-recapture.html>
- https://pyro.ai/examples/capture_recapture.html

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

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

BUGS, JAGS

<https://bcss.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>

Brief comparisons with other approaches

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)

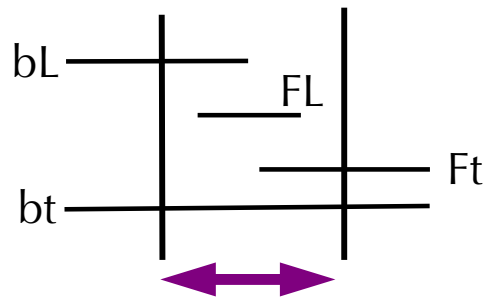
(2009) My own first capture recapture paleo-paper – I met Nichols in 2006; short course paper with Nichols

Silvestro, Schinitzler & 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)



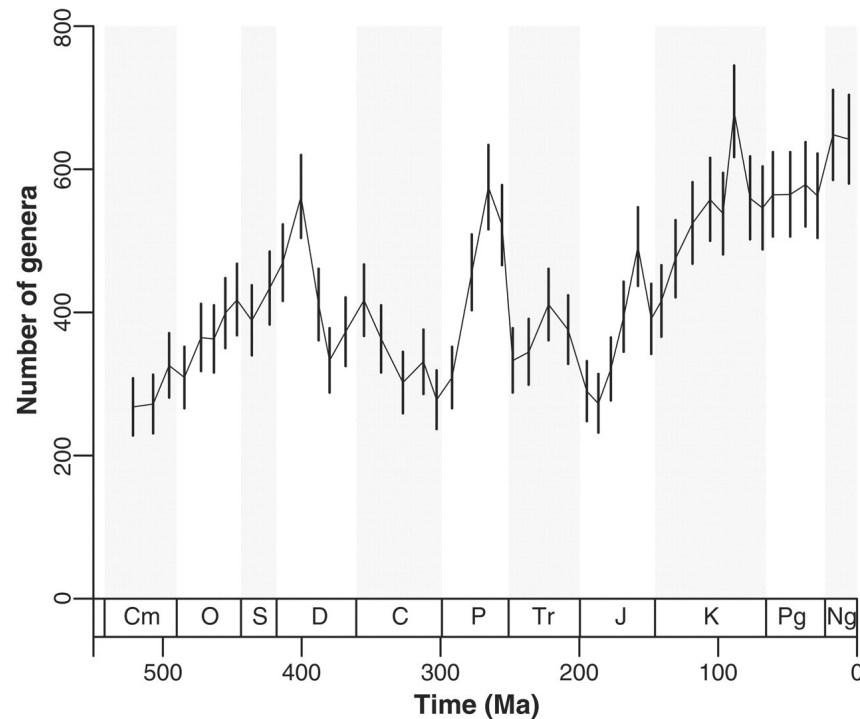
- Easy to use
- Lose information of “singletons” (FL class information not used)
- Hard to compare different models

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

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

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

Alroy “three-timer” and related methods

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

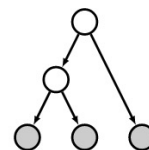
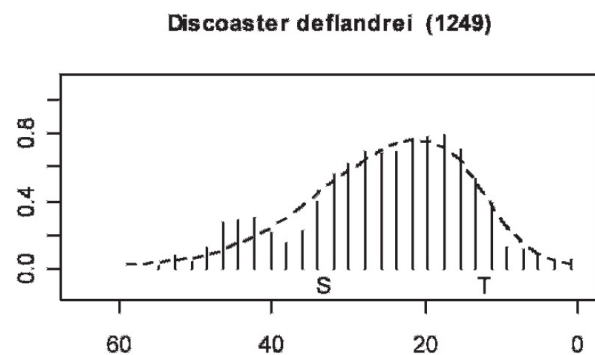
Smooths out temporal information

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

RevBayes

https://revbayes.github.io/tutorials/fbd_range/

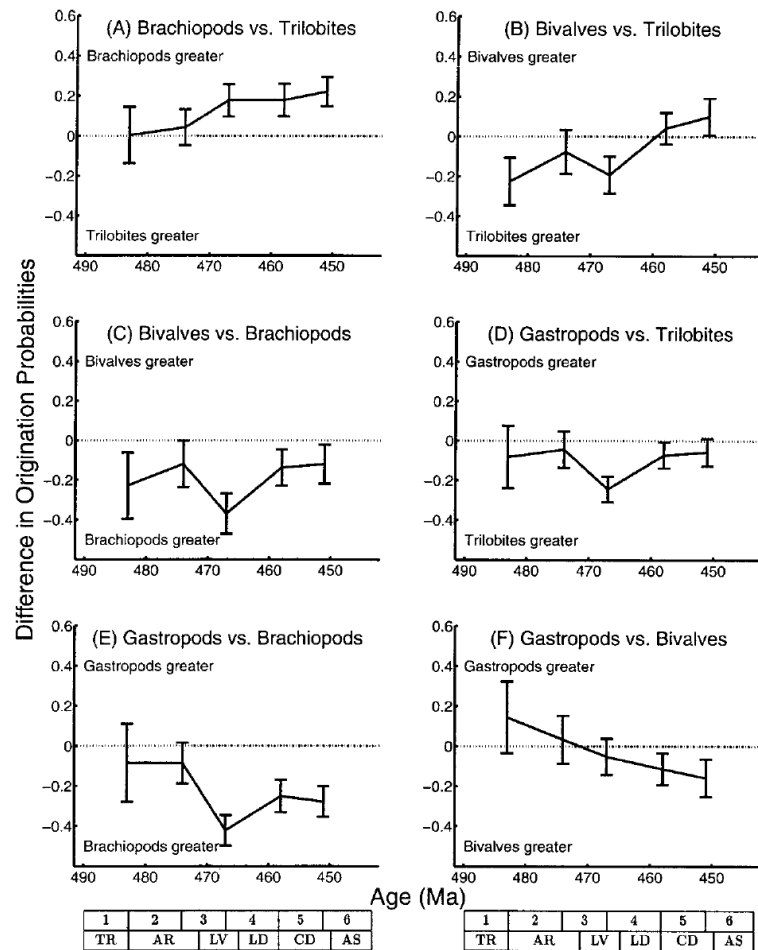
Rachel’s lecture!



RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language

Some paleo papers using CMR



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

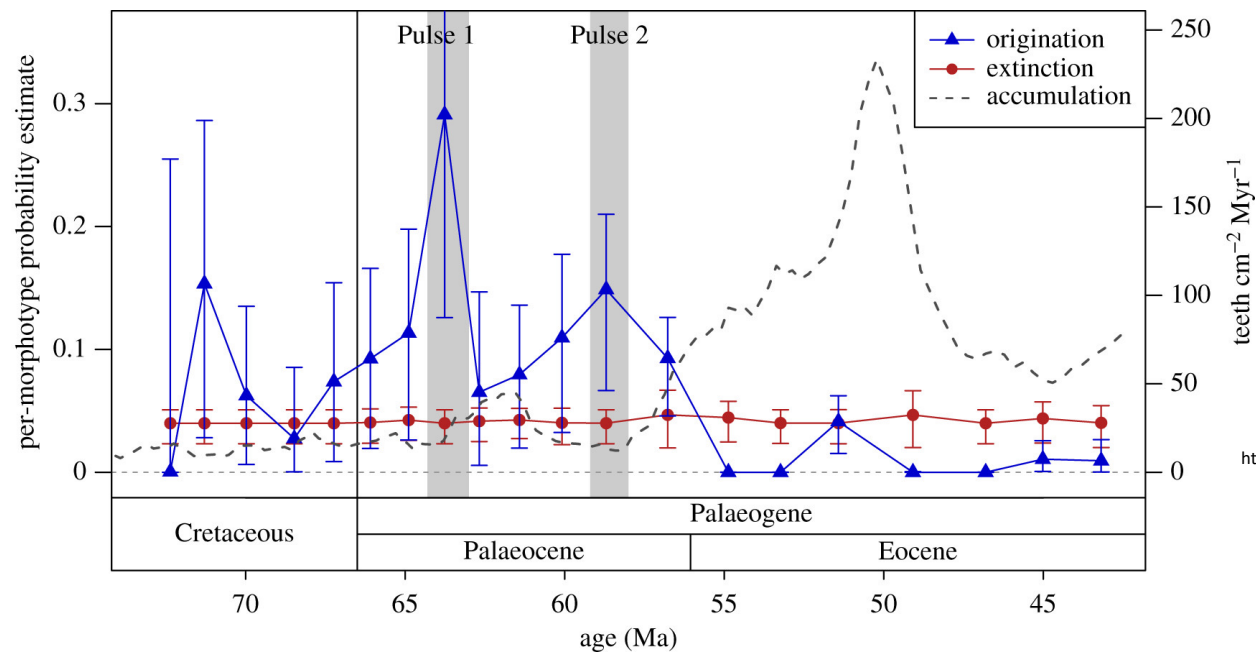
Connolly, S.R. and Miller, A.I. (2001) Joint estimation of sampling and turnover rates from fossil databases: Capture-Mark-Recapture methods revisited. *Paleobiology* 27, 751–767

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

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

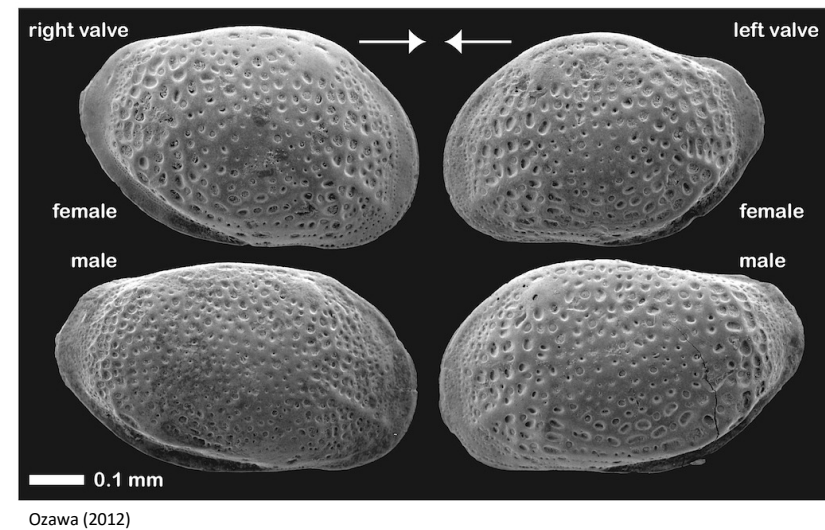
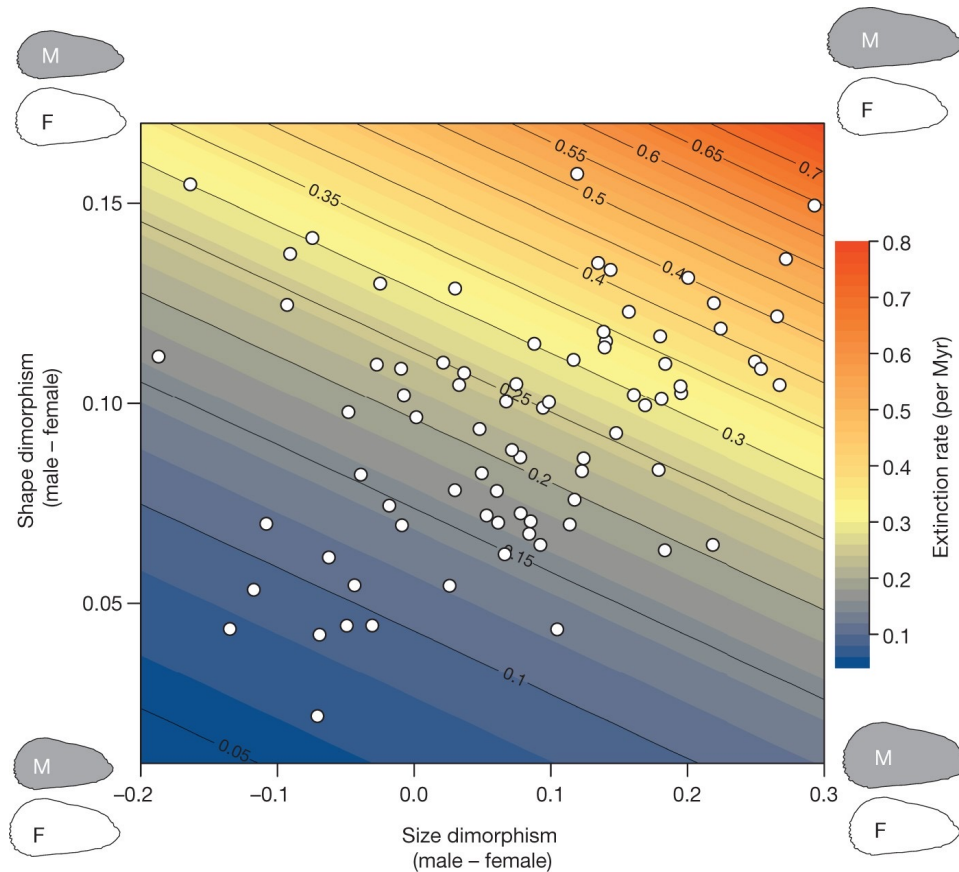
Some paleo papers using CMR



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

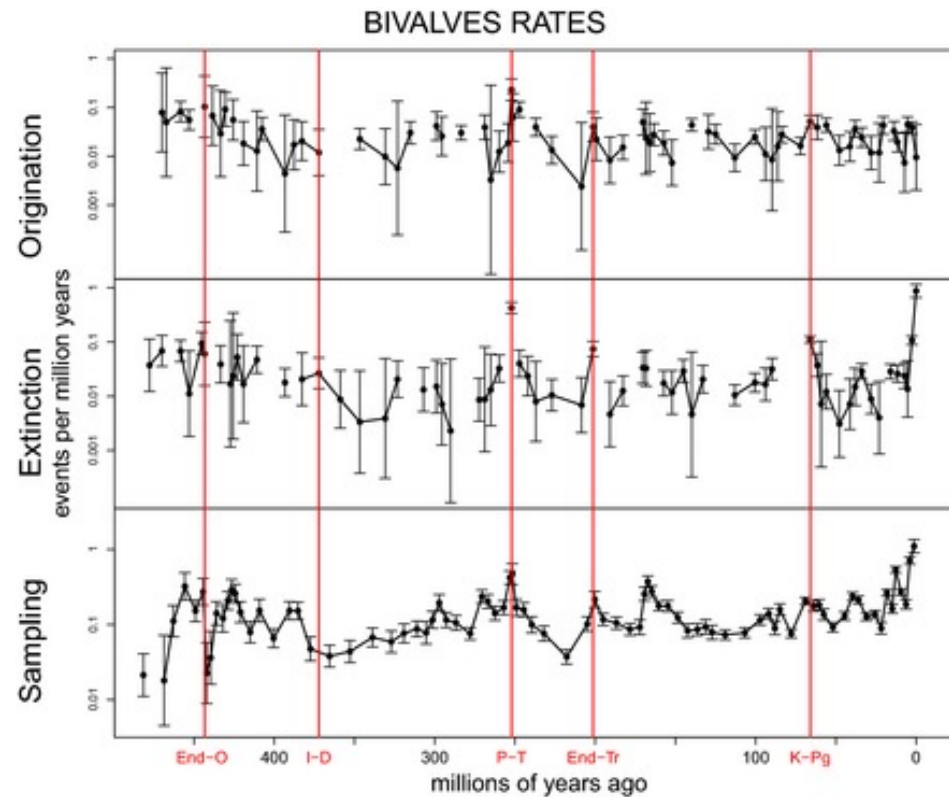
Sibert, E. *et al.* (2018) Two pulses of morphological diversification in Pacific pelagic fishes following the Cretaceous - Palaeogene mass extinction. *Proc. R. Soc. B-BIOLOGICAL Sci.* 285,

Some paleo papers using CMR



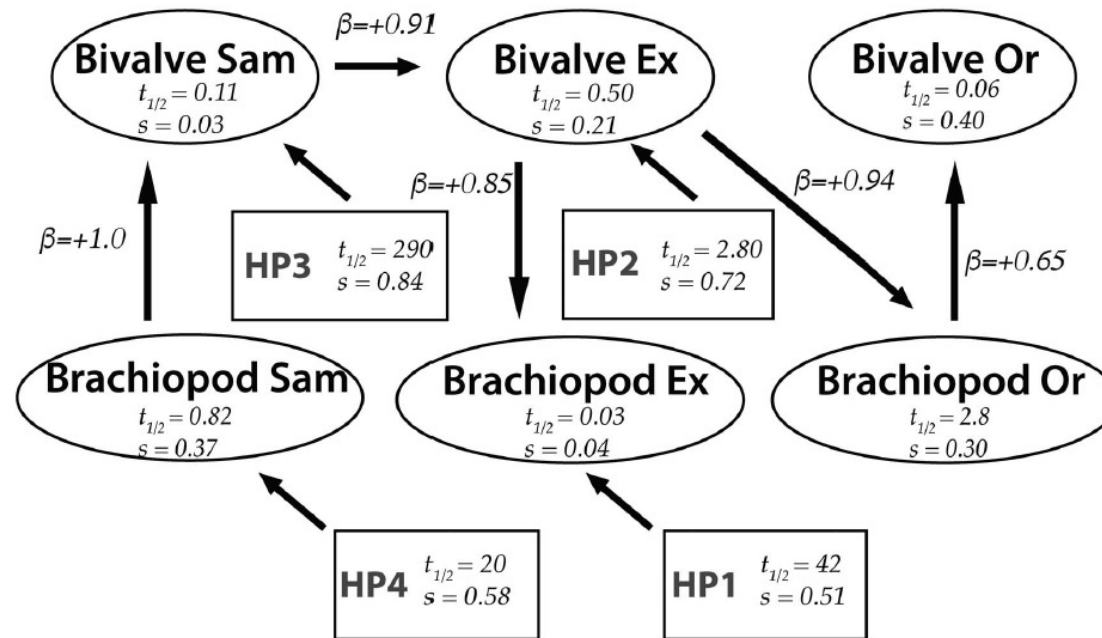
Martins, M.J.F. *et al.* (2018) High male sexual investment as a driver of extinction in fossil ostracods. *Nature*

Some paleo papers using CMR



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

Some paleo papers using CMR



Reitan, T. and Liow, L.H. (2017) An unknown Phanerozoic driver of brachiopod extinction rates unveiled by multivariate linear stochastic differential equations. *Paleobiology* DOI: 10.1017/pab.2017.11

layeranalyzer

Reitan, T. and Liow, L.H. (2019) layeranalyzer: Inferring correlative and causal connections from time series data in R.
Methods Ecol. Evol. 10, 2183–2188

