

How macroecology affects macroevolution: the interplay between extinction intensity and trait-dependent extinction in brachiopods.

Taxon occurrence as a function of both emergent biological traits and environmental context

Other projects

Moving forward

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## History

- ▶ presented at GSA 2015
- ▶ rejected from *Evolution*
  - ▶ encouraged resubmit
  - ▶ audience issues
  - ▶ difficult and transformative reviews
  - ▶ resubmitted 3 March

## New measure of taxon's environmental affinity

Probability of observing ( $\#$  epicontinental / total  $\#$  occurrences) given  $\text{Beta}(\alpha, \beta)$ .

$\alpha$  is the  $\#$  epicontinental background occurrences (+ 1).

$\beta$  is the  $\#$  open ocean background (+ 1).

## Measure of sampling and imputed values

Sampling is measured as the gap statistic  $r$ :  
(number of bins with an occurrence - 2) / (duration in bins)

Can only be estimated for taxa with duration of three or more.  
Have to impute (e.g. fill-in) the values for all other taxa  $r^*$ .

$$r \sim \text{Beta}(\phi, \lambda)$$

$$\phi = \text{logit}^{-1}(W\gamma)$$

$$r^* \sim \text{Beta}(\phi^*, \lambda)$$

$$\phi^* = \text{logit}^{-1}(W^*\gamma)$$

Note: Beta distribution parameterized in terms of mean  $\phi$  and total count  $\lambda$ .  
Also, this presentation excludes final (hyper)priors.

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# Empirical questions

## Theoretical underpinning

- ▶ changes in demographic structure of regional species pool
- ▶ intersection of macroecology and macroevolution
- ▶ fourth-corner type problem



# Fourth-corner problem

# Macroevolutionary phrasing of fourth-corner problem

# Analysis of Cenozoic mammal fossil record for NA

## individual-level

(genus  $i$  at time unit  $t$ )

- ▶ log-odds of occurrence probability at time  $t$
- ▶ effect of locomotor type
  - ▶ arboreal, digitigrade, plantigrade, unguligrade, fossorial, scansorial
- ▶ effect of dietary type
  - ▶ carnivore, herbivore, insectivore, omnivore
- ▶ body size  
(rescaled log body mass)

## group-level (2 My time unit $t$ )

- ▶ overall mean of log-odds of occurrence probability
- ▶ temperature record based on Mg/Ca estimates
  - ▶ mean and interquartile range of rescaled value
- ▶ plant community phase following Graham

# Model of taxon occurrence

- ▶ response is  $p/a$  of genus in NA at time  $t$ 
  - ▶ Bernoulli variable
  - ▶ probability is (observation prob) times (“true” presence)
- ▶ observation probability is effect of sampling/fossil record
- ▶ the latent discrete “true” presence modeled as a multi-level logistic regression
  - ▶ individual- and group-level

$$y_{i,t} \sim \text{Bernoulli}(\rho_t z_{i,t})$$

$$\text{logit}(\rho_t) \sim \mathcal{N}(\rho', \sigma_\rho)$$

$$z_{i,t} \sim \text{Bernoulli}(\theta_{i,t})$$

$$\text{logit}(\theta_{i,t}) = z_{i,t-1}(\alpha_t + X_i \beta_t) + \left( \prod_{k=1}^{t-1} 1 - z_{i,k} \right) (\alpha_t + X_i \beta_t)$$

$$\beta_{d,t} \sim \mathcal{N}(\mu_d, \sigma_d)$$

$$\alpha_t \sim \mathcal{N}(\mu + \phi_{p[t]} + U_t \gamma, \sigma_\mu)$$

$$\phi_p \sim \mathcal{N}(0, \sigma_\phi)$$

Note: My implementation in Stan marginalizes over all possible (range-through) values of  $z$  instead of estimating the discrete parameters, and also uses a noncentered parameterizations of the hierarchical effects for better posterior sampling behavior. Also, this presentation excludes final (hyper)priors.

# Posterior predictive model checking

- ▶ simulate fossil record given only  $y_{-t=1}$ , all its covariates, and  $\theta$ 
  - ▶ where  $\theta$  is the set of all parameters
- ▶ leave-one-out cross-validation for time series
  - ▶ Bayesian statement is  $p(\tilde{y}_{-(t+1)}|y_{-t}\theta)$
- ▶ ROC as measure of performance

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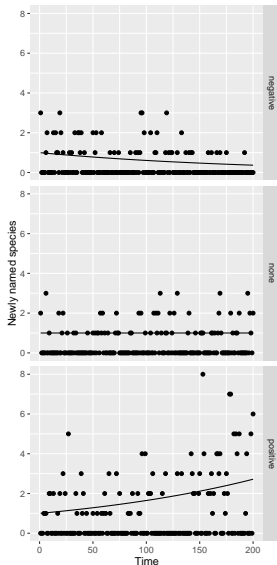
# How cryptic is cryptic diversity? Machine learning approaches to classifying morphological variation in the Pacific Pond Turtle (*Emys marmorata*)

- ▶ estimate which species classification is best supported by morphology
  - ▶ multiple machine learning approaches
  - ▶ focus on one turtle species complex
  - ▶ results compared against results from two other turtle datasets
  - ▶ comparison of in- and out-of-sample model performance
- ▶ collaboration with Ken, Jim Parham, and Bryan Stuart
- ▶ submitted to then rejected from Systematic Biology
- ▶ resubmitted soon



# Modeling the rate at which new species are named.

- ▶ collaboration with Stewart Edie; he's lead
- ▶ I developed the statistical model
  - ▶ zero-inflated Poisson model
  - ▶ both Bernoulli and Poisson modeled as time series
  - ▶ response is the number of species named per publication per year for each biogeographic province
- ▶ targets seem to be PNAS or Systematic Biology



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# Post-doc ideas

1. Miller Fellowship at Berkeley with Charles Marshall
  - ▶ Charles has met me a couple times.
2. Peter Buck Fellowship at Smithsonian with Gene Hunt (and Peter Wagner and Kate Lyons)
  - ▶ Gene, Pete, and Kate all know who I am.
3. Michigan Fellowship at University of Michigan with Matt Friedman
  - ▶ I don't know if he's actually moving there.
4. NIMBiOS Post-doc with Brian O'Meara
  - ▶ I don't know him.

# Research program