

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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Updates

- ▶ 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 $\text{Beta}(\alpha, \beta)$.

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

β 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 ϕ and total count λ . Also, this presentation excludes final (hyper)priors.

Results

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Empirical setup

- ▶ arboreal taxa are expected to have greatest extinction risk of the locomotor categories (Smits 2015 PNAS)
- ▶ two possible causes
 1. this effect is constant for all time
 2. Paleogene-Neogene transition
 - ▶ neutral effect of arboreality during Paleogene
 - ▶ strong selection against arboreality during Neogene
 - ▶ Neogene effect is stronger than Paleogene effect
 - ▶ means that overall mean effect is closer to Neogene
- ▶ former implies no appreciable demographic differences over Cenozoic
- ▶ latter implies a difference in demography between Paleogene and Neogene

The ground-dwelling problem

- ▶ “ground-dwelling” too broad a category
- ▶ following a suggestion from Graham, split by foot posture
 - ▶ based primarily on Carrano 1997 *ZJLS*
- ▶ allows for estimation of subtler shifts in demography within “ground-dwelling”

Theoretical underpinning

- ▶ changes in demographic structure of regional species pool
- ▶ intersection of macroecology and macroevolution
- ▶ fourth-corner type problem
 - ▶ trait- **and** environment-based assembly

Conceptual diagram of fourth-corner problem

GLMs for trait-based community assembly 397

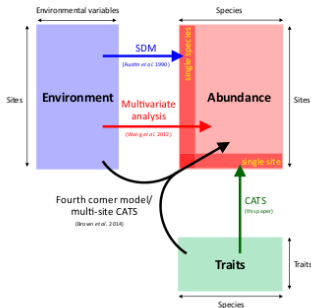
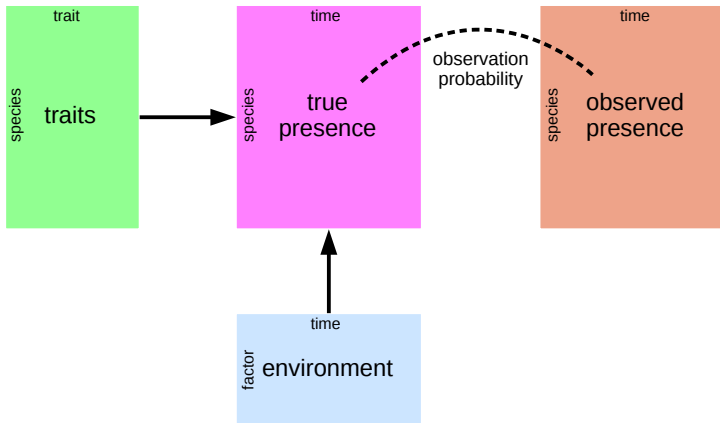


Fig. 4. Schematic diagram of the relationship of CATS and multisite CATS to species distribution modelling, multivariate analysis and fourth-corner models. All these methods can be understood as fitting predictive models for the abundance ('Abundance' table) of one or more species at one or more sites as a function of environmental variables ('Environment' table) and/or species traits ('Traits' table). In principle, any predictive modelling framework could be used to fit any of these models, but in each case, an example reference has been included which used generalized linear models.

(Warton, Shipley, and Hastie. 2015. *Methods in Ecology and Evolution*.)

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
- ▶ effect 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. I also uses a noncentered parameterizations of the hierarchical effects for better posterior sampling behavior. Finally, this presentation excludes final (hyper)priors.

Posterior predictive model checking

- ▶ simulate fossil record given only $y_{-t=1}$, all its covariates, and θ
 - ▶ where θ 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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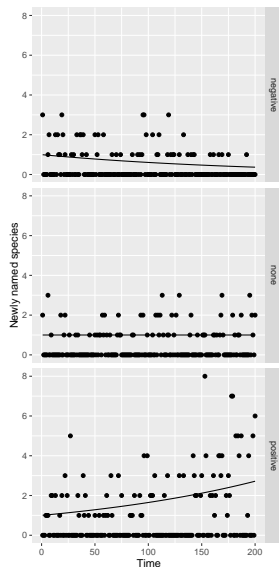
Moving forward

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 model
 - ▶ zero-inflated Poisson model
 - ▶ both Bernoulli and Poisson modeled as time series
 - ▶ response is the number of species named per publication per year by 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.

My “research program”