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 its 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 environmental affinity

Measure of sampling and imputed values

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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
  - 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

$$
\begin{aligned}
y_{i,t} &\sim \text{Bernoulli}(\rho_t z_{i,t}) \\
\text{logit}(\rho_t) &\sim \mathcal{N}(\rho^{'}, \sigma_\rho) \\
z_{i,t} &\sim \text{Bernoulli}(\theta_{i,t}) \\
\text{logit}(\theta_{i,t}) &= z_{i,t-1}(\alpha_t + X_i\beta_t) + (\prod_{k=1}^{t-1} 1 - z_{i,k})(\alpha_t + X_i\beta_t) \quad (1) \\
\beta_{d,t} &\sim \mathcal{N}(\mu_d, \sigma_d) \\
\alpha_t &\sim \mathcal{N}(\mu + \phi_{p[t]} + U_t\gamma, \sigma_\mu) \\
\phi_p &\sim \mathcal{N}(0, \sigma_\phi)
\end{aligned}
$$

Note: My implementation in Stan marginalizes over all possible values of z and takes advantage of noncentered parameterizations of the hierarchical effects for better posterior sampling behavior.

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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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
  - increasing, decreasing, or level?
- draft phase
- 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 statement

Modeling sources of variation in global and regional patterns of biodiversity over time.

- Intersection of macroevolution and macroecology.
- Species pool demography as focus.
- Paleontological data.