

Metacommunities, assembly, α and γ

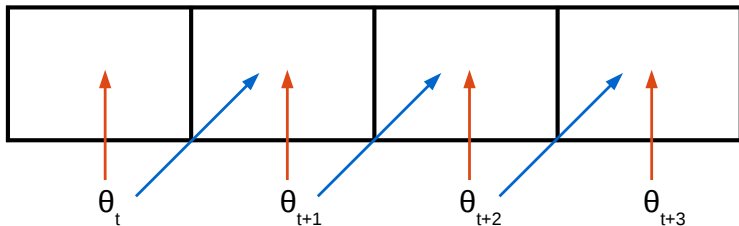
February 15, 2015

Species distribution across multiple localities

Questions

- ▶ How do mammal species traits effect co-occurrence patterns?
- ▶ What is the expected proportion of the mammal metacommunity pool present at a single locality?
- ▶ Have these relationships changed over the Cenozoic?

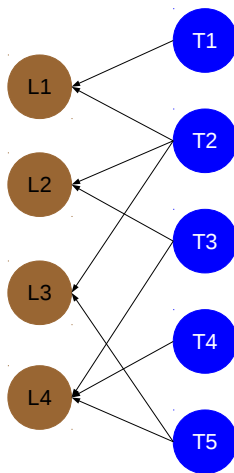
Analysis framework



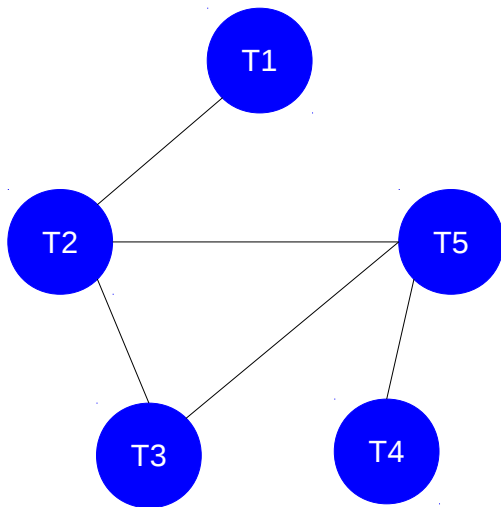
System

- ▶ Record
 - ▶ North American Cenozoic
 - ▶ 2 My bins
- ▶ Units
 - ▶ mammal species occurrence
 - ▶ 2x2 Lat-Long equal area grid cells
- ▶ Covariates
 - ▶ taxa: diet, locomotor, body size
 - ▶ localities: ??
- ▶ Hierarchical effects
 - ▶ spatial relation
 - ▶ phylogeny
- ▶ Relations to community assembly (e.g. requirements)
- ▶ Covariate hypotheses
 - ▶ carnivore greatest diet co-occur
 - ▶ ground dwelling > scansorial > arboreal
 - ▶ body size: positive
- ▶ Hierarchical effect interpretations
 - ▶ spatial effect: structured vs random
 - ▶ phylogeny: attract vs repel

Bipartite network



One-mode network



Modeling co-occurrence

Assumption and setup

y_i : # co-occurring species with species i per # of localities (offset).

Any species is equally likely to co-occur with any other species.

Consequence, node degree follows Poisson distribution (Erdos-Renyi random graph).

Modeling phylogenetic effect

Definition

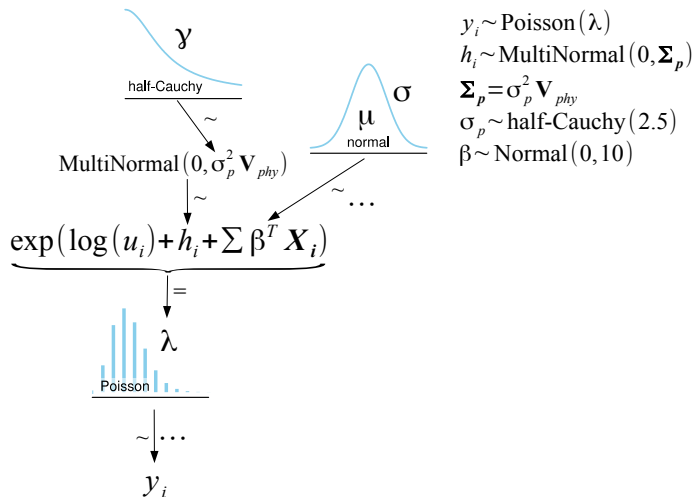
Assuming Brownian motion, effect drawn from multivariate normal distribution.

$$h \sim \mathcal{N}(0, \sigma_p^2 \mathbf{V}_p)$$

- ▶ Covariance known up to constant, σ_p .
- ▶ \mathbf{V}_p phylogenetic covariance matrix (shared branch lengths).

Follows Lynch 1991 *Evolution*, Housworth *et al.* 2004 *Am. Nat.*

Species co-occurrence model



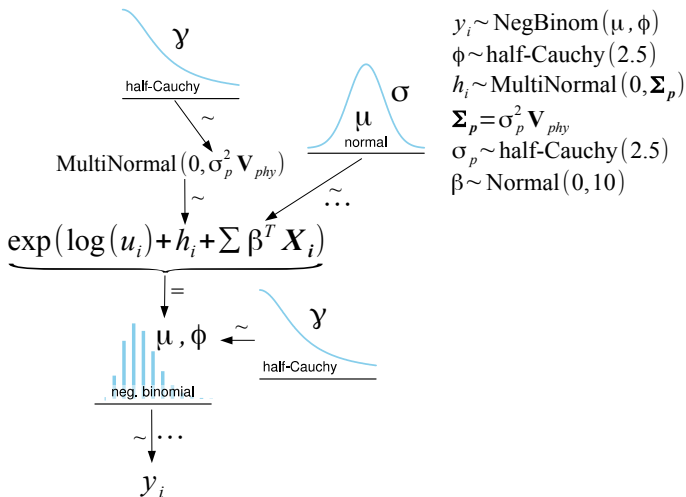
Modeling co-occurrence

Improvement

Poisson assumption $\frac{Var[y]}{E[y]} = 1$.

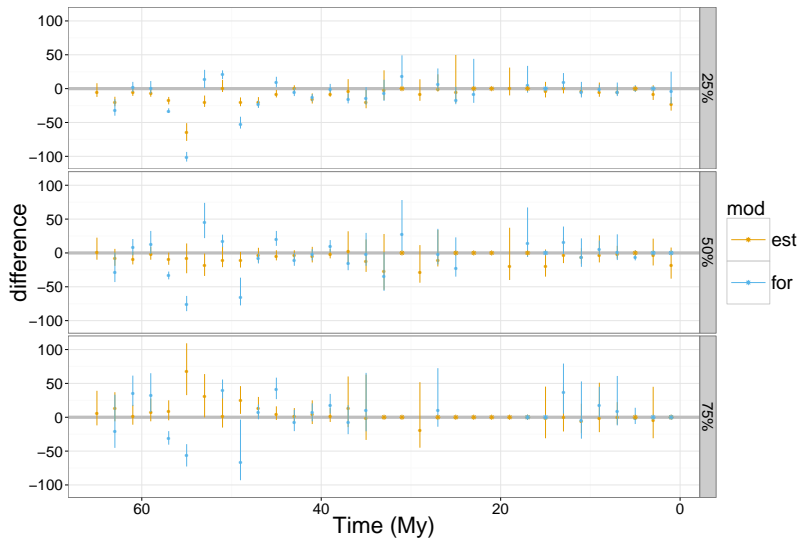
Relax assumption by modeling overdispersion ϕ .

Species co-occurrence model redux

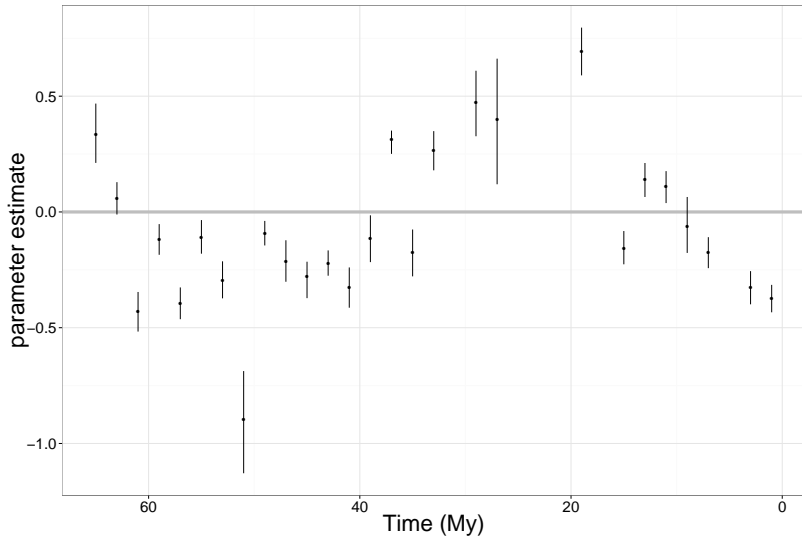


Model adequacy

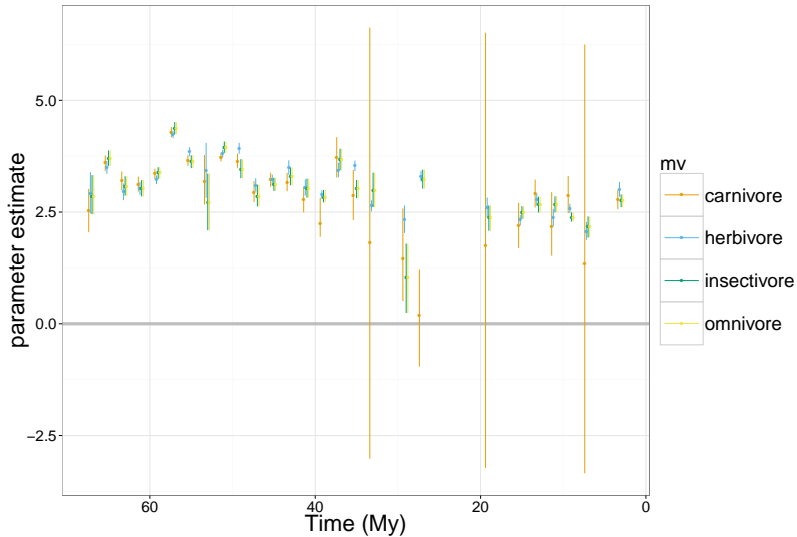
Forward prediction



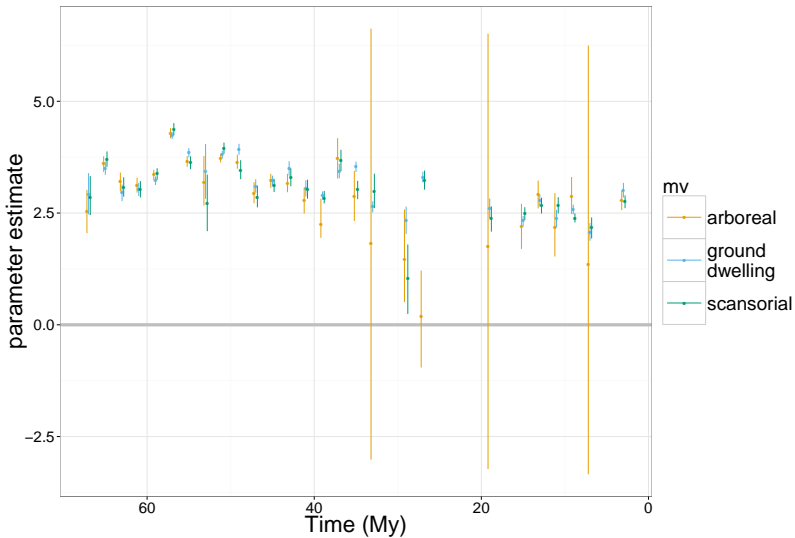
Mass effect



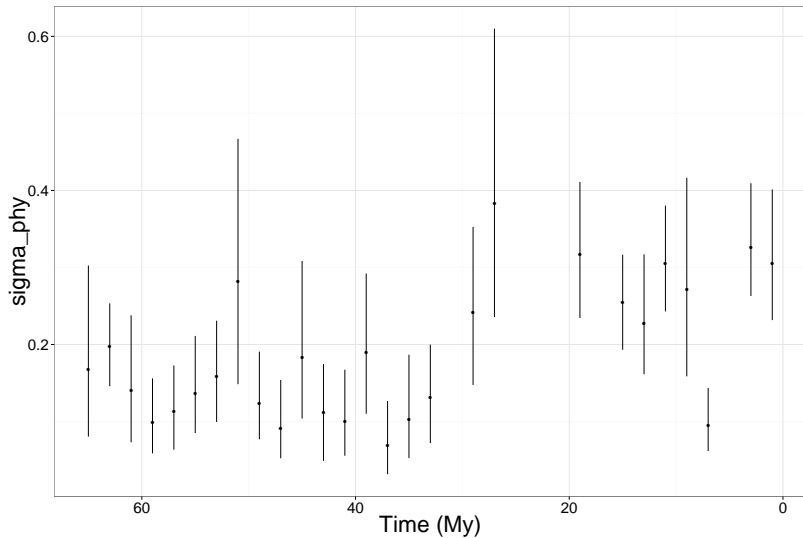
Diet effect



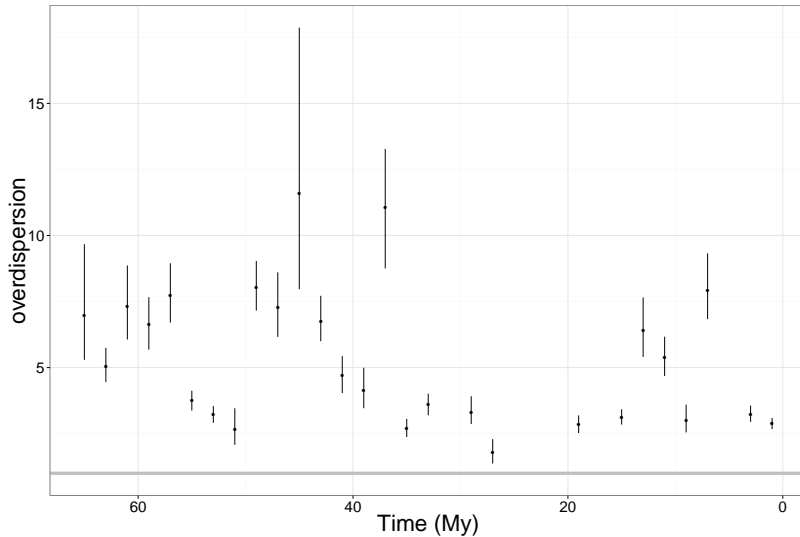
Locomotor effect



Phylogeny



Overdispersion



Modeling locality diversity

Assumption and setup

y_i : # species at locality i per # of species (offset).

y_i drawn from Poisson (or Negative Binomial) distribution.

Localities are from non-uniform lattice (areal units).

Definition

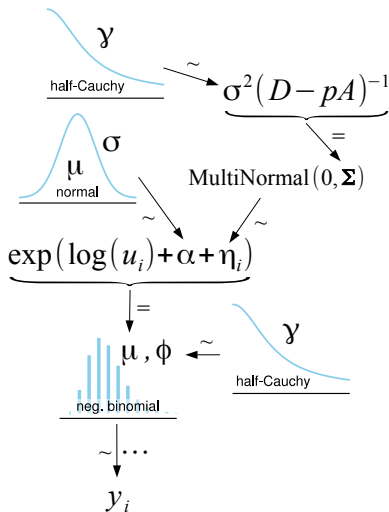
Autoregressive prior; spatial effect drawn from multivariate normal.

$$s \sim \mathcal{N}(0, \sigma_s^2 (D - pA)^{-1})$$

- ▶ σ_s is variance of spatial effect (size).
- ▶ D is diagonal matrix of neighbor count.
- ▶ A is adjacency matrix of localities.
- ▶ p is “strength” of spatial effect.

Assorted problems regarding propriety. See Banerjee *et al.* 2004 book.

Locality diversity model



$$\begin{aligned}
 y_i &\sim \text{NegBinom}(\mu, \phi) \\
 \phi &\sim \text{half-Cauchy}(2.5) \\
 \alpha &\sim \text{Normal}(0, 10) \\
 \eta_i &\sim \text{MultiNormal}(\vec{0}, \Sigma) \\
 \Sigma &= \sigma^2(D - pA)^{-1} \\
 \sigma &\sim \text{half-Cauchy}(2.5)
 \end{aligned}$$