

# Metacommunities, assembly, $\alpha$ and $\gamma$

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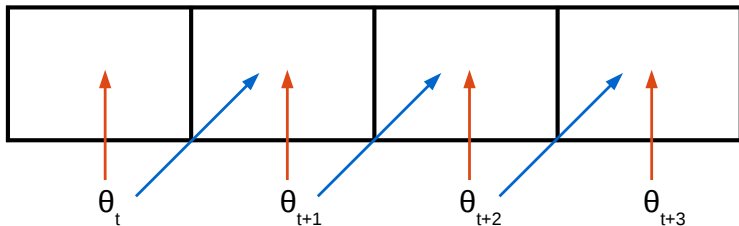
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# Species distribution across multiple localities

## 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?

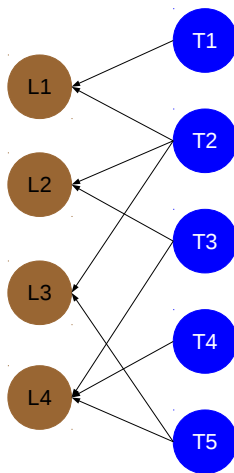
# Analysis framework



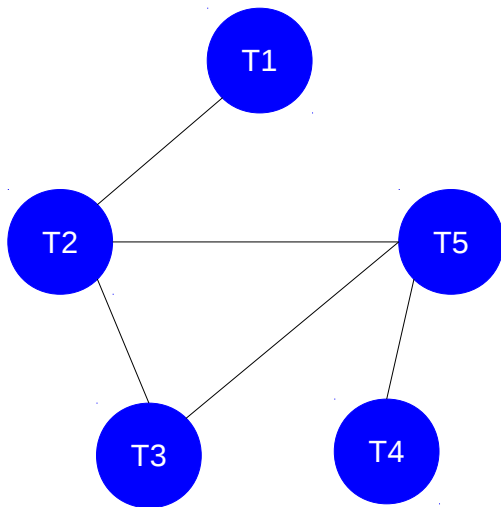
# System

- ▶ 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

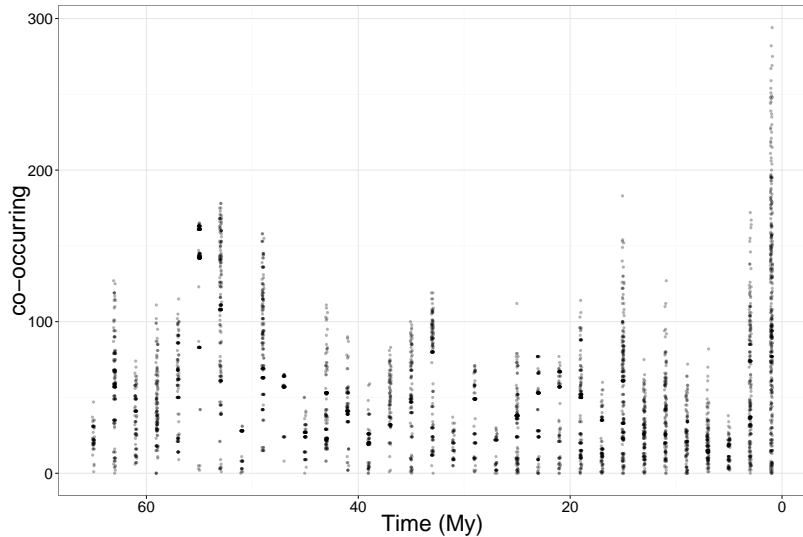
# Bipartite network



## One-mode network



# Co-occurrences



# 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

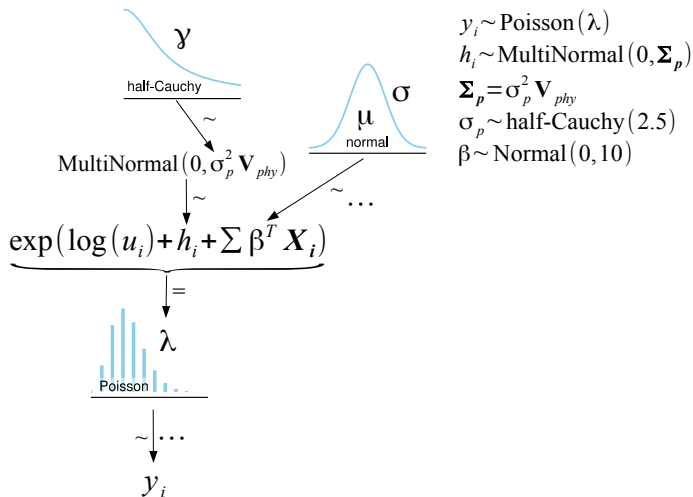
Assuming Brownian motion, effect drawn from multivariate normal distribution.

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

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

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

# Species co-occurrence model



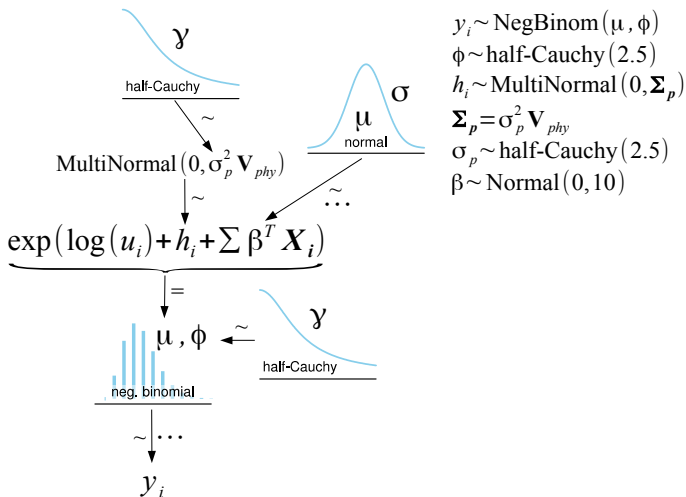
# Modeling co-occurrence

## Improvement

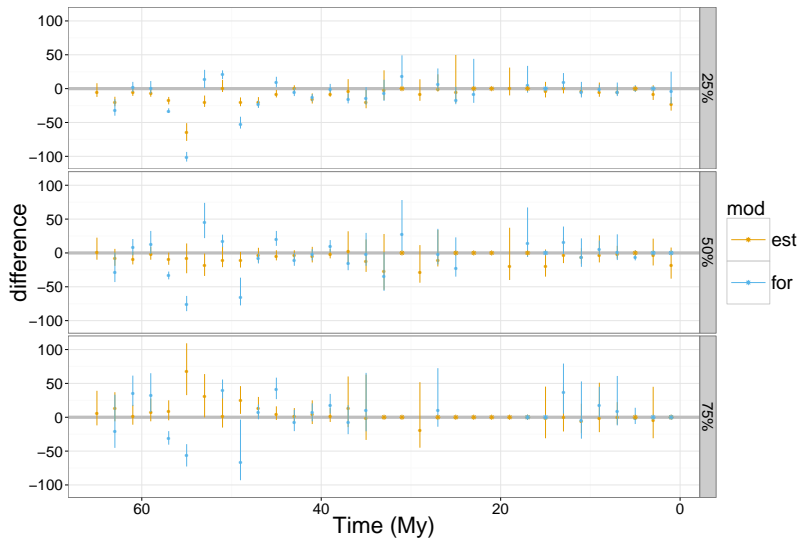
Poisson assumption  $\frac{Var[y]}{E[y]} = 1$ .

Relax assumption by modeling overdispersion  $\phi$ .

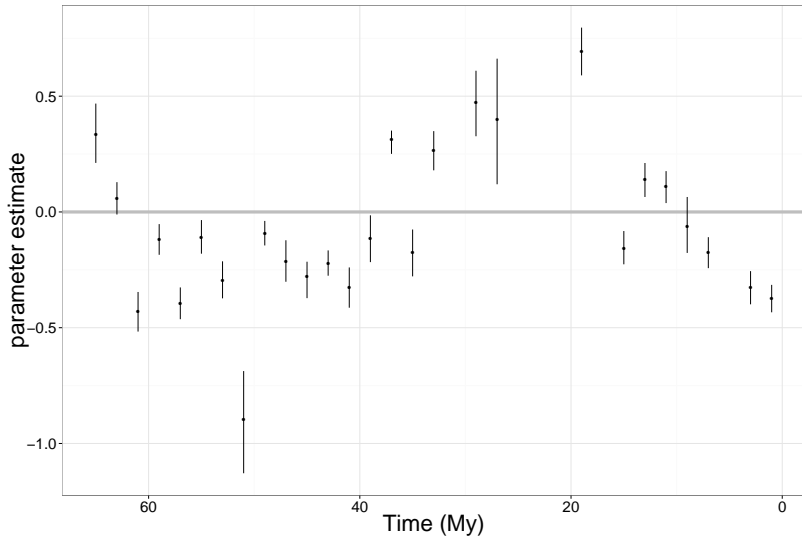
# Species co-occurrence model redux



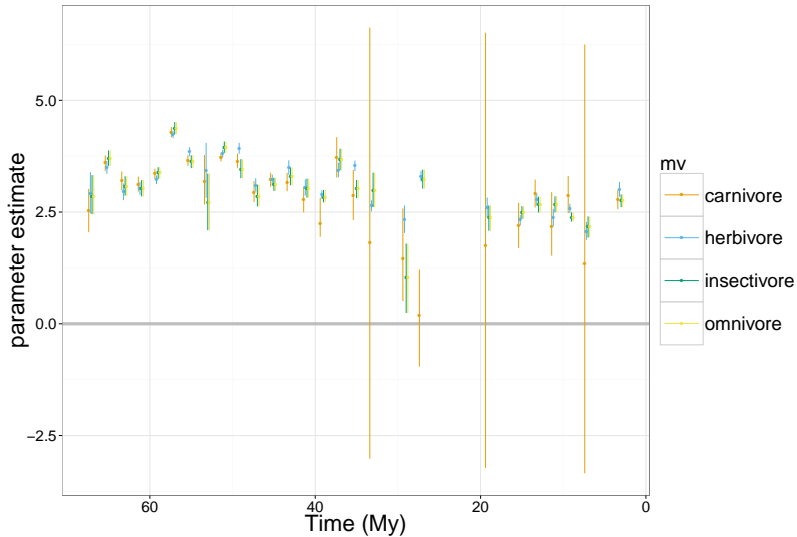
# Forward prediction



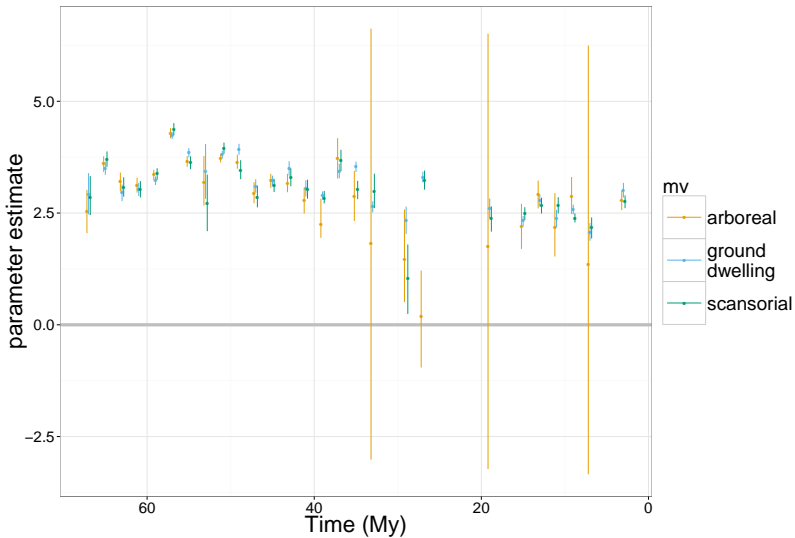
# Mass effect



# Diet effect

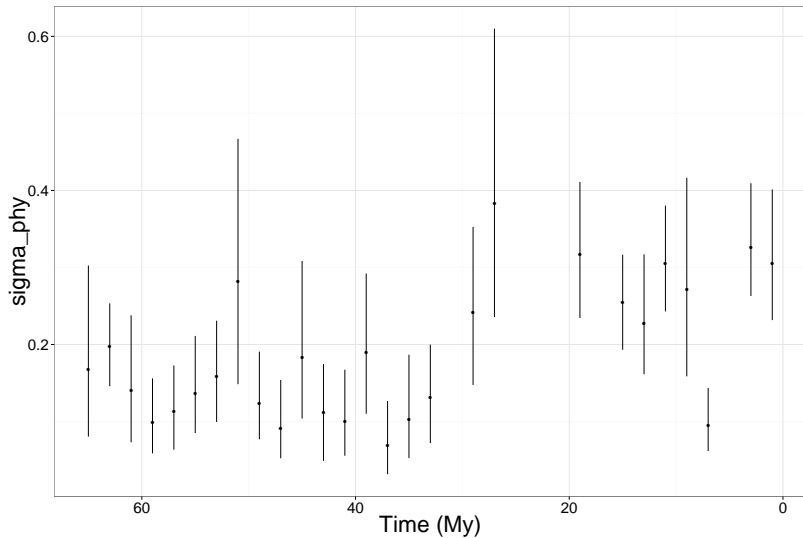


# Locomotor effect

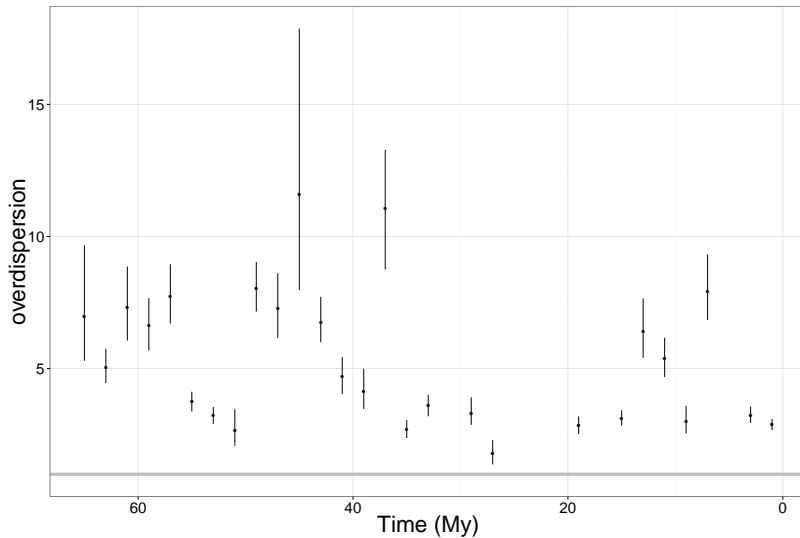




# Phylogeny



# 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

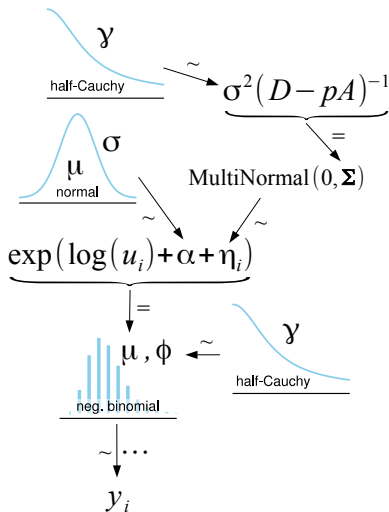
Autoregressive prior; spatial effect drawn from multivariate normal.

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

- ▶  $\sigma_s$  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



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