Metacommunities, assembly, α and γ

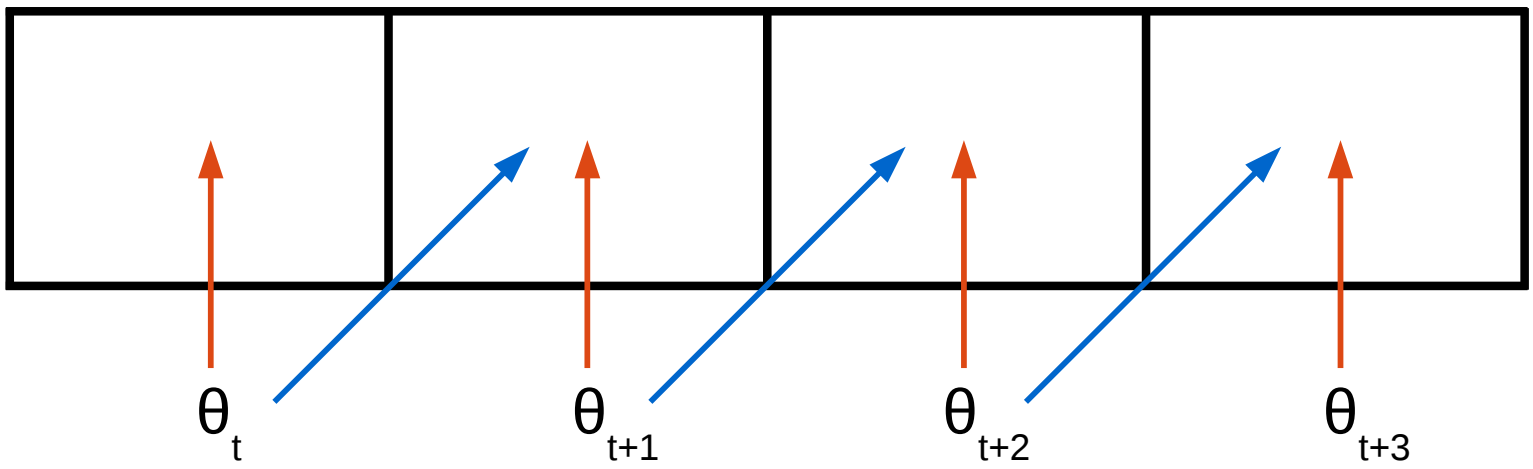
February 13, 2015

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?

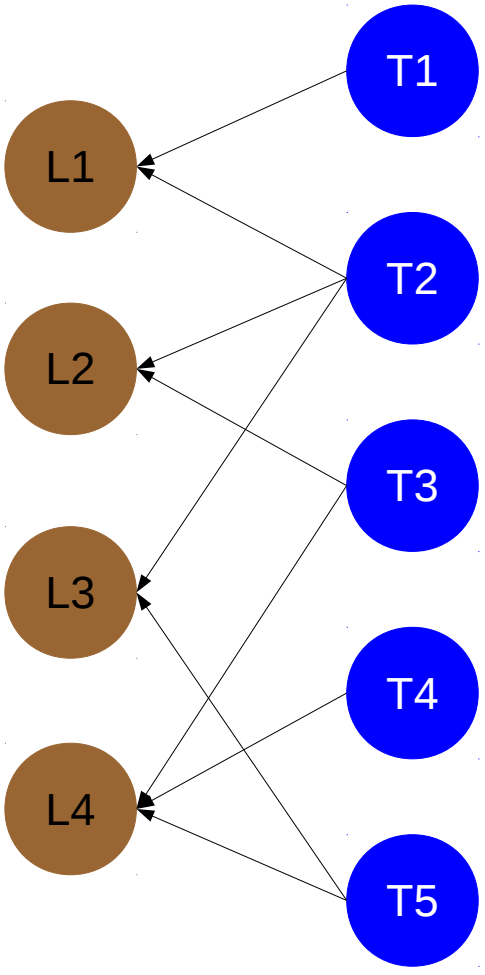
Analysis framework



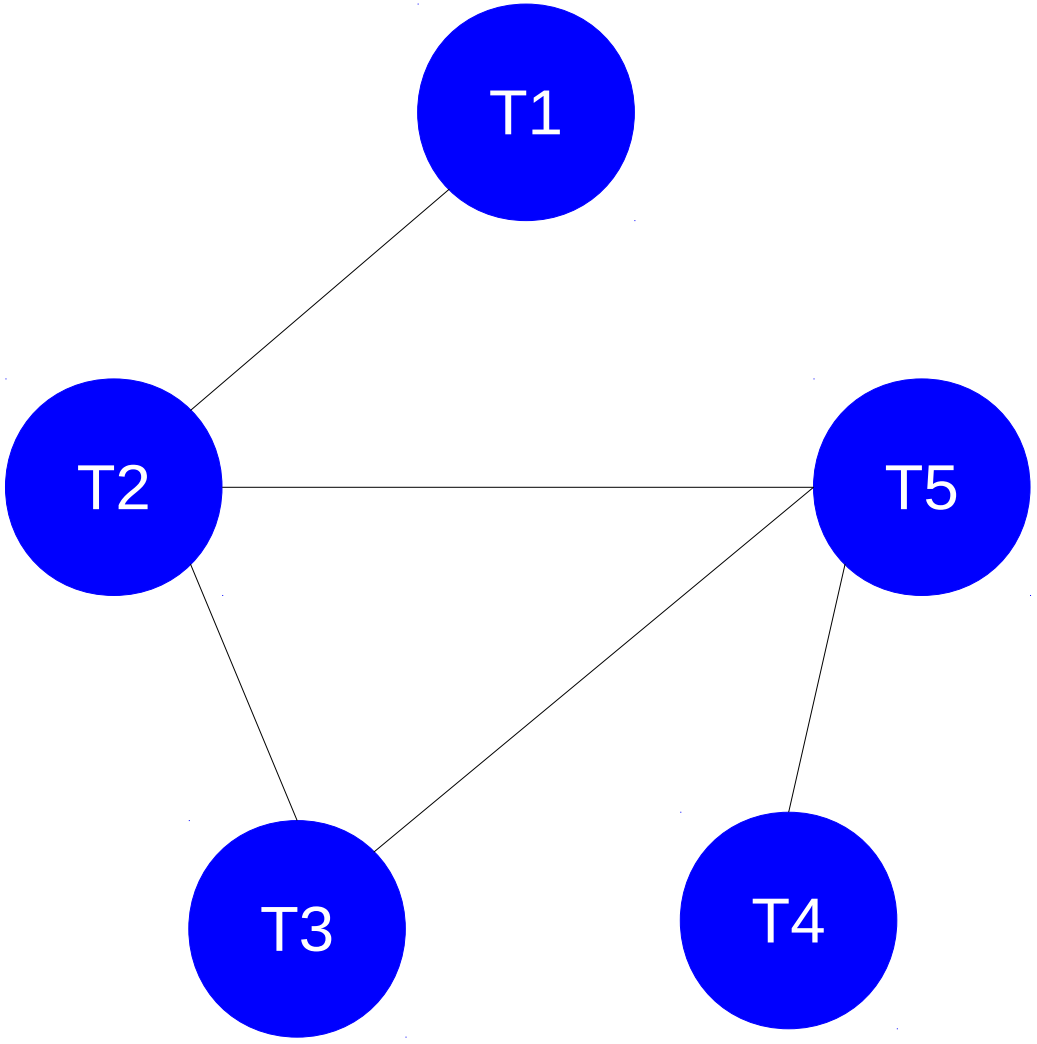
System

- Record
  - North American Cenozoic
  - 2 My bins
- Units
  - mammal species
  - 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

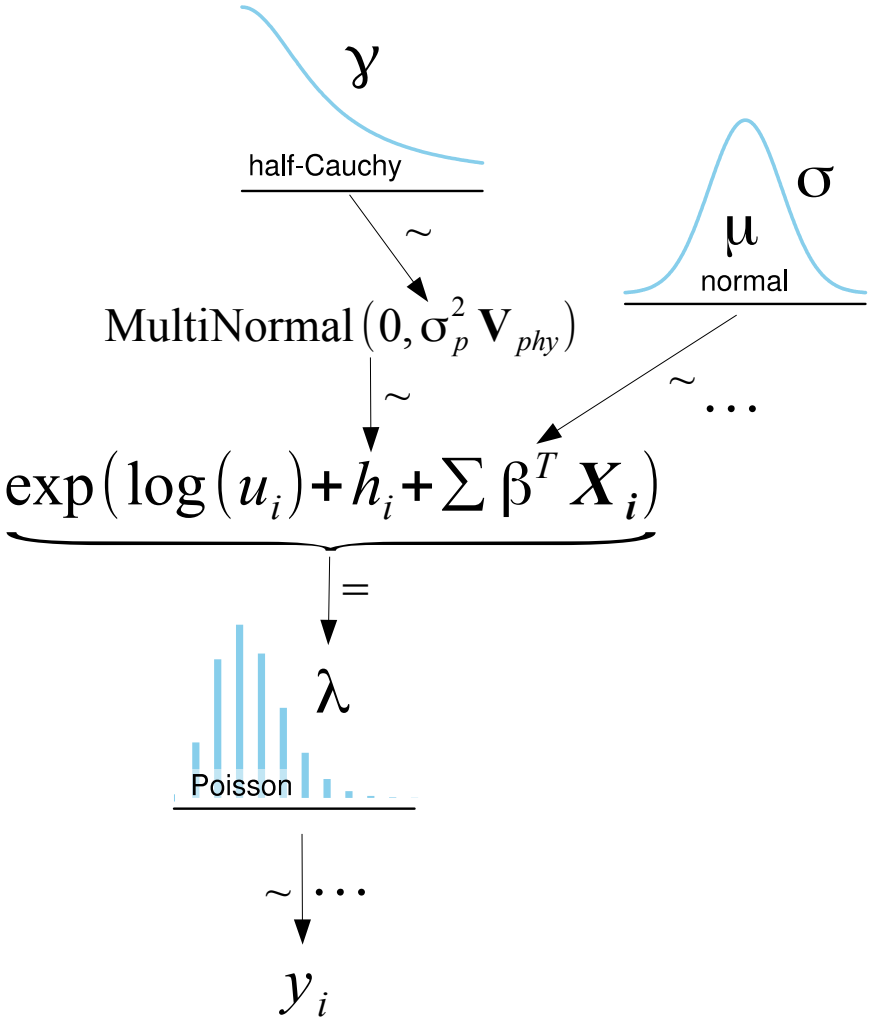
Assuming Brownian motion, effect drawn from multivariate normal distribution.

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

- 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



$$y_i \sim \text{Poisson}(\lambda)$$
$$h_i \sim \text{MultiNormal}(0, \boldsymbol{\Sigma}_p)$$
$$\boldsymbol{\Sigma}_p = \sigma_p^2 \mathbf{V}_{phy}$$
$$\sigma_p \sim \text{half-Cauchy}(2.5)$$
$$\beta \sim \text{Normal}(0, 10)$$

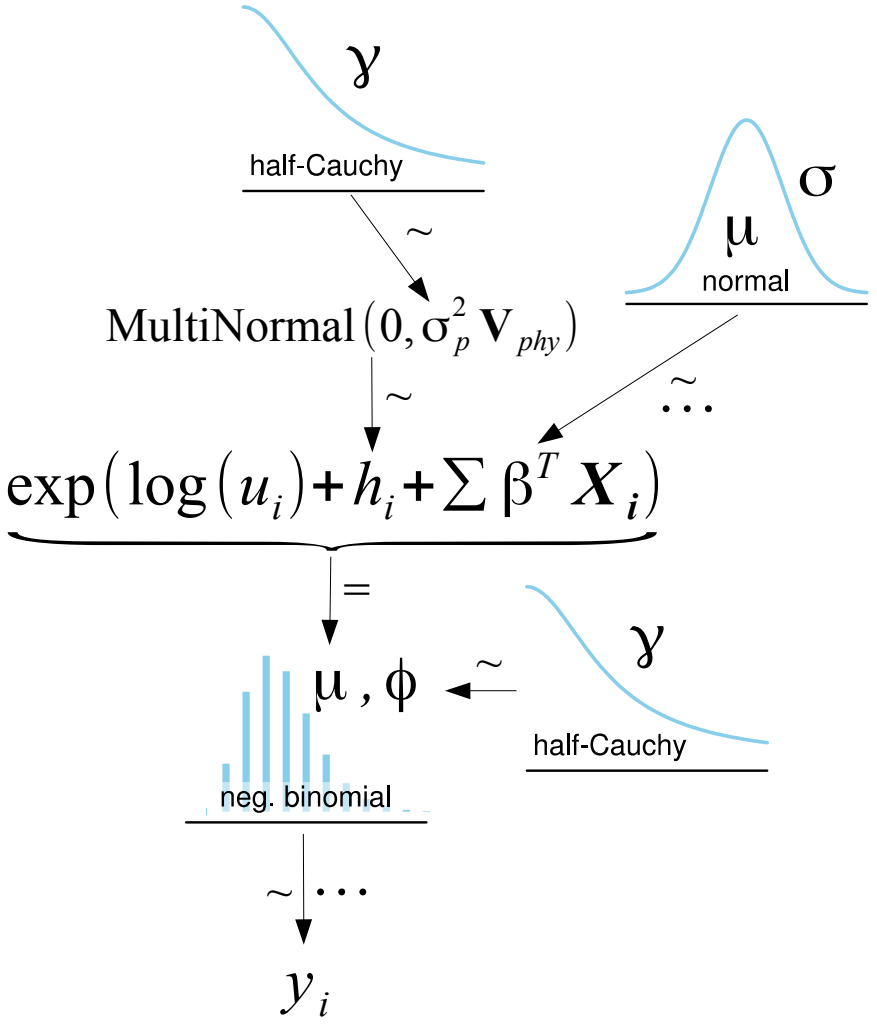
Modeling co-occurrence

Improvement

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

Relax assumption by modeling overdispersion ϕ.

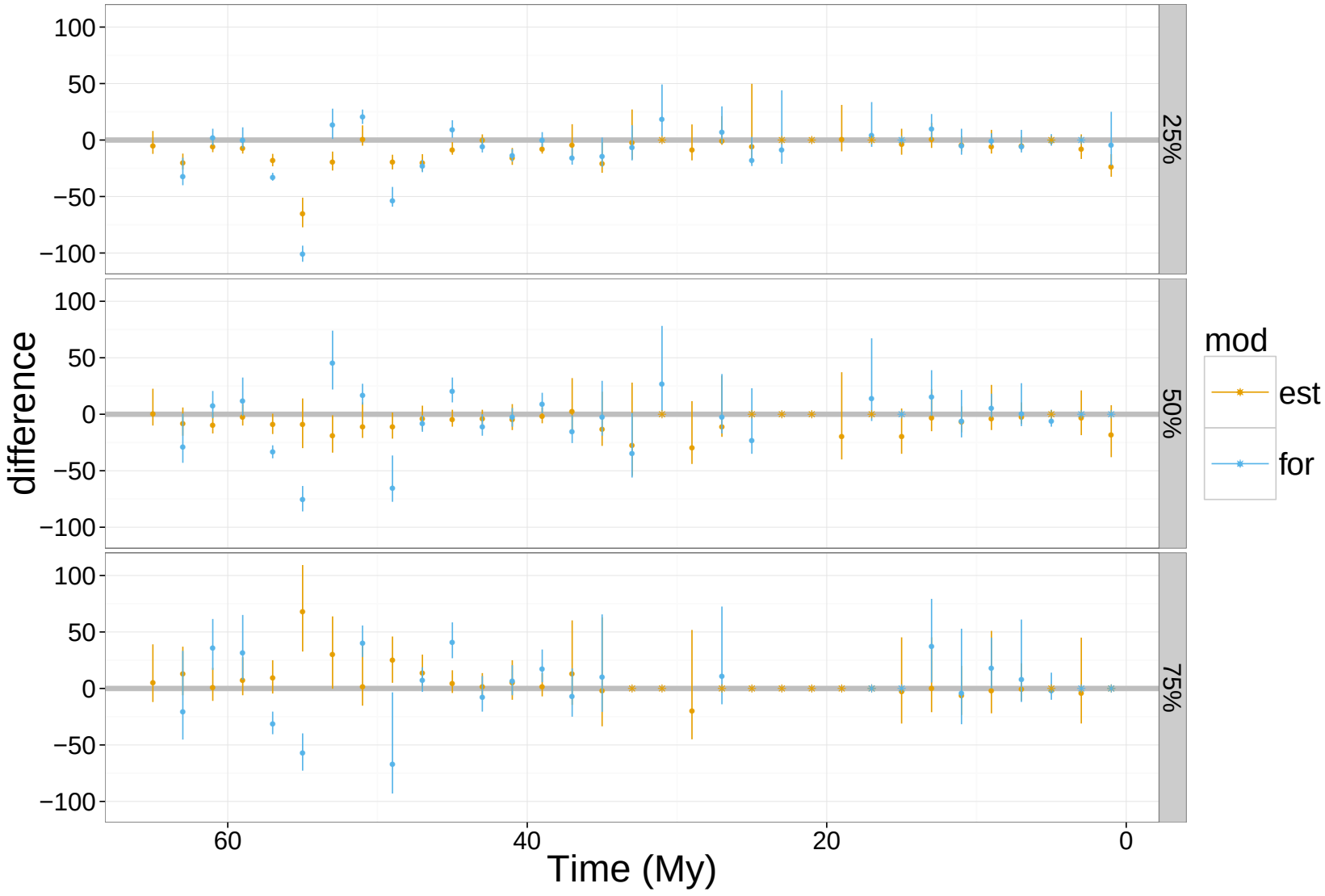
Species co-occurrence model redux



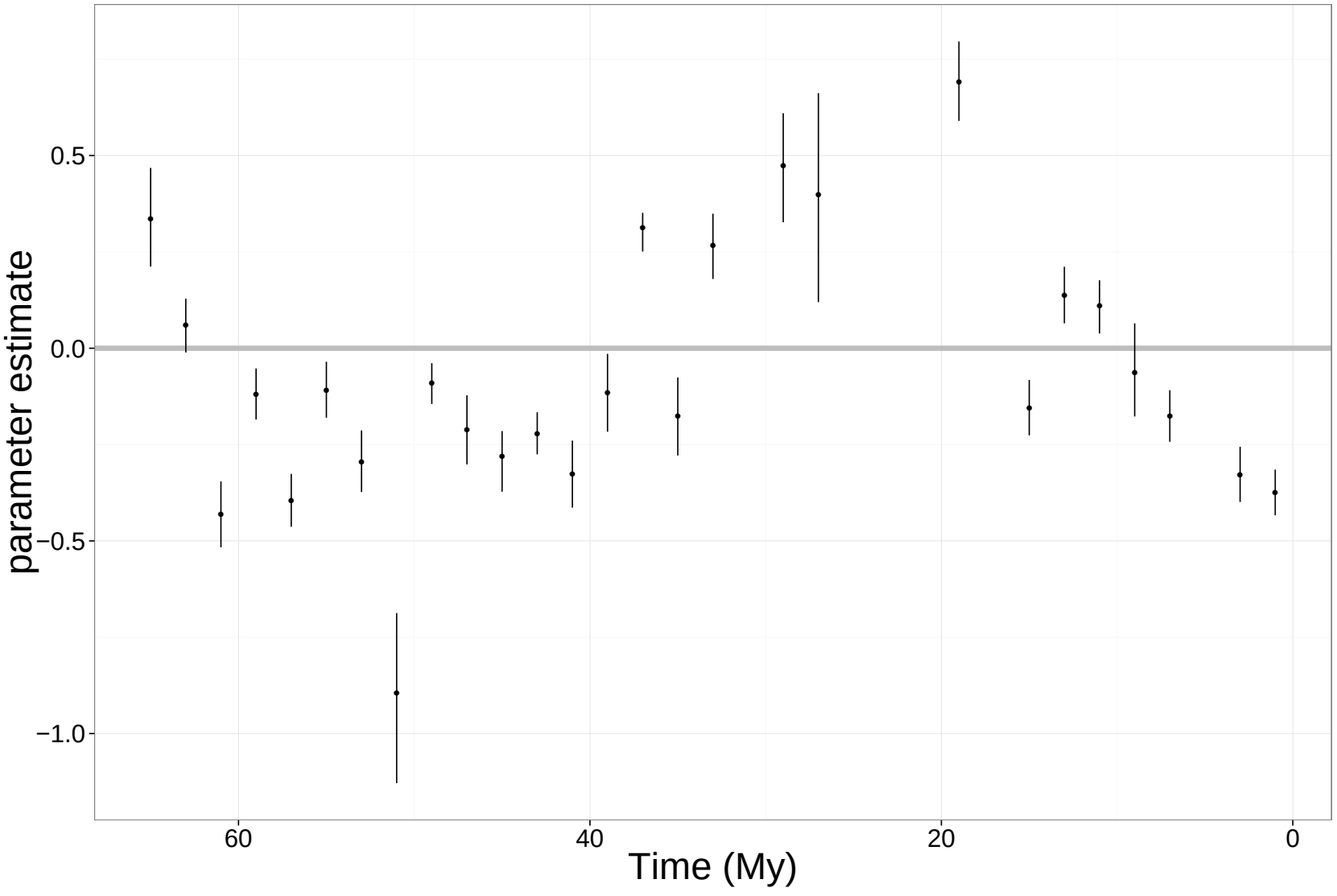
$$y_i \sim \text{NegBinom}(\mu, \phi)$$
$$\phi \sim \text{half-Cauchy}(2.5)$$
$$h_i \sim \text{MultiNormal}(0, \boldsymbol{\Sigma_p})$$
$$\boldsymbol{\Sigma_p} = \sigma_p^2 \mathbf{V}_{phy}$$
$$\sigma_p \sim \text{half-Cauchy}(2.5)$$
$$\beta \sim \text{Normal}(0, 10)$$

Model adequacy

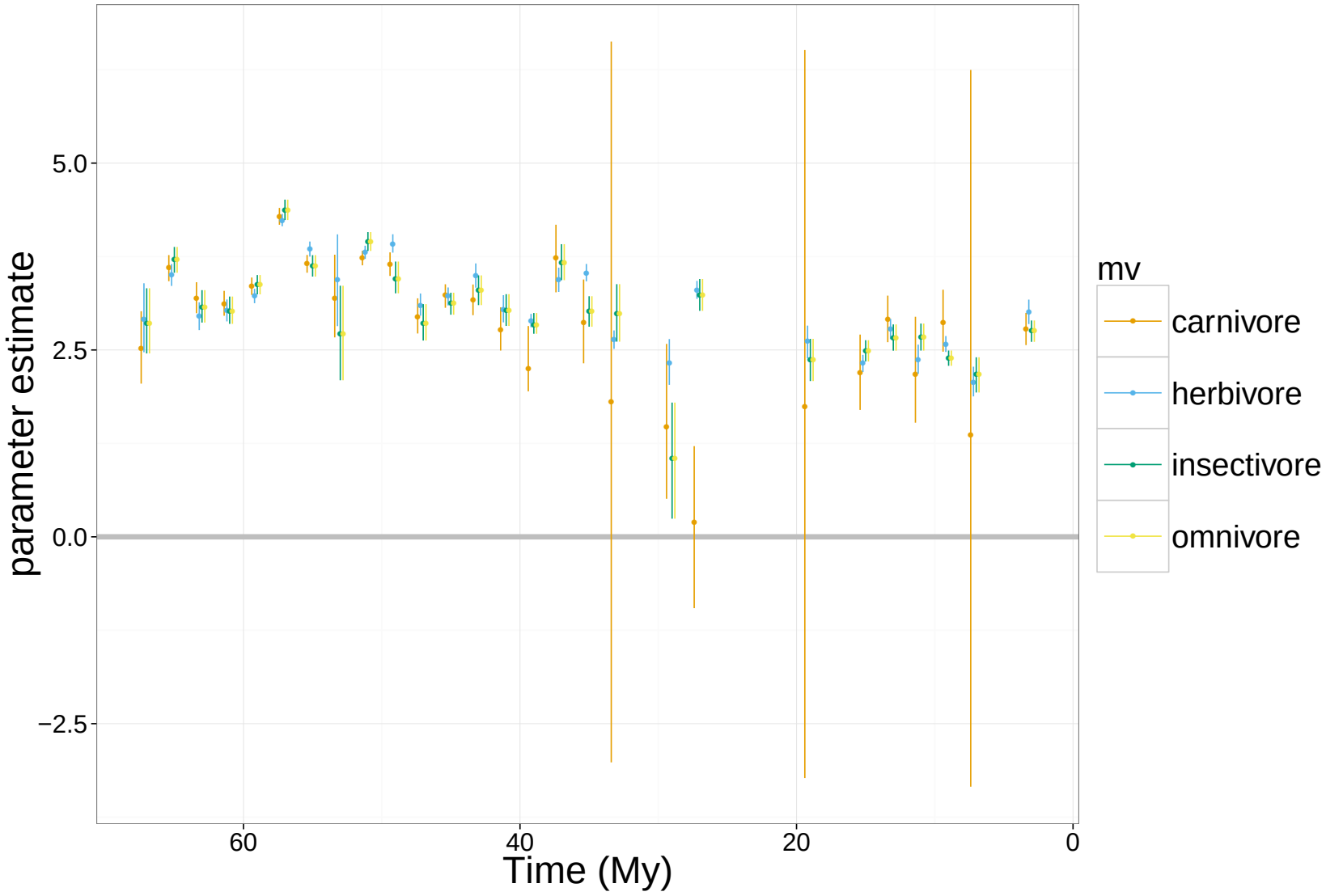
Forward prediction



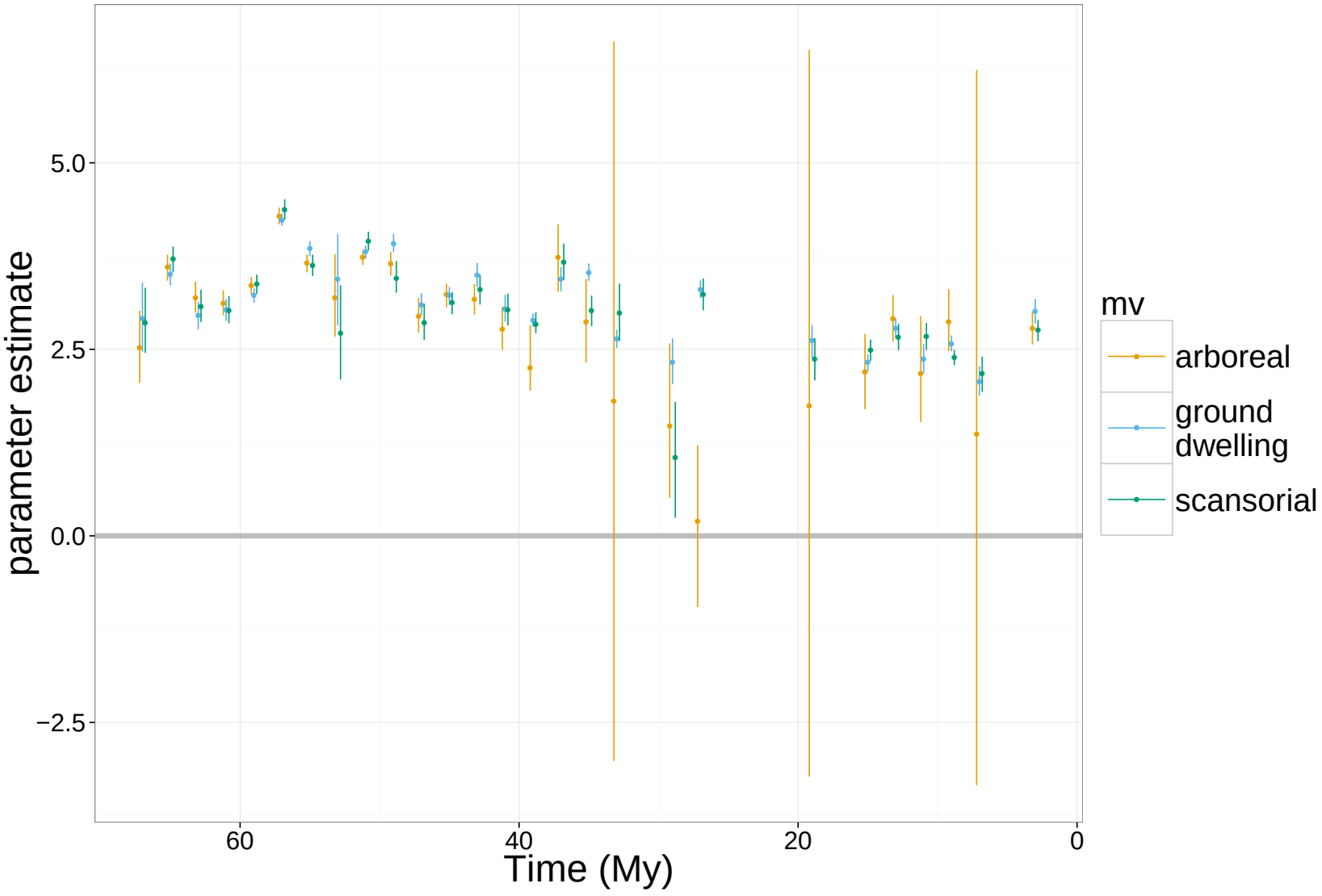
Mass effect



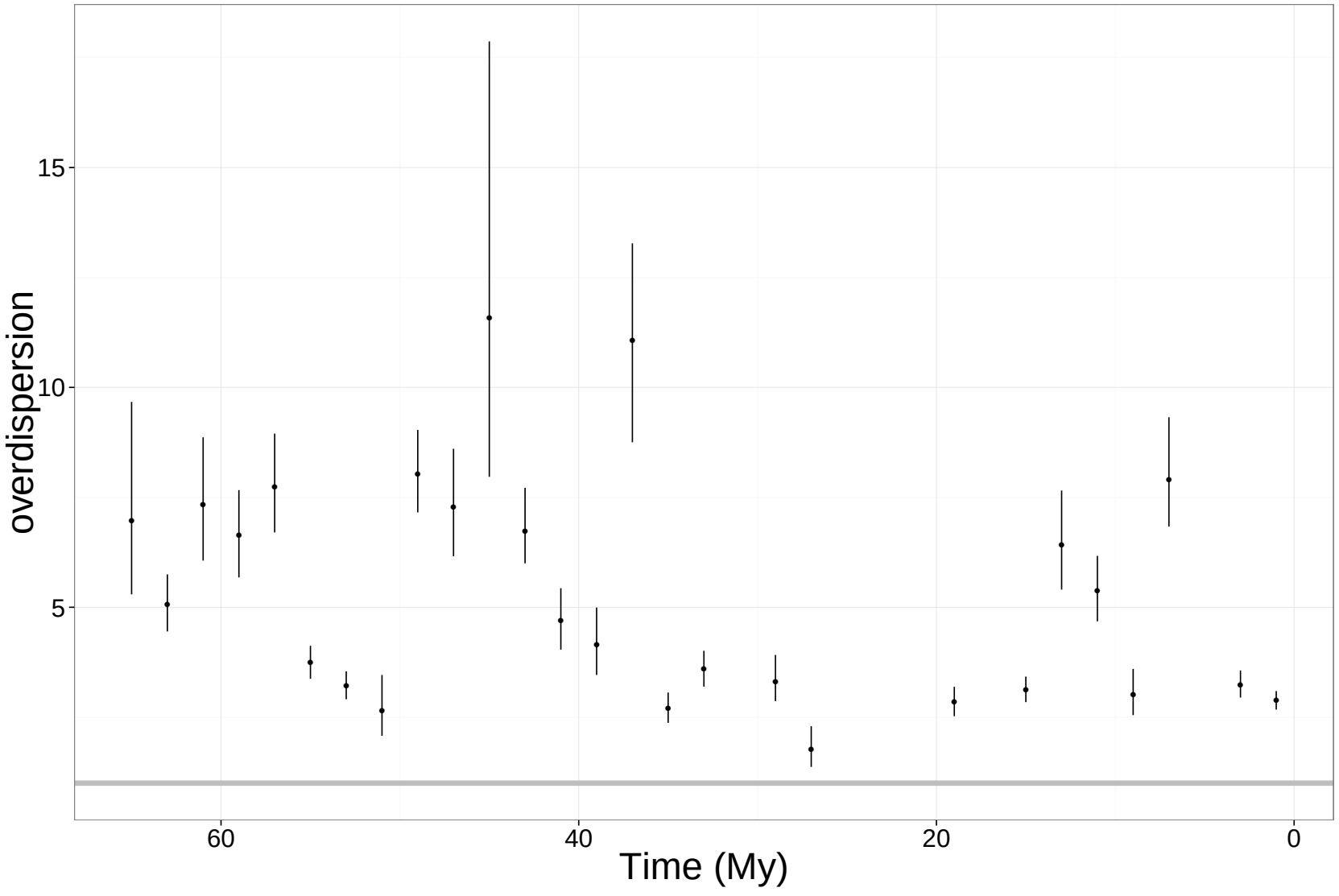
Diet effect


parameter estimate
5.0
2.5
0.0
−2.5
60
40
20
0
Time (My)
mv
carnivore
herbivore
insectivore
omnivore

Locomotor effect



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).

Spatial effect

Definition

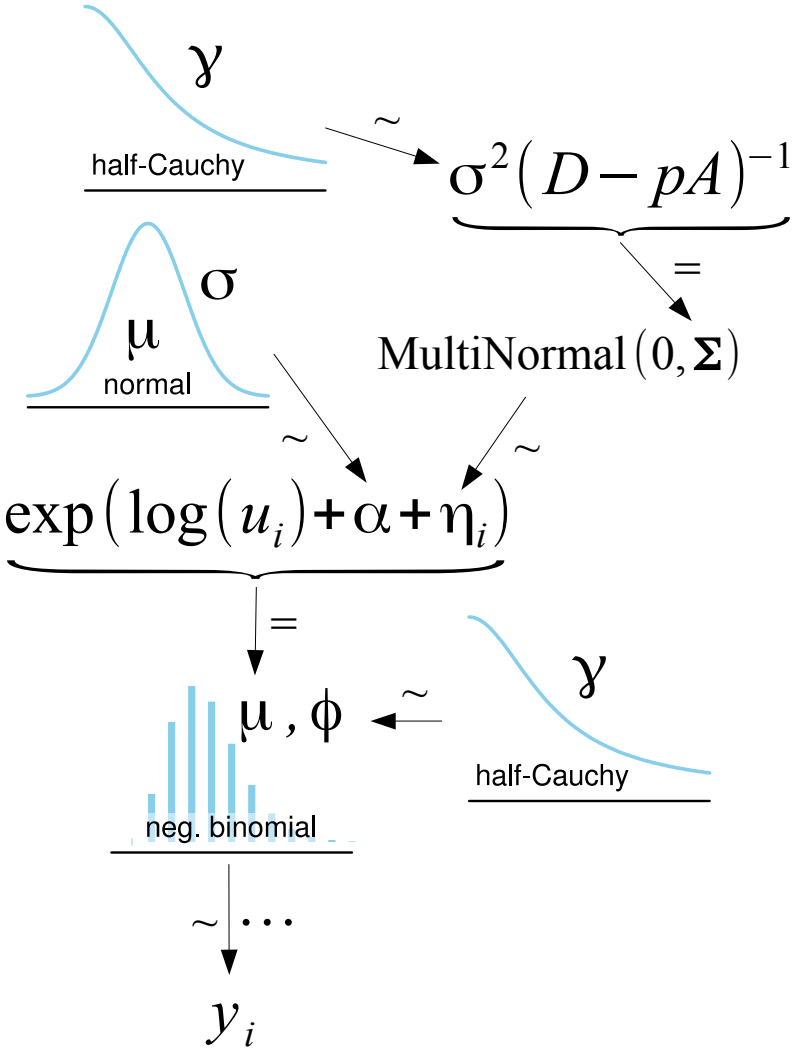
Autoregressive prior; spatial effect drawn from multivariate normal.

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

- 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.

Bunch of assorted problems regarding propriety. See Banerjee *et al.* 2004 book.

Locality diversity model



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