Talks

- Evolution 2014: basic comparison between NA and European mammal survival
- GSA 2014: current fully Bayesian model of brachiopod survival
  - lots of positive feedback, ideas

Travel and grants

- AMNH: tooth measures for all notoungulate specimens identified to species level
- DDIG: applied; travel to Argentina; collaboration with Rick Madden

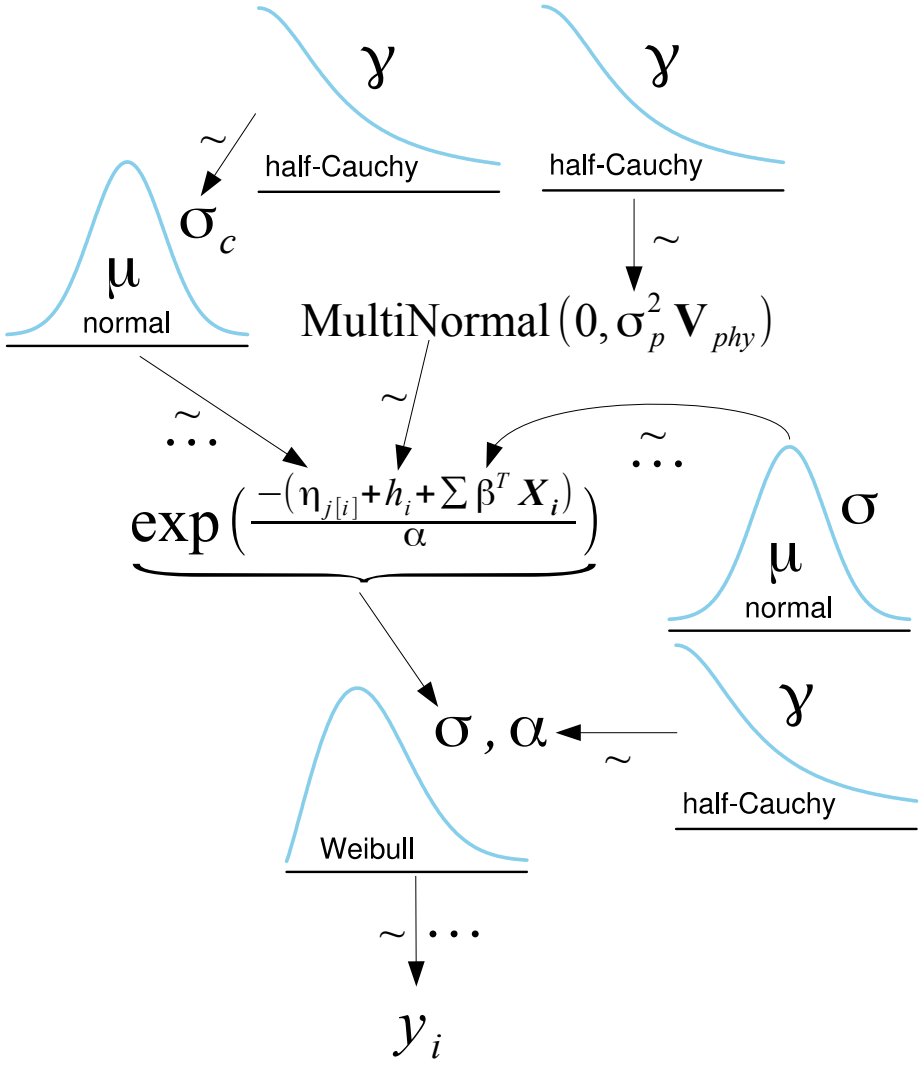
Death and taxa: time invariant differences in species duration

North American survival

- species duration as measure of survival
- traits
  - organismal: diet, locomotor categories
  - species: body size, bioprovince occupancy
- origination cohort
- phylogeny primarily based on taxonomy

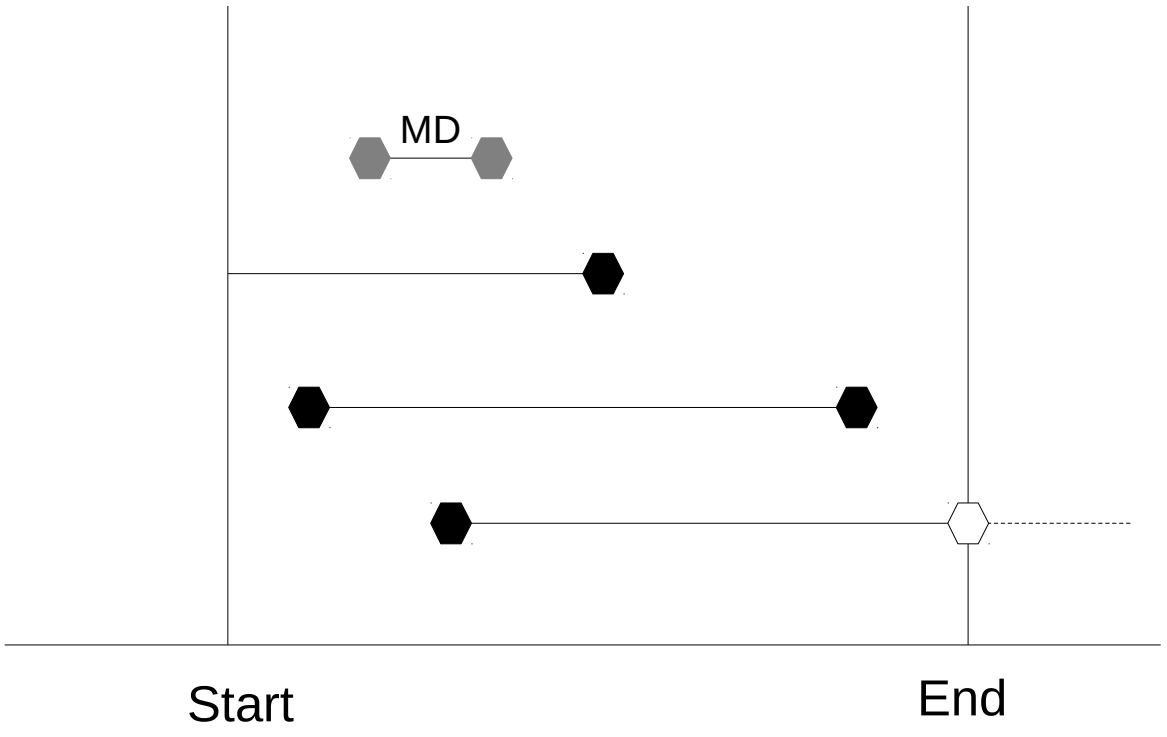
- duration defined as number of 2My bins from FAD to LAD, inclusive
- fully Bayesian hierarchical model
- censoring approach
  - if still extant, right censored
  - if not extant and duration of only 1 bin, left censored

Model diagram



$$y_i \sim \text{Weibull}(\sigma, \alpha)$$
$$\eta_{j[i]} \sim \text{Normal}(0, \sigma_c)$$
$$\sigma_c \sim \text{half-Cauchy}(2.5)$$
$$h_i \sim \text{MultiNormal}(0, \Sigma)$$
$$\Sigma = \sigma_p^2 \mathbf{V}_{phy}$$
$$\sigma_p \sim \text{half-Cauchy}(2.5)$$
$$\beta \sim \text{Normal}(0, 10)$$
$$\alpha \sim \text{half-Cauchy}(2.5)$$

Censoring



Modeling censored observations

Definition

$$S(t|\alpha,\sigma) = \exp\left(-\left(\frac{t}{\sigma}\right)^{\alpha}\right)$$

Right censored evaluated at $S(t)$, left at $1 - S(t)$.

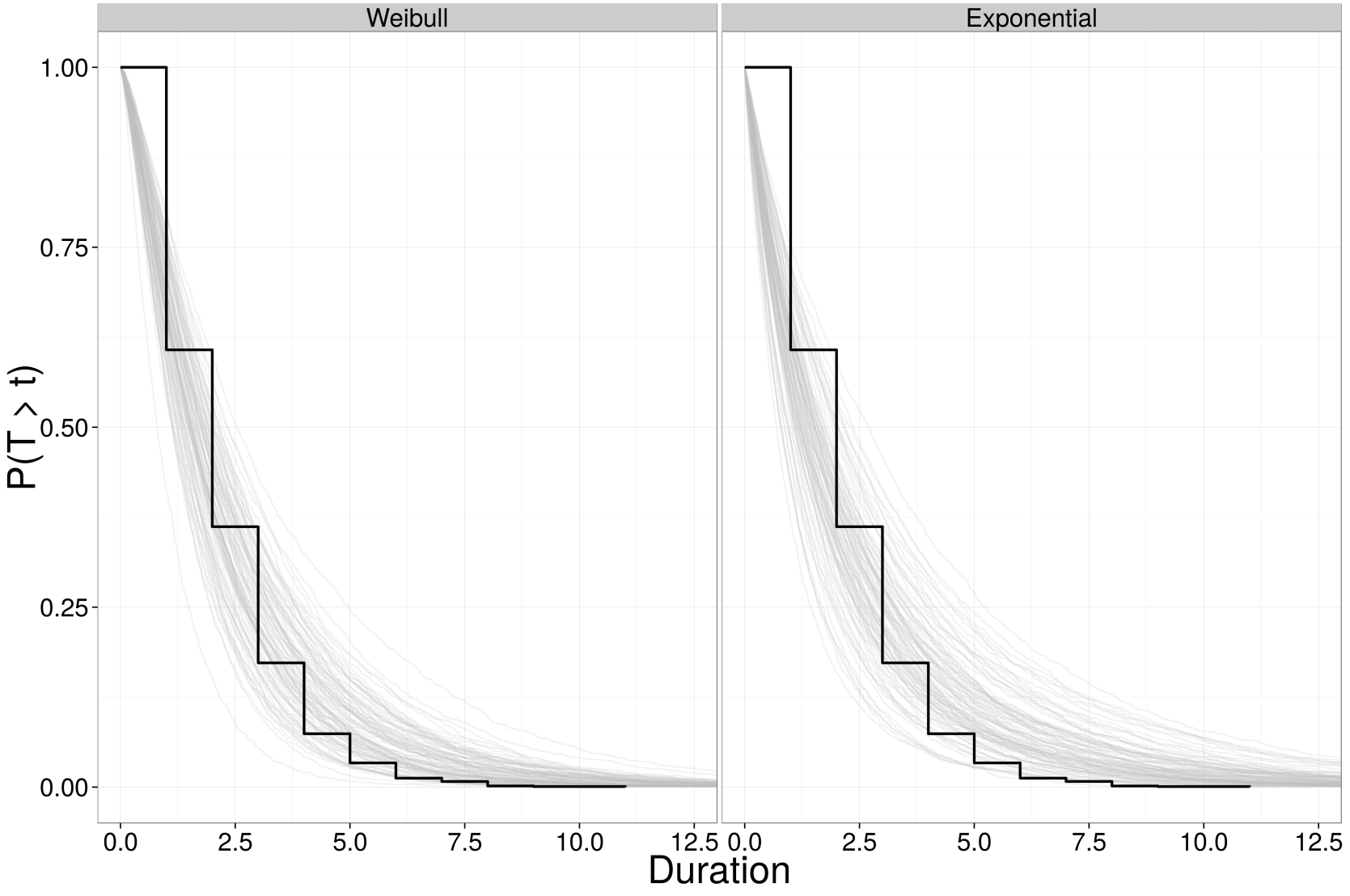
Equivalent to ccdf and cdf respectively.

Modeling censored observations

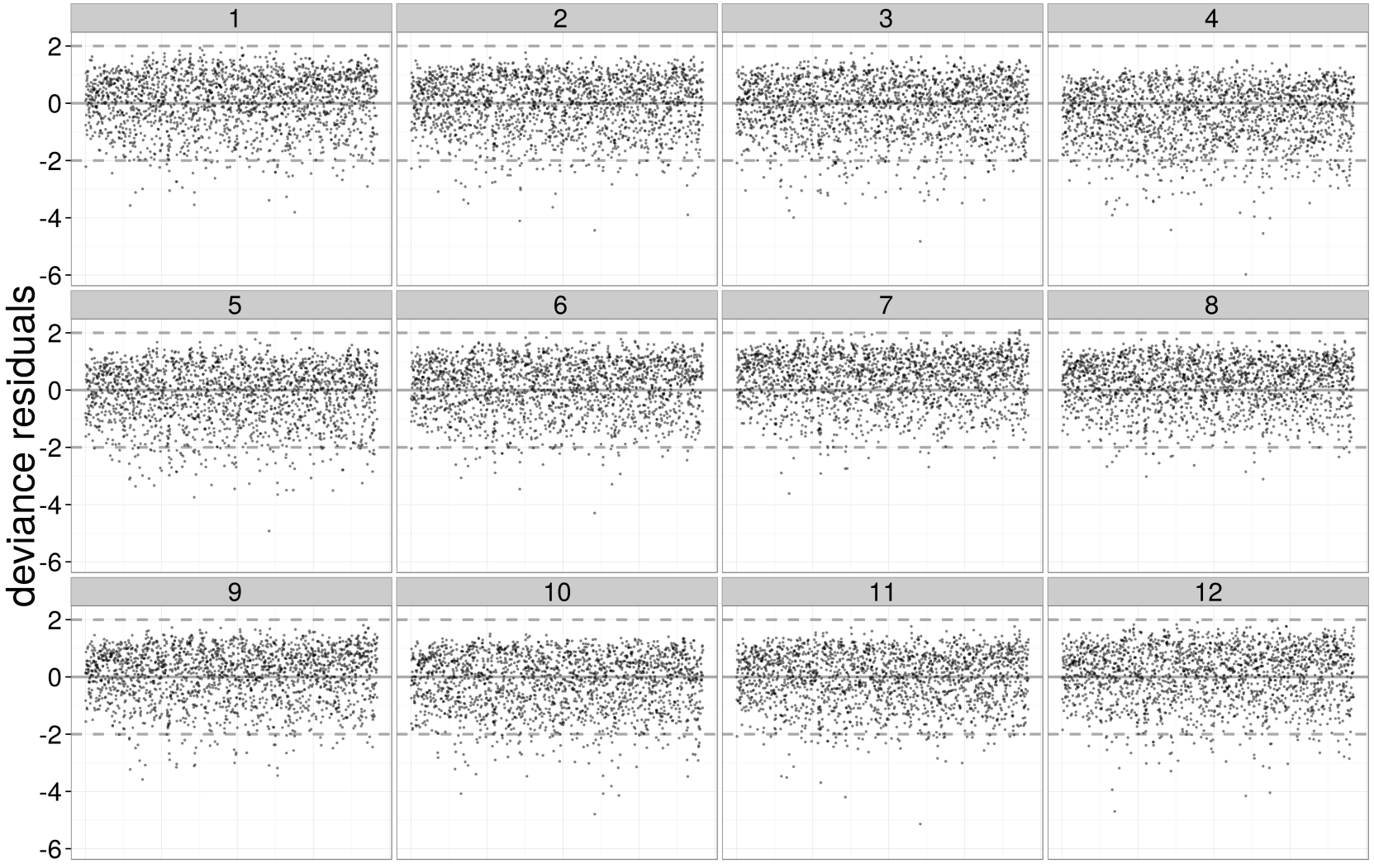
Likelihood

$$L \propto \prod_{i \in C} \text{Weibull}(y_i|\alpha, \sigma) \prod_{j \in R} S(y_j|\alpha, \sigma) \prod_{k \in L} (1 - S(y_k|\alpha, \sigma))$$

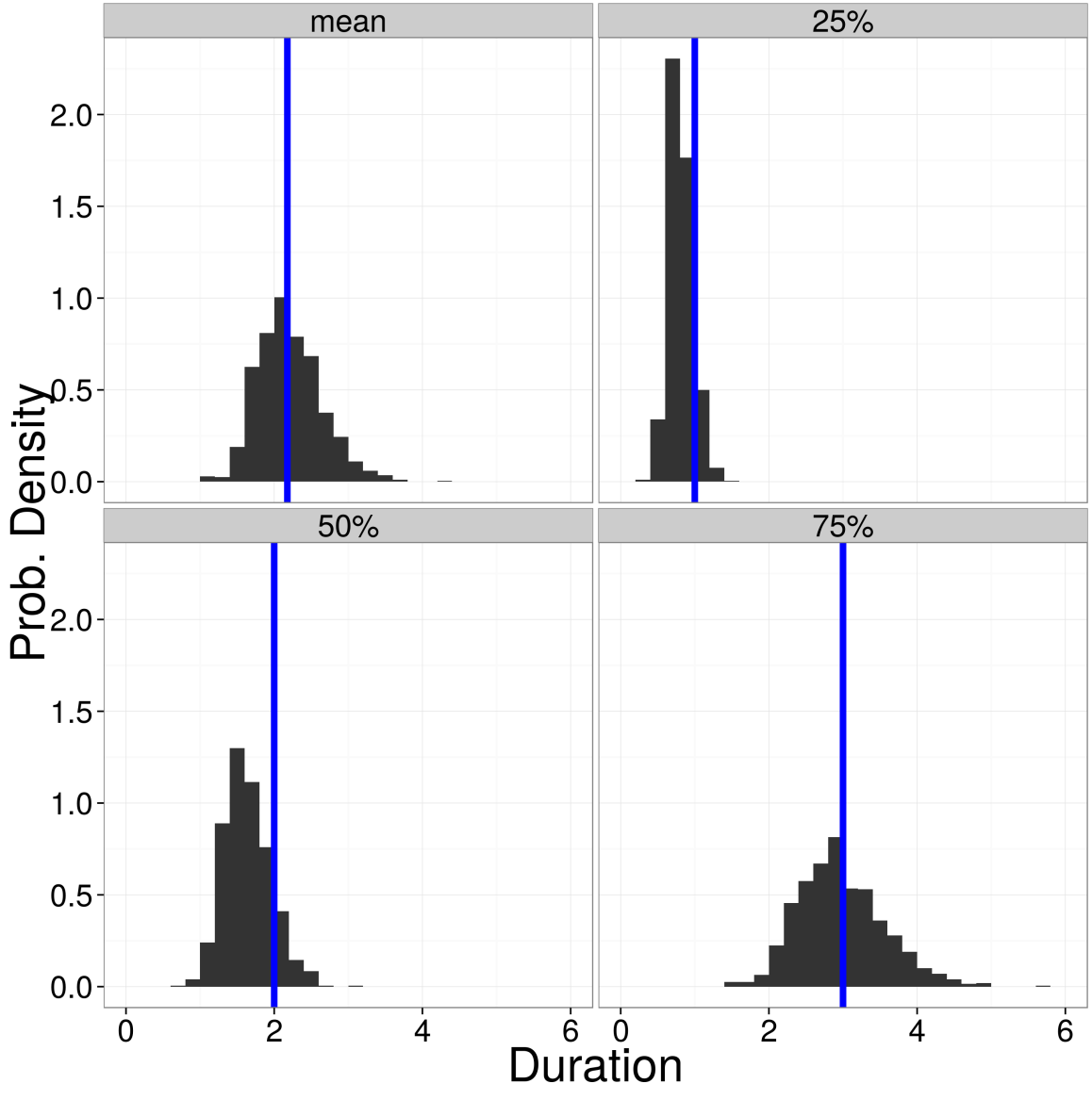
Posterior predictive checks: S(t)



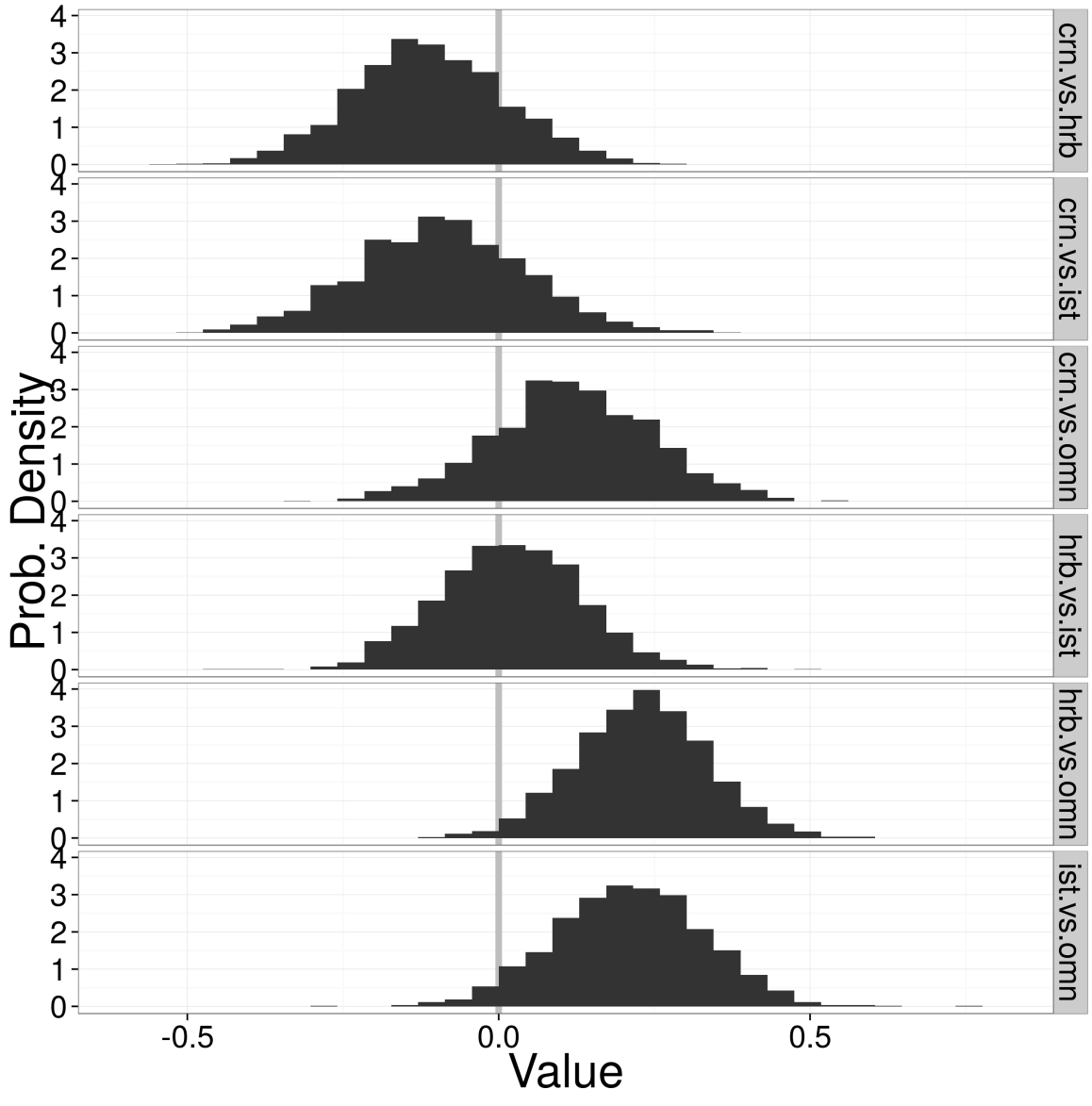
Posterior predictive checks: deviance residuals



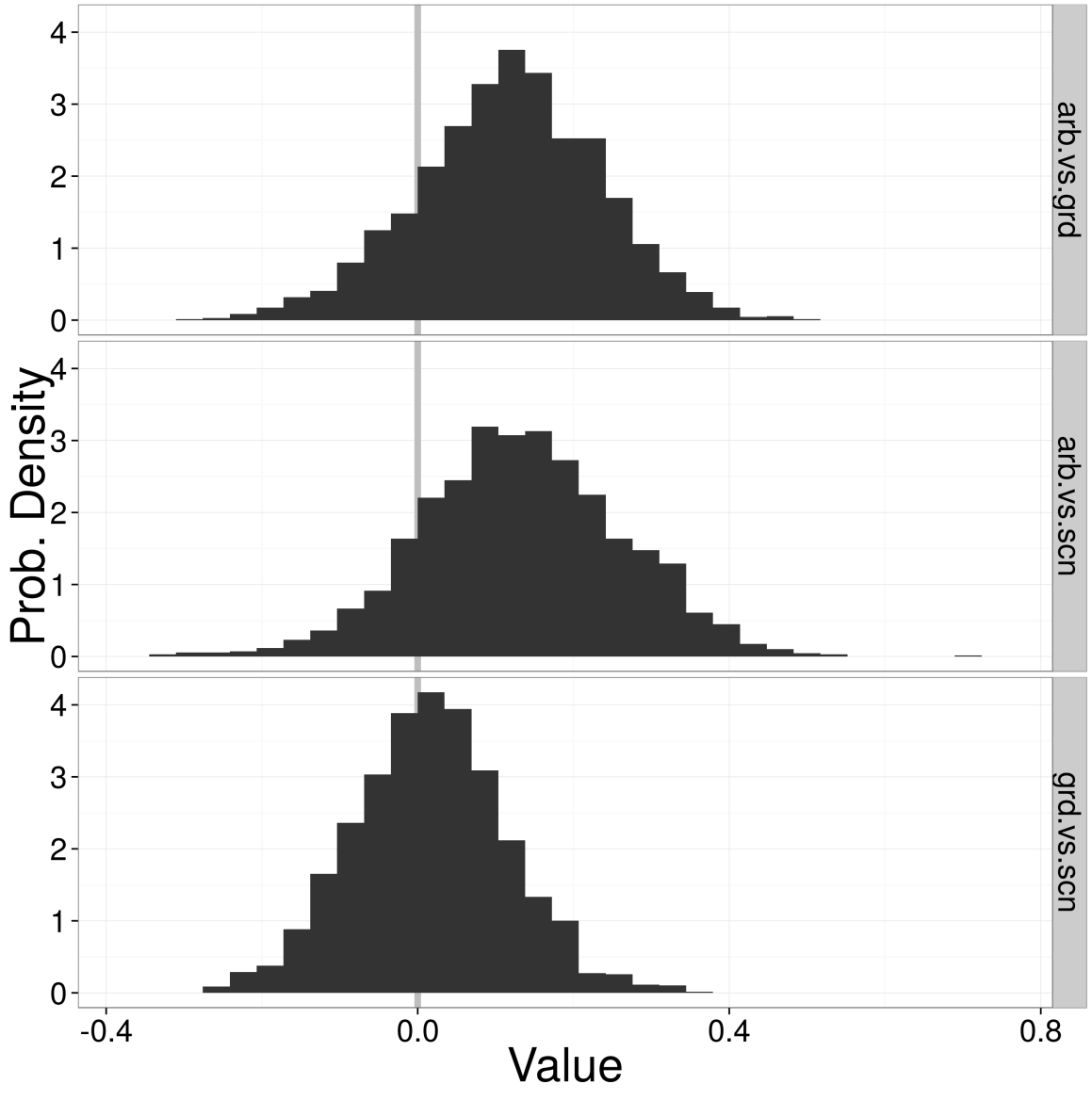
Posterior predictive checks: point checks



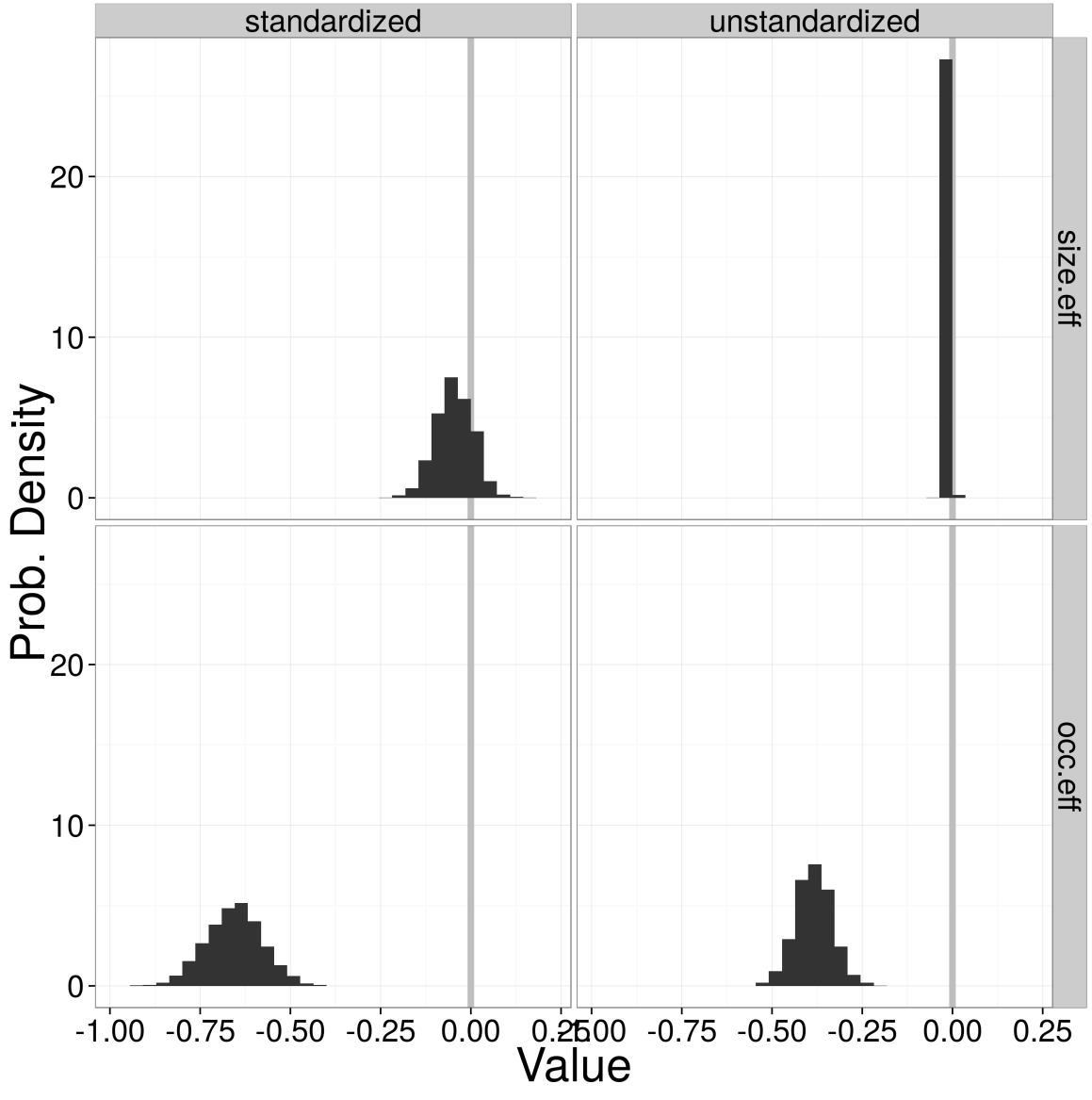
Pairwise differences of β, dietary category



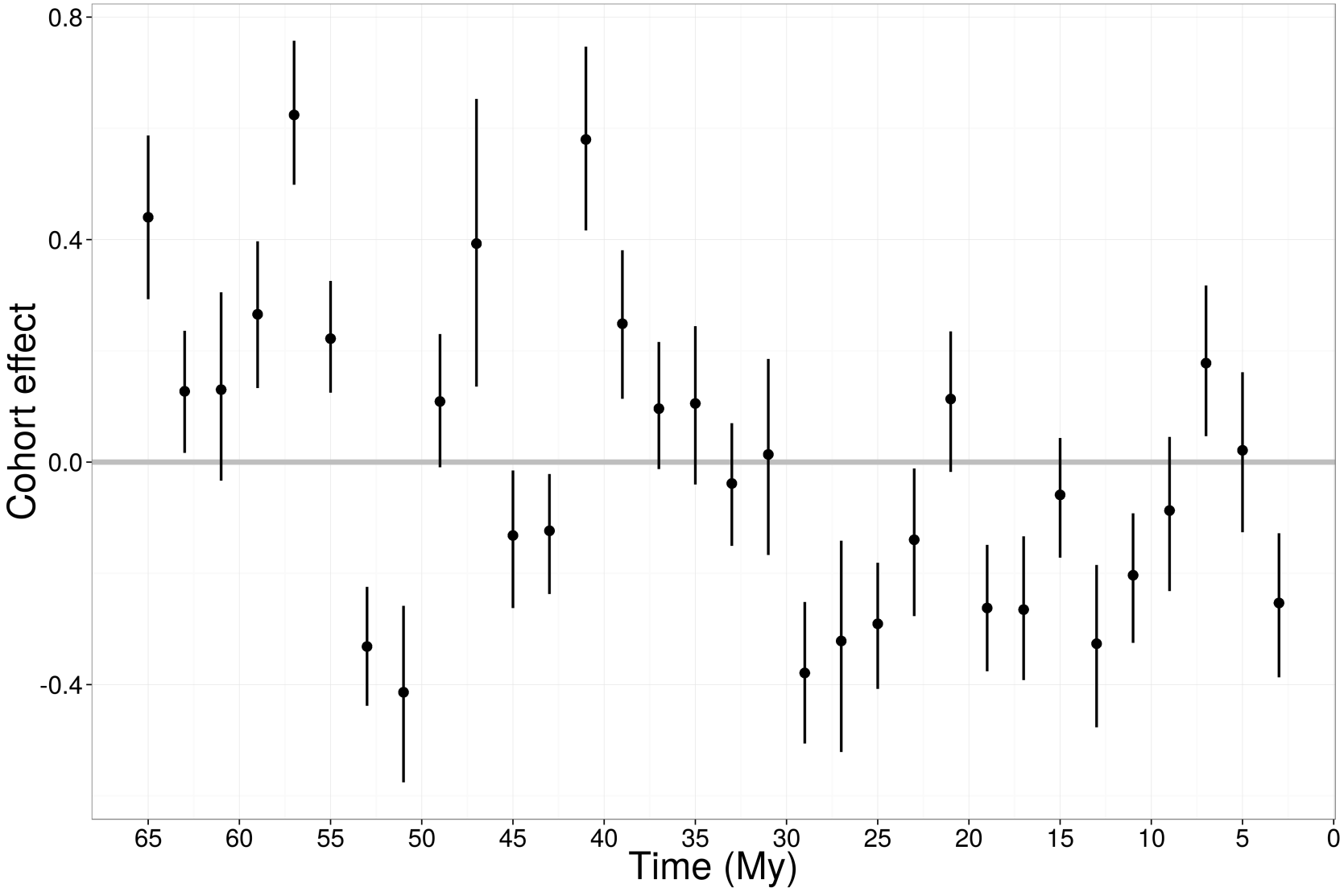
Pairwise differences of β, locomotor category



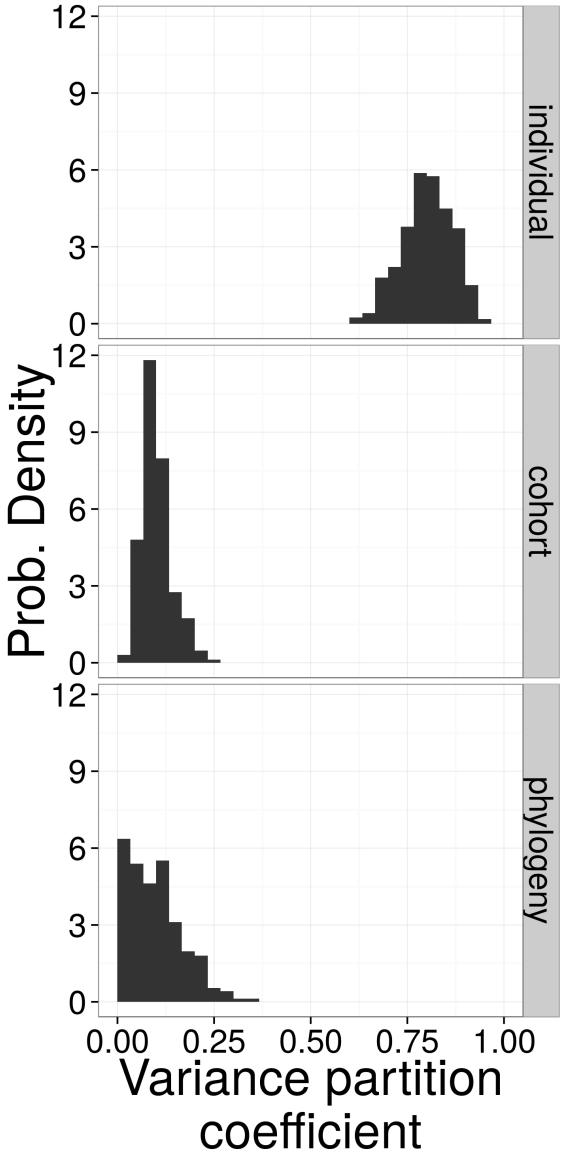
Other traits



Cohort effect

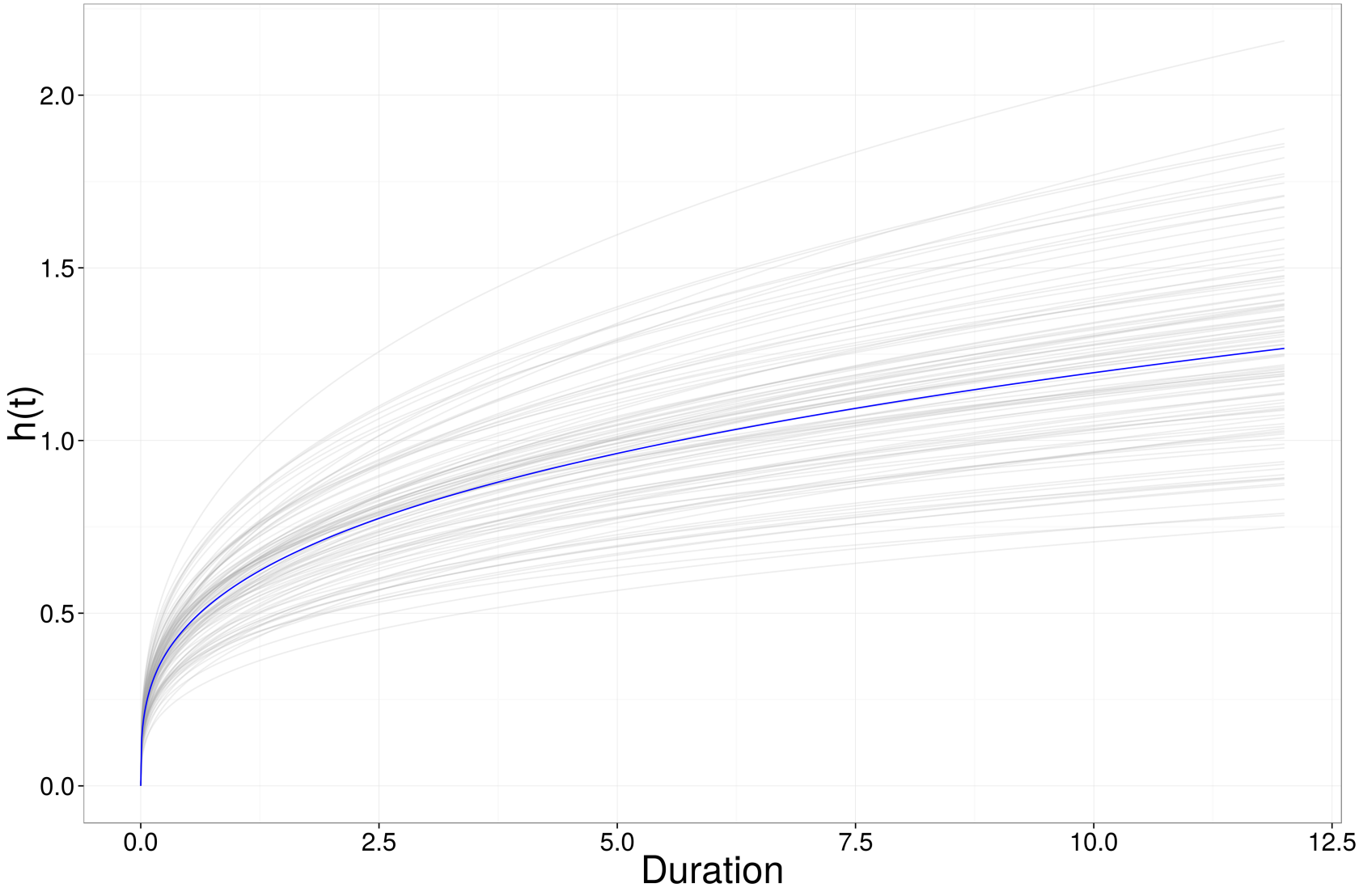


Variance partion coefficient



- Because GLMM, VPC approximated via simulation modified from Goldstein *et al.* '02 *Understanding Statistics*
- phylogenetic heritability, *sensu* Lynch '91 *Am. Nat.*, is a special case of VPC.

Hazard curvature



Meaning

Results

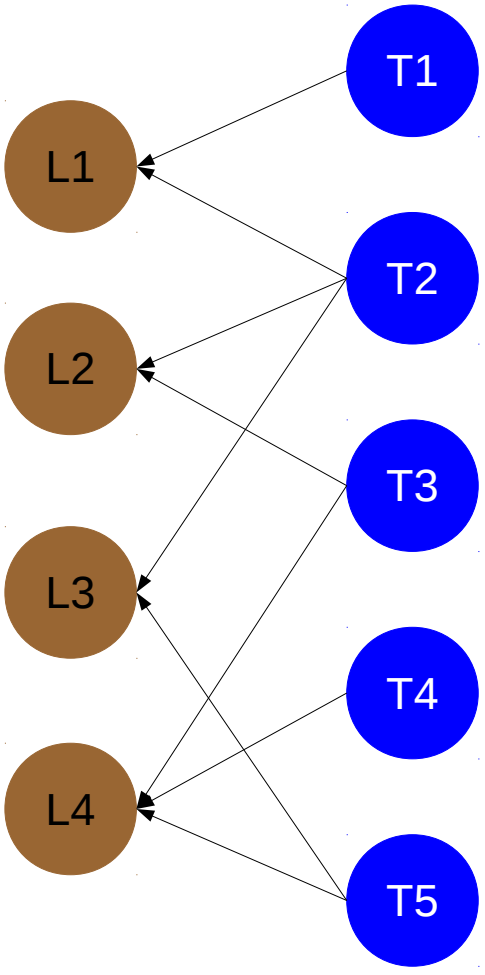
- model generally fits; no systematic biases in residuals
- comparable probabilistic statements of trait, temporal, and historical effects
  - individual level is major source of variance
  - phylogenetic, cohort effect similar
- weak decreasing cohort survival risk over Cenozoic
- $h(t)$ not constant over t, increases slowly

Interpretation

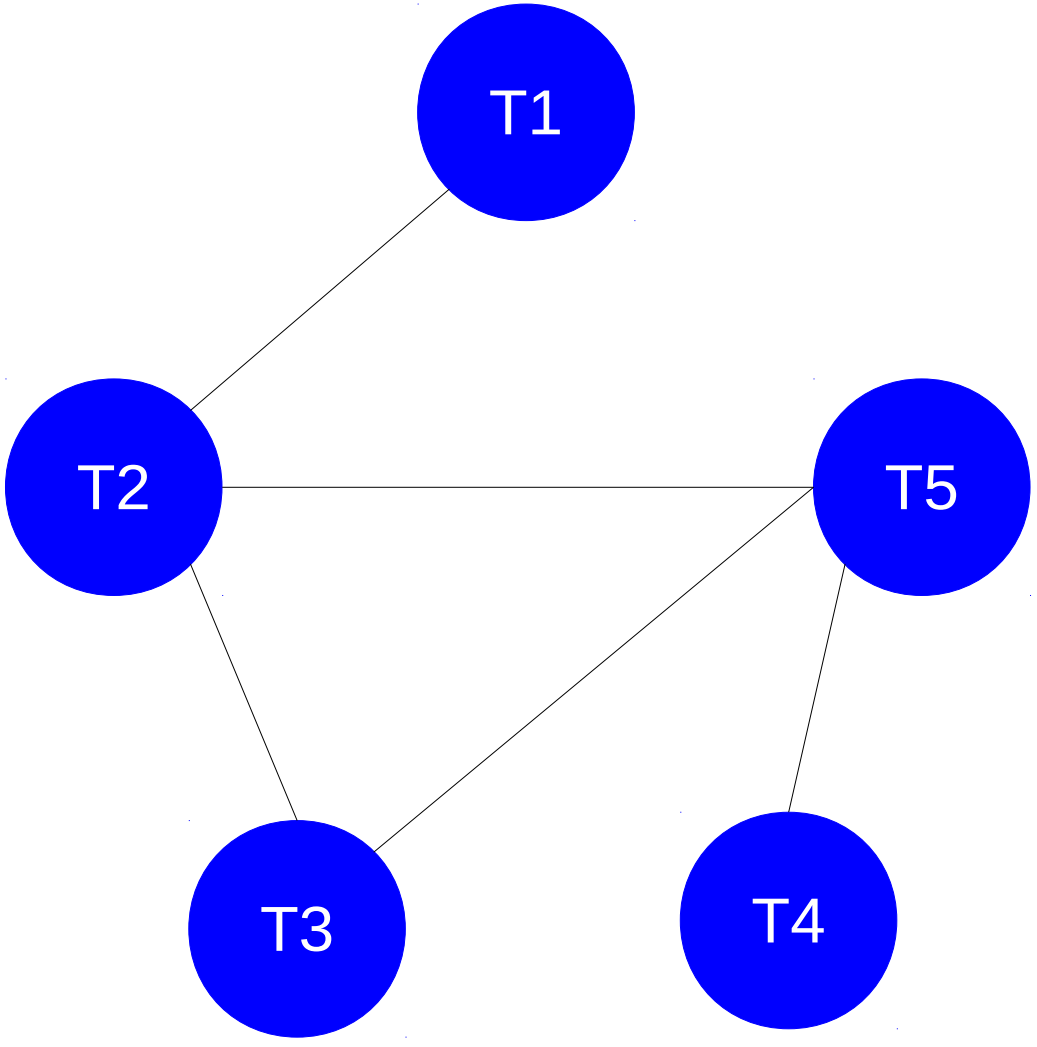
- non-zero temporal and historical effects, but very small
  - older lineages out-competed by younger (Wagner and Estabrook '14 *PNAS*)
- increasing extinction with group age (Quental and Marshall '13 *Science*)
- background extinction; no single mode of extinction
- relative effect of universality of covariate, levels of selection(?)

A model of biological, spatial, and phylogenic effects on Cenozoic mammal co-occurrence

Biogeographic network



Species adjacency

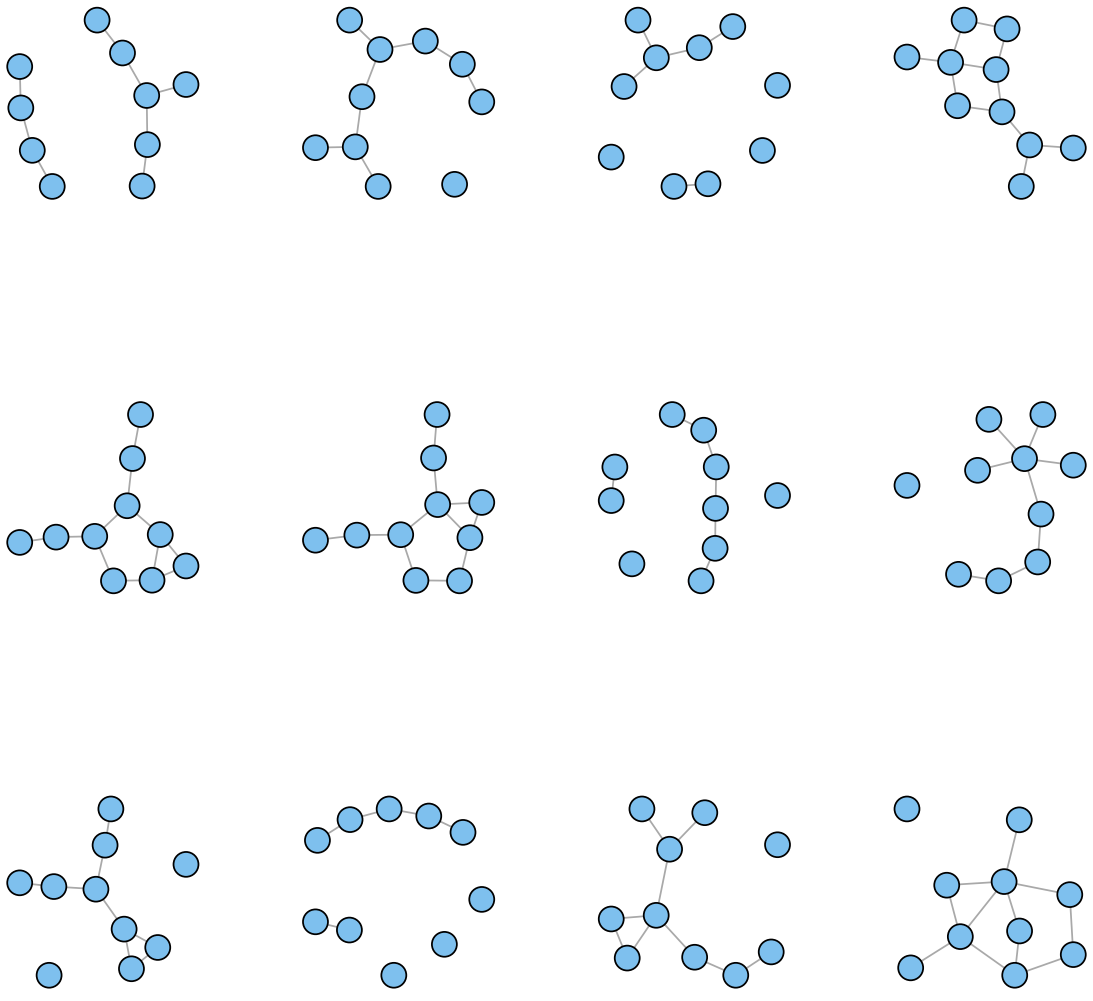


Autoregressive model

Adjacency is also a symmetric n by n matrix, A, with ones on the off-diagonals if the species co-occur.

CAR prior. Estimate spatial correlation (p) and hierarchical variance variance (sigmasq) as a multivariate normal effect with mean vector all 0 and covariance matrix = sigmasq * (I - p * A)

Erdos-Renyi graph $G(n, p)$



Overdispersion model

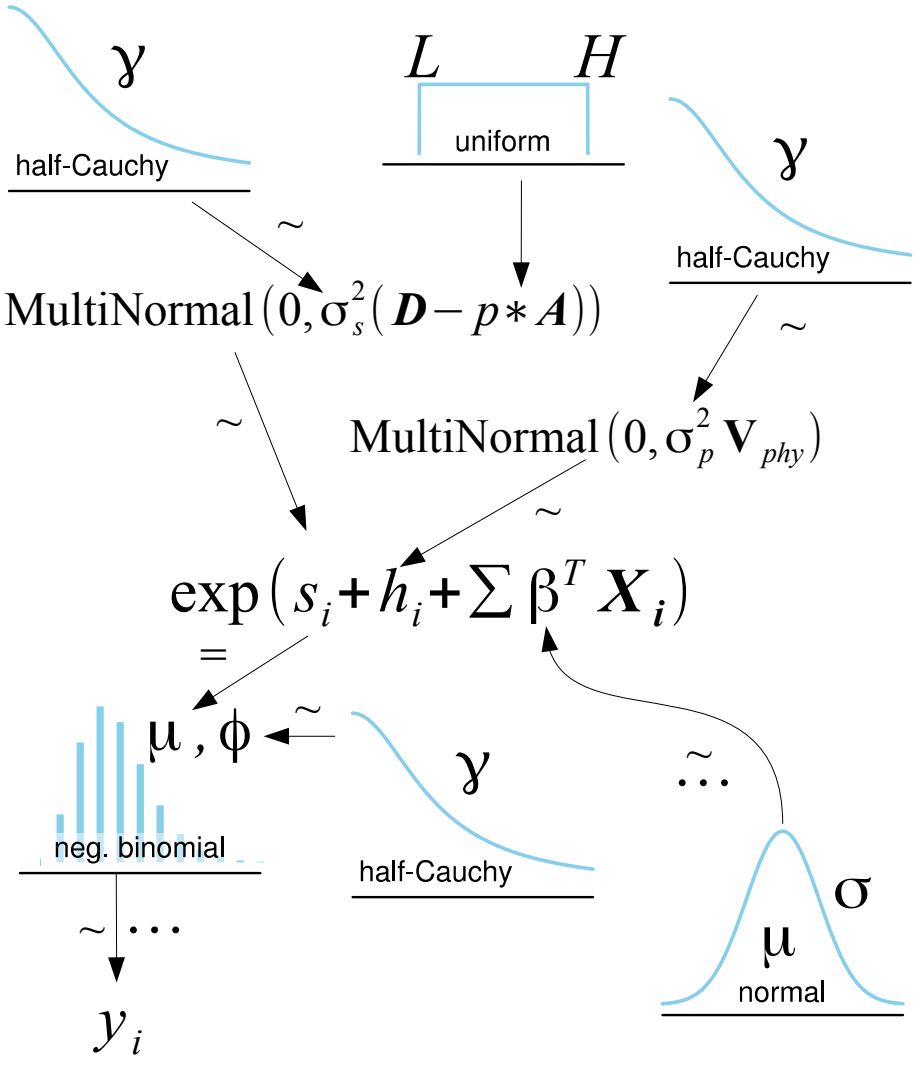
Negative Binomial

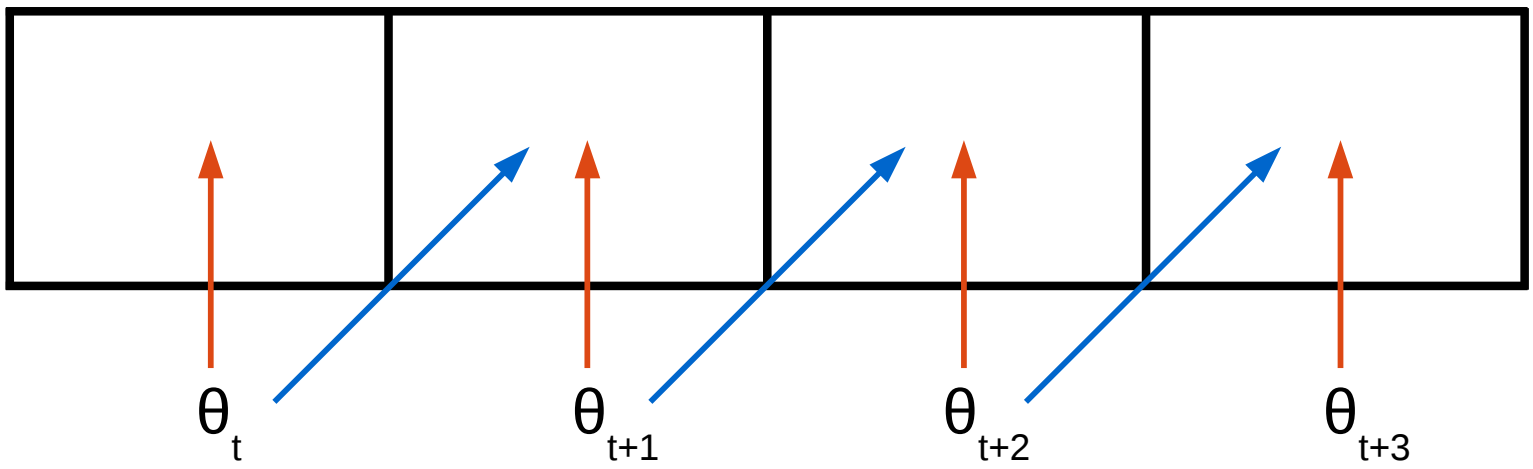
$$\text{NegBinom}(y|\alpha,\beta) = \binom{y+\alpha-1}{\alpha-1}\left(\frac{\beta}{\beta+1}\right)^{2}\left(\frac{1}{\beta+1}\right)^{y}$$

reparameterized

$$\text{NegBinom}(y|\mu,\phi) = \binom{y+\phi-1}{y}\left(\frac{\mu}{\mu+\phi}\right)^{y}\left(\frac{\phi}{\mu+\phi}\right)^{\phi}$$

Model diagram



$$y_i \sim \text{NegBinom}(\mu, \phi)$$
$$\phi \sim \text{half-Cauchy}(2.5)$$
$$s_i \sim \text{MultiNormal}(0, \Sigma_s)$$
$$\Sigma_s = \sigma_s^2(\boldsymbol{D} - p * \boldsymbol{A})$$
$$\sigma_s \sim \text{half-Cauchy}(2.5)$$
$$p \sim \text{Uniform}(0, 1)$$
$$h_i \sim \text{MultiNormal}(0, \Sigma_p)$$
$$\Sigma_p = \sigma_p^2 \mathbf{V}_{phy}$$
$$\sigma_p^2 \sim \text{half-Cauchy}(2.5)$$
$$\beta \sim \text{Normal}(0, 10)$$

Analysis framework