

- ▶ 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

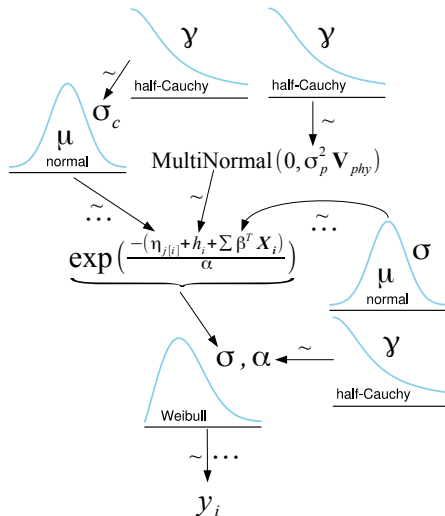
- ▶ AMNH: tooth measures for all notoungulate specimens identified to species level
- ▶ DDIG: applied; travel to Argentina; collaboration with Rick Madden

Death and taxa: time invariant differences in species duration

North American survival

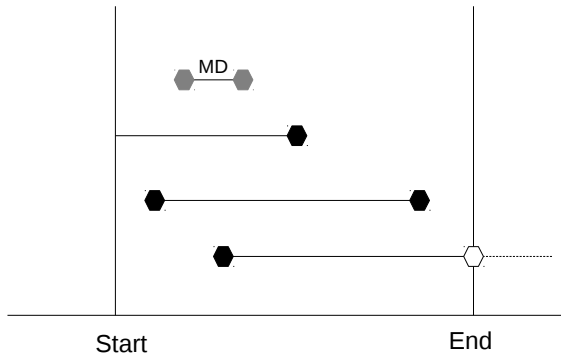
- ▶ species duration as measure of survival
- ▶ traits of interest
 - ▶ organismal: diet, locomotor categories
 - ▶ species: body size, bioprovince occupancy
- ▶ origination cohort
- ▶ phylogeny primarily based on taxonomy
- ▶ duration defined as number of 2My bins from FAD to LAD, inclusive
- ▶ fully Bayesian hierarchical model
- ▶ censoring approach
 - ▶ if still extant, right censored
 - ▶ if not extant and duration of only 1 bin, left censored

Model diagram



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

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 $1 - S(t)$.

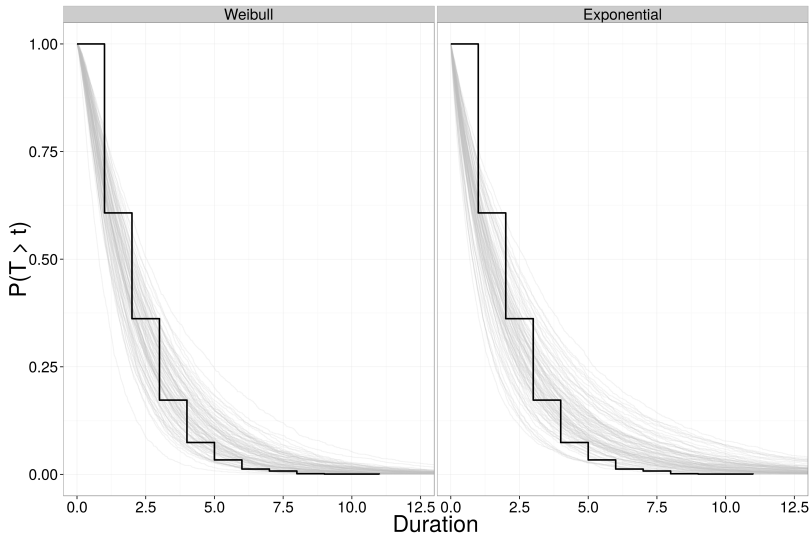
Equivalent to ccdf and cdf respectively.

Modeling censored observations

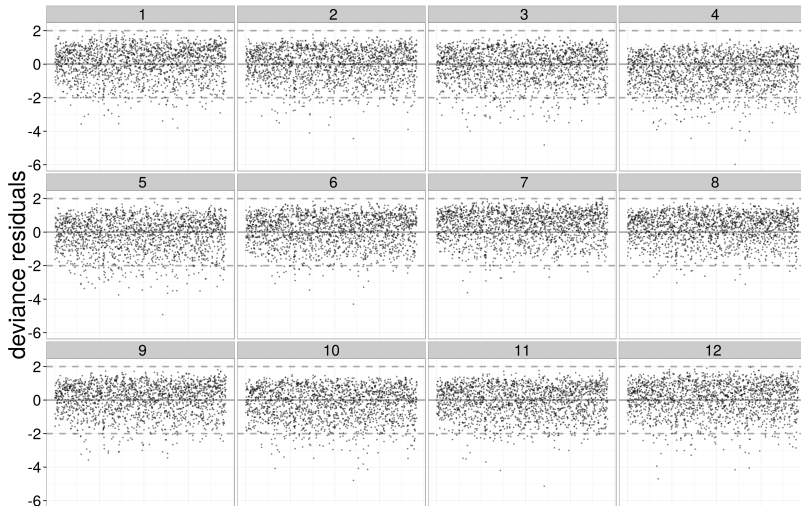
Likelihood

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

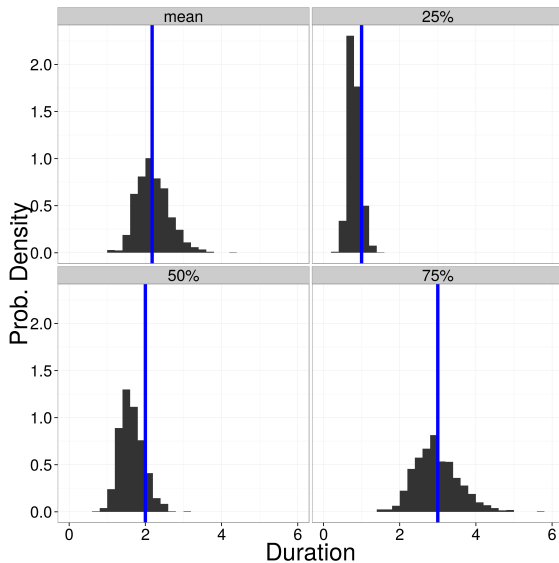
Posterior predictive checks: $S(t)$



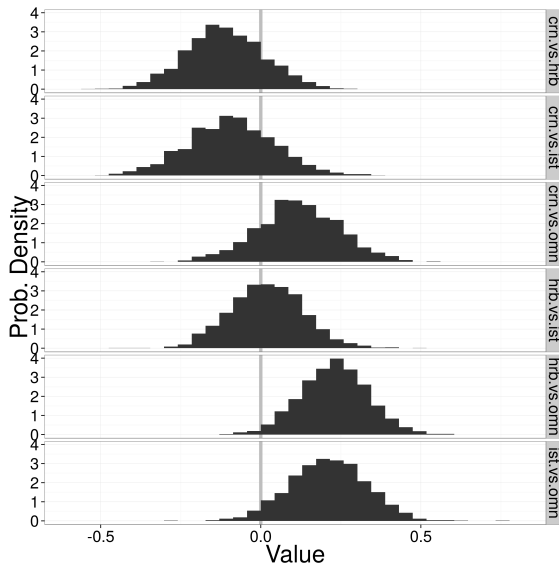
Posterior predictive checks: deviance residuals



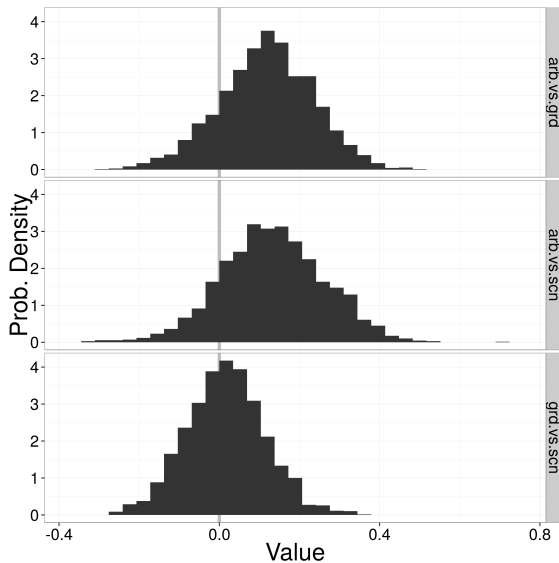
Posterior predictive checks: point checks



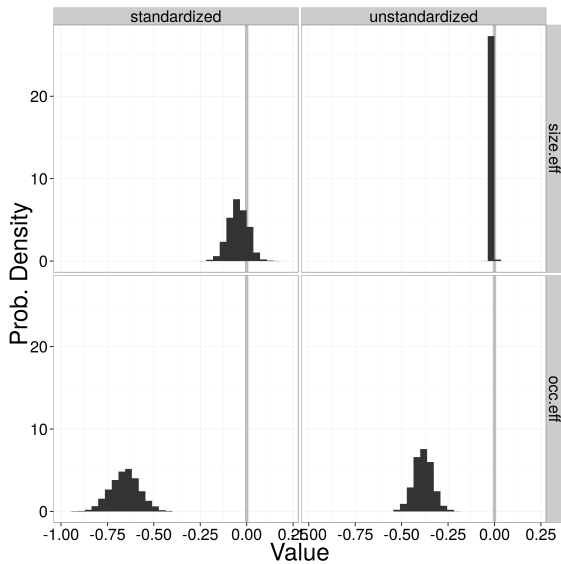
Pairwise differences of β , dietary category



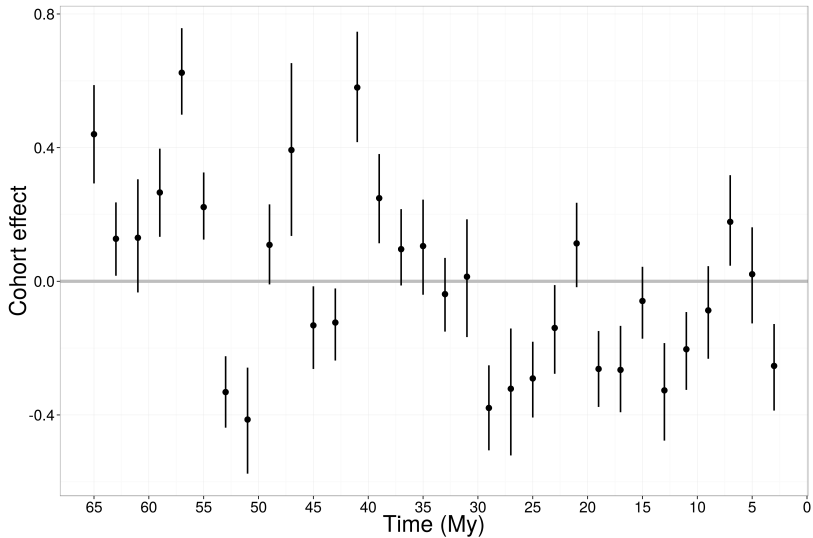
Pairwise differences of β , locomotor category



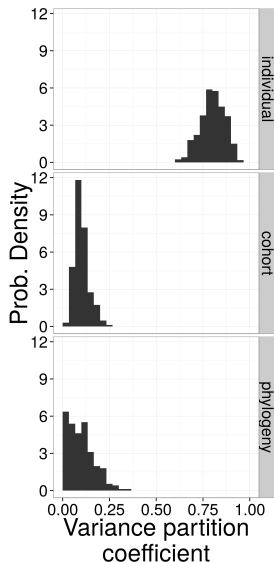
Other traits



Cohort effect

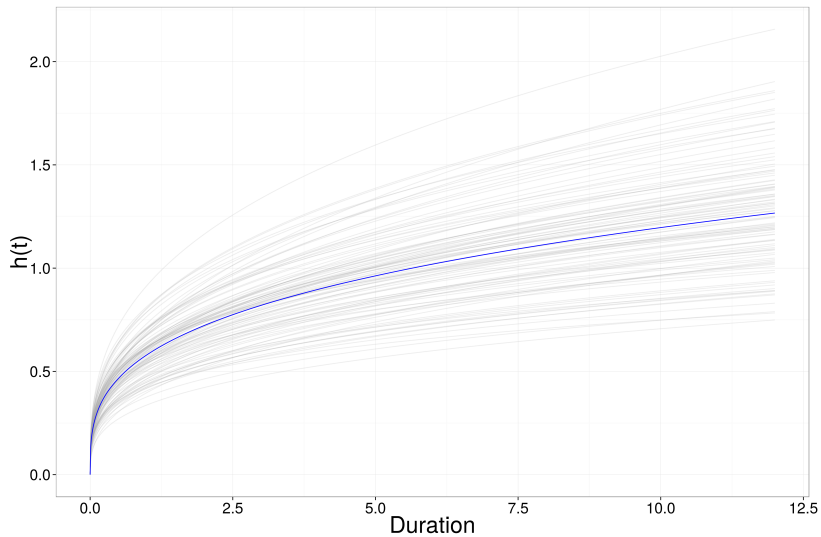


Variance partition coefficient



- ▶ 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

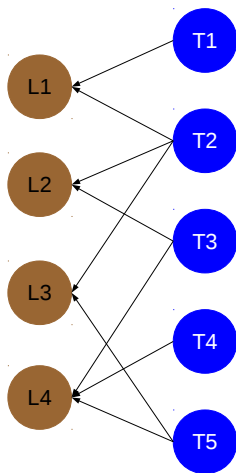
- ▶ model adequate
- ▶ comparable probabilistic statements of trait, temporal, and historical effects
 - ▶ individual level is major source of variance
 - ▶ phylogenetic, cohort effect similar
- ▶ weak decreasing cohort survival risk over Cenozoic
- ▶ $h(t)$ not constant over t , increases slowly

Interpretation

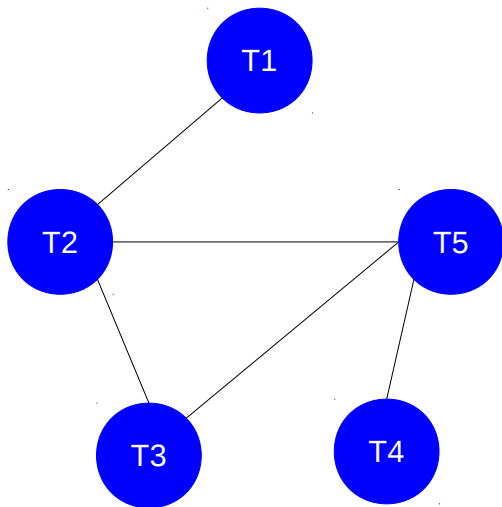
- ▶ non-zero temporal and historical effects, but very small
 - ▶ older lineages out-competed by younger (Wagner and Estabrook '14 *PNAS*)
- ▶ increasing extinction with group age (Quental and Marshall '13 *Science*)
- ▶ background extinction; no single mode of extinction
- ▶ relative effect of universality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

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

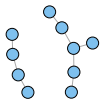
Biogeographic network



Species adjacency



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



Overdispersion model

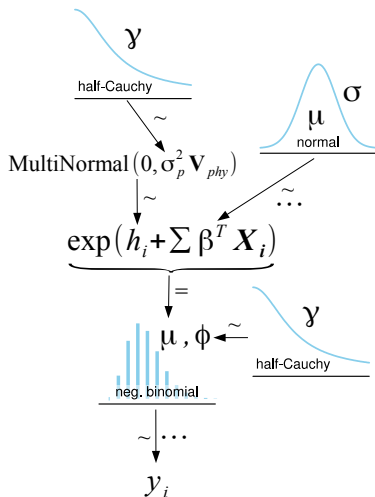
Negative Binomial

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

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



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

Analysis framework

