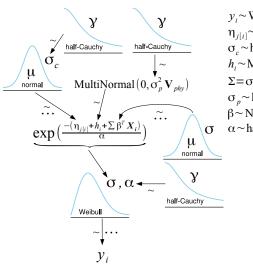
Death and taxa: time invariant differences in mammal species duration

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

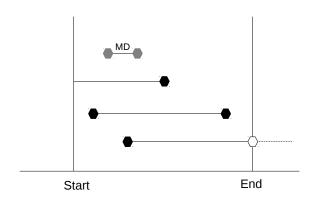
- duration defined as number of 2My bins from FAD to LAD, inclusive
- fully Bayesian hierarchical model
- censoring approach
 - if still extant, right censored
 - if not extant and duration of only 1 bin, left censored

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).

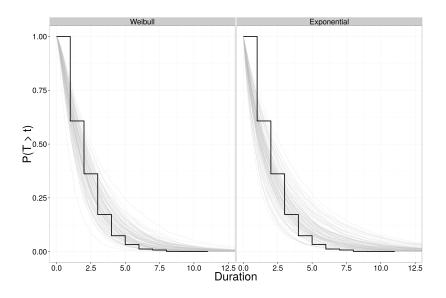
Equivalent to ccdf and cdf respectively.

Modeling censored observations

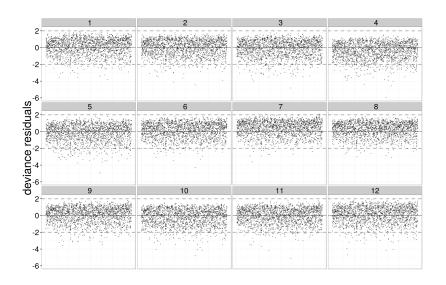
Likelihood

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

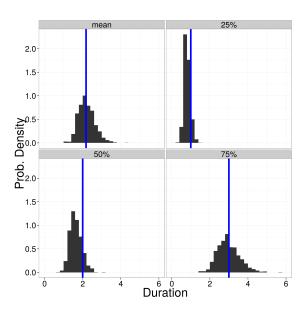
Posterior predictive checks: S(t)



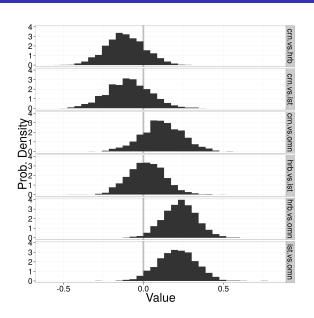
Posterior predictive checks: deviance residuals



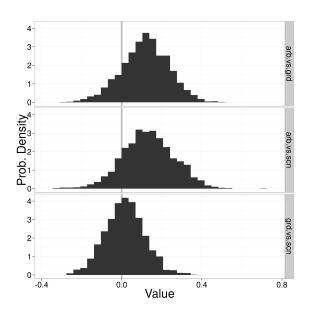
Posterior predictive checks: point checks



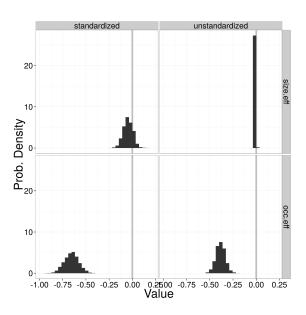
Pairwise differences of β , dietary category



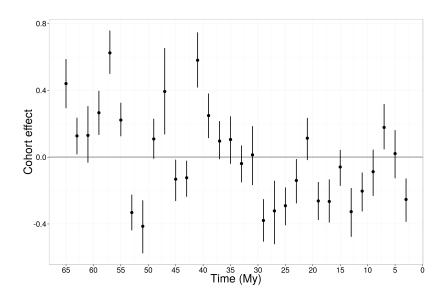
Pairwise differences of β , locomotor category



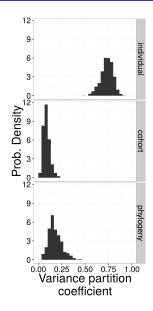
Other traits



Cohort effect

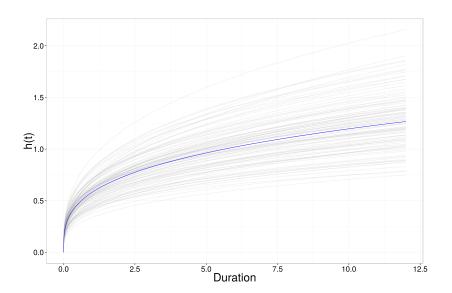


Variance partion coefficient



- 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

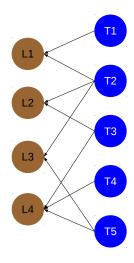
- model adequate
- comparable probabilistic statements of trait, temporal, and historical effects
 - individual level is major source of variance
 - phylogenetic, cohort effect similar
- weak decreasing cohort survival risk over Cenozoic
- h(t) not constant over t, increases slowly

Interpretation

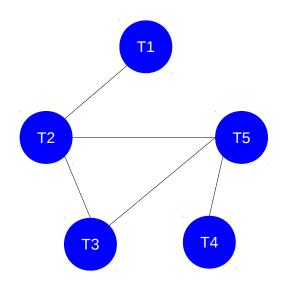
- non-zero temporal and historical effects, but very small
 - older lineages out-competed by younger (Wagner and Estabrook '14 PNAS)
- increasing extinction with group age (Quental and Marshall '13 Science)
- background extinction; no single mode of extinction
- relative effect of universality of covariate,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

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

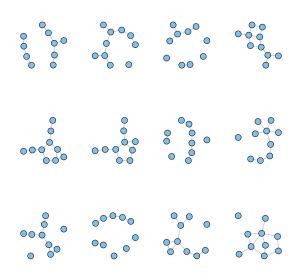
Biogeographic network



Species adjacency



Erdos-Renyi graph G(n, p)



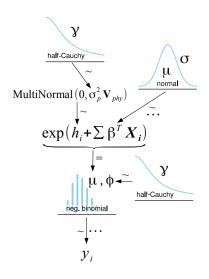
Overdispersion model

Negative Binomial

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

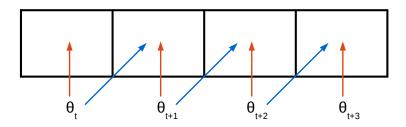
NegBinom
$$(y|\mu,\phi) = {y+\phi-1 \choose y} \left(\frac{\mu}{\mu+\phi}\right)^y \left(\frac{\phi}{\mu+\phi}\right)^{\phi}$$

Model diagram



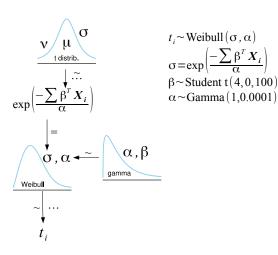
 $y_i \sim \text{NegBinom}(\mu, \phi)$ $\phi \sim \text{half-Cauchy}(2.5)$ $h_i \sim \text{MultiNormal}(0, \Sigma_p)$ $\Sigma_p = \sigma_p^2 \mathbf{V}_{phy}$ $\sigma_p \sim \text{half-Cauchy}(2.5)$ $\beta \sim \text{Normal}(0, 10)$

Analysis framework

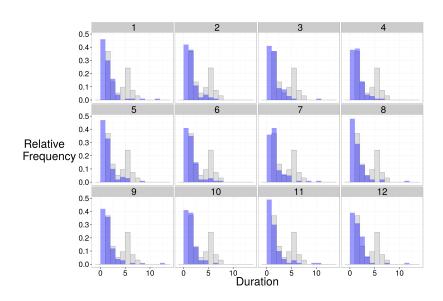


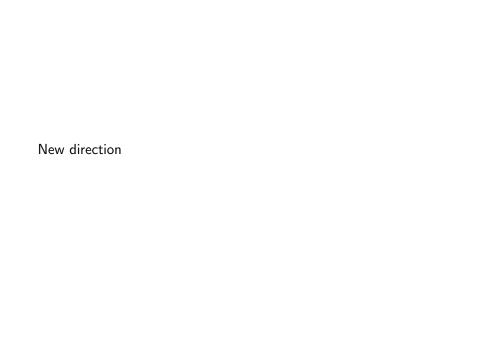


Current brachipod survival model



Current results...





Counting process of fossil occurrence

Hierarchical Poisson model of absolute sighting rate.

fossils (i) of genus (j) in order (k) in a stage $\sim \mathsf{Poisson}(\lambda_{k[j[i]]})$