

# Supplementary Text for “Death and Taxa”

Peter D Smits

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## 1 Materials and Methods

### 2 1.1 Species occurrence and covariate information

Fossil occurrence information was downloaded from the Paleobiology Database (PBDB; <http://paleodb.org/>). Occurrence, taxonomic, stratigraphic, and biological information was downloaded for all North American mammals. This data set was filtered so that only occurrences identified to the species-level, excluding all “sp.”-s. All aquatic and volant taxa were also excluded. Additionally, all occurrences without latitude and longitude information were excluded from the sample.

Species dietary and locomotor category assignments were done using the assignments in the PBDB, which were then reassigned into coarser categories (Table S2). This was done to improve interpretability, increase sample size per category, and make results comparable to previous studies (1, 2).

All individual fossil occurrences were assigned to 2 My bins ranging through the entire Cenozoic. Taxon duration was measured as the number of 2 My bins from the first occurrence to the last occurrence, inclusive. This bin size was chosen because it approximately reflects the resolution of the North American Cenozoic mammal fossil record (3–5). Species originating in the youngest cohort, 0–2 My, were excluded from analysis because every species duration would be both left and right censored, which is illogical.

#### 1.1.1 Body size

Species body size estimates in grams were sourced from a large selection of primary literature and database compilations. Databases used include the PBDB, PanTHERIA (6), and the Neogene Old World Mammal database (NOW; <http://www.helsinki.fi/science/now/>). Major sources of additional compiled body size estimates include (7–12). These were then supplemented with an additional literature search to try and fill in the remaining gaps. In many cases, species body mass was estimated using various published regression equations based on tooth or skull measurements (Table S3). If multiple specimens were measured, I used the mean of specimen measures as the species mean. The See Supplementary Table S4 for a complete list of individual measures and sources.

### 32 1.1.2 Biogeographic network

Species geographic extent was measured as the mean of the relative number of  
34 bioprovinces occupied by a species for each 2 My bin the species was present.  
Bioprovinces were identified using a network-theoretic approach that has pre-  
36 viously been applied to paleontological data (13, 14). This approach relies on  
defining a biogeographic bipartite network of taxa and localities. In this study,  
38 taxa were defined as species and localities were grid cells from a regular lattice on  
a global equal-area cylinder map projection. The regular lattice was defined as  
40 a 70 x 34 global grid where each cell corresponds to approximately 250000 km<sup>2</sup>.  
This network is considered bipartite because taxa are connected to localities  
42 based on their occurrence but taxa are not connected to taxa nor are localities  
connected to localities.

44 A biogeographic network was constructed for each of the 2 My bins used in this  
study. Emergent bioprovinces were then identified using the map equation (15, 16)  
46 as has been done before (13, 14, 17). These bioprovinces correspond to taxa and  
localities that are more interconnected with each other than with other nodes.

48 The map projection and regular lattice were made using shape files from  
<http://www.naturalearthdata.com/> and the **raster** package for R (18). The  
50 map equation and other network related analysis was done using the **igraph**  
package for R (19).

### 52 1.1.3 Supertree

As there is no single, combined formal phylogenetic hypothesis of all Cenozoic  
54 fossils mammals from North America, it was necessary to construct a semi-  
formal supertree. This was done by combining taxonomic information for all the  
56 observed species and a few published phylogenies.

The initial taxonomic classification of the observed species was based on the  
58 associated taxonomic information from the PBDB. This information was then  
updated using the Encyclopedia of Life (<http://eol.org/>) which collects and col-  
60 lates taxonomic information in a single database. This was done programatically  
using the **taxize** package for R (20). Finally, this taxonomic information was  
62 further updated using a published taxonomy of fossil mammals (21, 22).

This taxonomy serves as an initial phylogenetic hypothesis which was then  
64 combined with a selection of species-level phylogenies (10, 23) in order to better  
constrain a minimum estimate of the actual phylogenetic relationships of the  
66 species. The supertree was inferred via matrix representation parsimony imple-  
mented in the **phytools** package for R (24). While four most parsimonious trees  
68 were found, I selected a single of these for use in analysis.

Polytomies were resolved in order of species first appearance in order to  
70 minimize stratigraphic gaps. The resulting tree was then time scaled using the  
**paleotree** package via the “minimum branch length” approach with a minimum  
72 length of 0.1 My (25). The minimum length is necessary to avoid zero-length  
branches which cause the phylogenetic covariance matrix not to be positive  
74 definite, which is important for computation (see below). While other time

scaling approaches are possible (26, 27) this method was chosen for its simplicity and not requiring additional information about diversification rates which are the interest of this study.

## 1.2 Survival model

Presented here is the model development process used to formulate the two survival models used in this study.

First, define  $y$  as a vector of length  $n$  where the  $i$ th element is the duration of species  $i$ , where  $i = 1, \dots, n$ .

The simplest survival model where durations are assumed to follow an exponential distribution with a single “rate” or inverse-scale parameter  $\lambda$  (28). This is written out as

$$\begin{aligned} p(y|\lambda) &= \lambda \exp(-\lambda y) \\ y &\sim \text{Exp}(\lambda). \end{aligned} \tag{1}$$

The exponential distribution corresponds to situations where extinction risk is independent of age. To understand this, we need to define two functions: the survival function  $S(t)$  and the hazard function  $h(t)$ .

$S(t)$  corresponds to the probability that a species having existed for  $t$  2 My bins will not have gone extinct while  $h(t)$  corresponds to the instantaneous extinction rate for some taxon age  $t$  (28). For an exponential model,  $S(t)$  is defined

$$S(t) = \exp(-\lambda t) \tag{2}$$

and  $h(t)$  is defined

$$h(t) = \lambda \tag{3}$$

The choice of the exponential distribution corresponds directly to the Law of Constant Extinction (29) as the right side of Eq. 3 does not depend on species age  $t$ .

The current sampling statement (Eq. 1) assumes that all species share the same rate parameter with no variation. To allow for variation in  $\lambda$  associated with relevant covariate information like species body size,  $\lambda$  is reparameterized as  $\lambda_i = \exp(\sum \beta^T \mathbf{X}_i)$  with  $i$  indexing a given observation and its covariates,  $\beta$  is a vector of regression coefficients, and  $\mathbf{X}$  is a matrix of covariates. This is a standard regression formulation, where one column of  $\mathbf{X}$  is all 1-s and its corresponding  $\beta$  coefficient is the intercept. This approach is essentially a generalized linear model (GLM) approach where instead of normally distributed errors there are exponentially distributed errors (28).

To relax the assumption of age-independent extinction of the Law of Constant Extinction we substitute the Weibull distribution for the exponential (28). The Weibull distribution has a shape parameter  $\alpha$  and scale parameter  $\sigma$ . Conceptually,  $\sigma$  is the inverse of  $\lambda$ .  $\alpha$  modifies the impact of taxon age on extinction risk. When  $\alpha > 1$  then  $h(t)$  is a monotonically increasing function,

108 but when  $\alpha < 1$  then  $h(t)$  is a monotonically decreasing function. When  $\alpha = 1$   
 then the Weibull distribution is equivalent to the exponential.

The Weibull distribution and sampling statement were defined

$$p(y|\alpha, \sigma) = \frac{\alpha}{\sigma} \left(\frac{y}{\sigma}\right)^{\alpha-1} \exp\left(-\left(\frac{y}{\sigma}\right)^\alpha\right)$$

$$y \sim \text{Weibull}(\alpha, \sigma). \quad (4)$$

The corresponding  $S(t)$  and  $h(t)$  functions are defined

$$S(t) = \exp\left(-\left(\frac{t}{\sigma}\right)^\alpha\right) \quad (5)$$

$$h(t) = \frac{\alpha}{\sigma} \left(\frac{t}{\sigma}\right)^{\alpha-1}. \quad (6)$$

110 To allow for  $\sigma$  to vary with a given observation's covariate information it is  
 reparameterized in a similar fashion to  $\lambda$  with a few key differences. Because  
 112  $\sigma = 1/\lambda$  in order to preserve the interpretation of  $\beta$ , while taking  $\alpha$  into account,  
 $\sigma$  is reparameterized as

$$\sigma_i = \exp\left(\frac{-(\beta_0)}{\alpha}\right) \quad (7)$$

114 where  $\beta_0$  is the intercept term.

The model described here was the final model at the end of a continuous  
 116 model development framework where the sampling and prior distributions were  
 iteratively modified to best reflect theory, knowledge of the data, the inclusion  
 118 of important covariates, and the fit to the data. This follows the approach  
 described in (30) and (31). A survival model was fit in a Bayesian context  
 120 where species duration were assumed to be drawn from either an exponential  
 or Weibull distribution (Eq. 4) with shape  $\alpha$  and scale  $\sigma$  parameters.  $\alpha$  was  
 122 assumed constant, which is standard practice in survival analysis (28).  $\alpha$  was  
 given a weakly informative half-Cauchy ( $C^+$ ) prior.  $\sigma$  was reparameterized as  
 124 an exponentiated regression model (Eq. 7). This was further expanded (Eq. 8)  
 to allow for two hierarchical factors as discussed below. This is written

$$\sigma_i = \exp\left(\frac{-(h_i + \eta_{j[i]} + \sum \beta^T \mathbf{X}_i)}{\alpha}\right) \quad (8)$$

126 where equivalent statement for the exponential distribution is defined

$$\lambda_i = \exp\left(h_i + \eta_{j[i]} + \sum \beta^T \mathbf{X}_i\right). \quad (9)$$

$\mathbf{X}$  is an  $n \times K$  matrix of species-level covariates. Three of the covariates of  
 128 interest are the logit of mean relative occupancy, and the logarithm of body size  
 (g). The discrete covariate index variables of dietary and locomotor category  
 130 were transformed into  $n \times (k - 1)$  matrices where each column is an indicator  
 variable (0/1) for that species's category,  $k$  being the number of categories of

the index variable (3 and 4, respectively). Only  $k - 1$  indicator variables are necessary as the intercept takes on the remaining value. Finally, a vector of 1-s was included in the matrix  $\mathbf{X}$  whose corresponding  $\beta$  coefficient is the intercept, making  $K$  equal eight.

$\beta$  is the vector of regression coefficients. The intercept term was given a weak normal prior,  $\beta_0 \sim \mathcal{N}(0, 10)$  while all of these other coefficients were slightly more informative priors, e.g.  $\beta_{mass} \sim \mathcal{N}(0, 5)$ . These priors were chosen because it is expected that the effect size of each variable on duration will be small, as is generally the case with binary covariates (30).

Regression coefficients are not directly comparable without first standardizing the input variables to have equal standard deviations. This is accomplished by subtracting the mean of the covariate from all values and then dividing by the standard deviation, resulting in a variable with mean of zero and a standard deviation of one. This linear transform greatly improves the interpretability of the coefficients as expected change in mean duration given a difference of one standard deviation in the covariate (32). Additionally, this makes the intercept directly interpretable as the estimate of mean (transformed)  $\sigma$  (Eq. 7). However, because the expected standard deviation for a random binary variable is 0.5, in order to make comparisons between the binary and continuous variables, the continuous inputs must instead be divided by twice their standard deviation (33).

### 1.2.1 Hierarchical effects

The two hierarchical effects of interest in this study are origination cohort and shared evolutionary history, or phylogeny. Hierarchical modeling can be considered an intermediate between complete and no pooling of groups (30), where complete pooling is when the differences between groups are ignored and no pooling is where different groups are analyzed separately. By allowing for partial pooling, we are modeling the appropriate compromise between these two extremes, allowing for better and potentially more informative overall inference. This is done by having all of the groups share the same normal prior with mean 0 and a scale parameter estimated from the data, which then acts as an indicator of the amount of pooling. A scale of 0 and  $\infty$  indicate complete and no pooling, respectively. The choice of mean 0 allows for the individual group estimates to be interpreted as deviations from the intercept. Hierarchical modeling is analogous to mixed-effects modeling (30).

Origination cohort is defined as the group of species which all originated during the same 2 My temporal bin. Because the most recent temporal bin, 0-2 My, was excluded, there are 32 different cohorts. The effect of origination cohort  $j$  was modeled with each group being a sample from a common cohort effect,  $\eta_j$ , which was considered normally distributed with mean 0, and standard deviation  $\sigma_c$ . The value of  $\sigma_c$  was then estimated from the data itself, corresponding to the amount of pooling in the individual estimates of  $\eta_j$ . This approach is a conceptual and statistical unification between dynamic and cohort survival analysis in paleontology (34–38), with  $\sigma_c$  acting as a measure of compromise between these two end members.

$$\begin{aligned}\eta_j &\sim \mathcal{N}(0, \sigma_c) \\ \sigma_c &\sim \text{C}^+(0, 2.5)\end{aligned}$$

176 The choice of the half-Cauchy prior on  $\sigma_c$  follows (39).

178 The impact of shared evolutionary history, or phylogeny, was modeling as an individual effect where each observation,  $i$ , is modeled as a multivariate normal,  $h$ , where the covariance matrix  $\Sigma$  is known up to a constant,  $\sigma_p^2$  (40, 41). This is written

$$\begin{aligned}h &\sim \text{multivariate } \mathcal{N}(0, \Sigma) \\ \Sigma &= \sigma_p^2 \mathbf{V}_{phy} \\ \sigma_p &\sim \text{C}^+(0, 2.5).\end{aligned}$$

182  $\mathbf{V}_{phy}$  is the phylogenetic covariance matrix defined as an  $n \times n$  matrix where the diagonal elements are the distance from root to tip, in branch length, for each observation and the off-diagonal elements are the amount of shared history, measured in branch length, between observations  $i$  and  $j$ .  $\sigma_p$  was given a weakly informative half-Cauchy hyperprior. Note that because the phylogeny used here is primarily based on taxonomy, estimates of  $\sigma_p$  represent minimum estimates (40, 41). Improved phylogenetic estimates of all fossil Cenozoic mammals would greatly improve this estimate.

### 1.2.2 Censored observations

190 An important part of survival analysis is the inclusion of censored observations where the failure time has not been observed (28, 42). The most common censored observation is right censored, where the point of extinction had not yet been observed in the period of study, such as taxa that are still present in the most recent time bin (0-2 My). Left censored observations, on the other hand, correspond to observations that went extinct any time between 0 and some known point. In order to account for the minimum resolution of the fossil record encountered here, taxa that occurred in only a single time bin were left censored.

200 Censored data are modeled using the survival function of the distribution,  $S(t)$ , defined earlier for the Weibull distribution (Eq. 5) with  $\sigma$  defined as above (Eq. 8).  $S(t)$  is the probability that an observation will survive longer than a given time  $t$ . The likelihood of uncensored observations is evaluated as normal using Equation 4 while right censored observations are evaluated at  $S(t)$  and left censored observations are evaluated at  $1 - S(t)$ . Note,  $1 - S(t)$  is equivalent to the cumulative distribution function and  $S(t)$  is equivalent to the complementary cumulative distribution function (31).

The full likelihood for both uncensored and both right and left censored observations is written

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

where  $C$  is the set of uncensored observations,  $R$  is the set of right censored observations, and  $L$  is the set of left censored observations.

### 1.2.3 Estimation

Parameter posteriors were approximated using a Markov-chain Monte Carlo (MCMC) routine implemented in the Stan programming language (43). Stan implements a Hamiltonian Monte Carlo using a No-U-Turn sampler (44). Posterior approximation was done using four parallel MCMC chains run for 30000 steps, thinned to every thirtieth sample, split evenly between warm-up and sampling. Convergence was evaluated using the scale reduction factor,  $\hat{R}$ . Values of  $\hat{R}$  close to 1, or less than or equal to 1.1, indicate approximate convergence. Convergence means that the chains are approximately stationary and the samples are well mixed (31).

In order to speed up the posterior approximation, a custom multivariate normal sampler was used to estimate the unknown constant term in the covariance matrix. This is necessary because inverting and solving the complete covariance matrix on every iteration is a memory intense procedure. The custom sampler limits the necessary number of operations and matrix inversions per iteration.

## 1.3 Posterior predictive checks

The most basic assessment of model fit is that simulated data generated using the fitted model should be similar to the observed. This is the idea behind posterior predictive checks. Using the covariates from each of the observed durations, and randomly drawn parameter estimates from their marginal posteriors, a simulated data set  $y^{rep}$  was generated. This process was repeated 1000 times and the distribution of  $y^{rep}$  was compared with the observed (31).

An example posterior predictive check used in this study is a graphical comparison between the Kaplan-Meier (K-M) survival curve estimated from the observed data and the K-M survival curves estimated from 1000 simulation sets. K-M survival curves are non-parametric estimates of  $S(t)$  (28). Other posterior predictive checks used here include comparison of the mean and quantiles of the observed durations to the distributions of the same quantities from the simulations, and inspection of the deviance residuals, defined below.

In standard linear regression, residuals are defined as  $r_i = y_i - y_i^{est}$ . For the model used here, this definition is inadequate. The equivalent values for survival analysis are deviance residuals. To define how deviance residuals are calculated, we first define the cumulative hazard function (28). Given  $S(t)$  (Eq. 5), we define the cumulative hazard function as

$$\Lambda(t) = -\log(S(t)).$$

Next, we define martingale residuals  $m$  as

$$m_i = I_i - \Lambda(t_i).$$

238  $I$  is the inclusion vector of length  $n$ , where  $I_i = 1$  means the observation is completely observed and  $I_i = 0$  means the observation is censored. Martingale  
240 residuals have a mean of 0, range between 1 and  $-\infty$ , and can be viewed as the difference between the observed number of deaths between 0 and  $t_i$  and the  
242 expected number of deaths based on the model. However, martingale residuals are asymmetrically distributed, and can not be interpreted in the same manner  
244 as standard residuals.

The solution to this is to use the deviance residuals,  $D$ . This is defined as a function of martingale residuals and takes the form

$$D_i = \text{sign}(m_i) \sqrt{-2[m_i + I_i \log(I_i - m_i)]}.$$

Deviance residuals have a mean of 0 and a standard deviation of 1 by definition.

#### 246 1.4 Model comparison

The exponential and Weibull models were compared for out-of-sample predictive  
248 accuracy using the widely-applicable information criterion (WAIC) (45). Because the Weibull model reduces to the exponential model when  $\alpha = 0$ , our interest is  
250 not in choosing between these models. Instead comparison of WAIC values is useful for better understanding the effect of model complexity on out-of-sample  
252 predictive accuracy. The calculation of WAIC used here corresponds to the “WAIC 2” formulation recommended by (31).

254 WAIC can be considered fully Bayesian alternative to the Akaike information criterion, where WAIC acts as an approximation of leave-one-out cross-validation  
256 which acts as a measure of out-of-sample predictive accuracy. WAIC is calculated starting with the log pointwise posterior predictive density calculated as

$$\text{lppd} = \sum_{i=1}^n \log \left( \frac{1}{S} \sum_{s=1}^S p(y_i | \Theta^s) \right), \quad (10)$$

258 where  $n$  is sample size,  $S$  is the number posterior simulation draws, and  $\Theta$  represents all of the estimated parameters of the model. This is similar to  
260 calculating the likelihood of each observation given the entire posterior. A correction for the effective number of parameters is then added to lppd to adjust  
262 for overfitting. The effective number of parameters is calculated, following derivation and recommendations of (31), as

$$p_{\text{WAIC}} = \sum_{i=1}^n V_{s=1}^S (\log p(y_i | \Theta^s)). \quad (11)$$

264 where  $V$  is the sample posterior variance of the log predictive density for each data point.



266 Given both equations 10 and 11, WAIC is then calculated

$$\text{WAIC} = \text{lppd} - p_{\text{WAIC}}. \quad (12)$$

268 When comparing two or more models, lower WAIC values indicate better out-of-sample predictive accuracy. Importantly, WAIC is just one way of comparing models. When combined with posterior predictive checks it is possible to get a  
270 more complete understanding of model fit.

## 1.5 Variance partitioning

272 There are three different variance components in this model: sample  $\sigma_y^2$ , cohort  $\sigma_c^2$ , and phylogenetic  $\sigma_p^2$ . The sample variance,  $\sigma_y^2$ , is similar to the residual  
274 variance from a normal linear regression. Partitioning the variance between these sources allows the relative amount of unexplained variance of the sample  
276 to be compared. However, the Weibull based model used here (Eq. 4) does not include an estimate of the sample variance,  $\sigma_y^2$ . Partitioning the variance  
278 between these three components was approximated via a simulation approach modified from (46).

280 The procedure is as follows:

- 282 1. Simulate  $w$  (50,000) values of  $\eta$ ;  $\eta \sim \mathcal{N}(0, \sigma_c)$ .
- 284 2. For a given value of  $\beta^T \mathbf{X}$ , calculate  $\sigma^{c*}$  (Eq. 7) for all  $w$  simulations, holding  $h$  constant at 0.
- 286 3. Calculate  $v_c$ , the Weibull variance (Eq. 13) of each element of  $\sigma^{c*}$  with  $\alpha$  drawn from the posterior estimate.
- 288 4. Simulate  $w$  values of  $h$ ;  $h \sim \mathcal{N}(0, \sigma_p)$ .
- 290 5. For a given value of  $\beta^T \mathbf{X}$ , calculate  $\sigma^{p*}$  (Eq. 7) for all  $w$  simulations, holding  $\eta$  constant at 0.
- 292 6. Calculate  $v_p$ , the Weibull variance (Eq. 13) of each element of  $\sigma^{p*}$  with  $\alpha$  drawn from the posterior estimate.
7.  $\sigma_{y*}^2 = \frac{1}{2} \left( \left( \frac{1}{w} \sum_i^w v_{pi} \right) + \left( \frac{1}{w} \sum_j^w v_{cj} \right) \right)$ .
8.  $\sigma_{c*}^2 = \text{var}(v_c)$  and  $\sigma_{p*}^2 = \text{var}(v_p)$ .

294 The simulated values of  $h$  were drawn from a univariate normal distribution because each simulated value is in isolation, so there is no concern of phylogenetic autocorrelation. The chosen value for  $\beta^T \mathbf{X}$  was a draw from the posterior  
296 estimate of the intercept. Because input variables were standardized prior to model fitting, the intercept corresponds to the estimated effect on survival of  
298 the sample mean.

Weibull variance is calculated as

$$var(x) = \sigma^2 \left( \Gamma \left( 1 + \frac{2}{\alpha} \right) - \left( \Gamma \left( 1 + \frac{1}{\alpha} \right) \right)^2 \right), \quad (13)$$

where  $\Gamma$  is the gamma function.

The variance partitioning coefficients are then calculated, for example, as  $VPC_{phylo} = \frac{\sigma_{p*}^2}{\sigma_{y*}^2 + \sigma_{c*}^2 + \sigma_{p*}^2}$  and similarly for the other components.

I used variance partitioning coefficients (VPC) to estimate the relative importance of the different variance components (30). Phylogenetic heritability,  $h_p^2$  (40, 41), is identical to the VPC of the phylogenetic effect. Additionally, because phylogenetic effect was estimated using a principally taxonomy based tree the estimates derived here can be considered minimum estimates of the phylogenetic effect.

## 2 Model adequacy and comparison

With all marginal posterior estimates having converged ( $\hat{R} < 1.1$ ) it is possible to examine the quality of model fit (Table S1). If the model is an adequate descriptor of the observed data, then relatively confident inference can be made (31).

Visual examination of the deviance residuals from twelve different sets of posterior predictive simulations indicates a systematic weakness estimating durations greater than 3 2-My bins (Fig. S1). However, posterior predictive estimates of the 25th, 50th, and 75th quantiles of the observed indicate adequate fit. (Fig. S2). Importantly, this indicates that the model has approximate fit for 50+% of the data. Because, the inferred model can be inferred to be approximately adequate at capturing the observed variation.

The Weibull model (VALUE) also had a much lower WAIC score than the Exponential model (VALUE). This difference indicates that the Weibull model probably has the lower out-of-sample predictive accuracy of the two.

## 3 Concerns surrounding estimates of $\alpha$

The estimate of the Weibull shape parameter,  $\alpha$ , is greater than 1 meaning that extinction risk is expected to increase with taxon age (Table S1). As the value of  $\alpha$  is between 1 and 1.5, extinction risk for a given species only gradually increases with age (Fig. S3). There are three possible explanations for this result: 1) older taxa being out competed by younger taxa (47); or 2) this is an artifact of the minimum resolution of the fossil record (48).

An additional concern is that there may be an upward bias in estimates of  $\alpha$  at this sample size, similar to that for scale parameters (31). The plausibility of third possibility in this example can be explored in simulation. I simulated from 10, 100, 1000, and 10000 samples from a Weibull( $alpha = 1.3$ ,  $\sigma = 1$ ) 100 times each. For each of these simulated datasets, I then estimated the values

of  $\alpha$  and  $\sigma$  in a Bayesian context, giving each of them weak  $C^+$  distributions  
336 (e.g.  $\alpha \sim C^+(2.5)$ ). The means of the marginal posterior estimate for the  
simulated datasets were then compared to the known values. The results from  
338 these simulations demonstrate that the estimates of  $\alpha$  in the above analyses  
(Table S1) should not be overly biased based on my sample size of approximately  
340 2000 species.

The model used in this analysis, however, is unable to distinguish between  
342 the remaining two hypotheses (47, 48). Further work on how to better constrain  
estimates  $\alpha$  is necessary. A possibly is somehow incorporating these hypotheses  
344 as prior information.

## 4 Supplementary figures

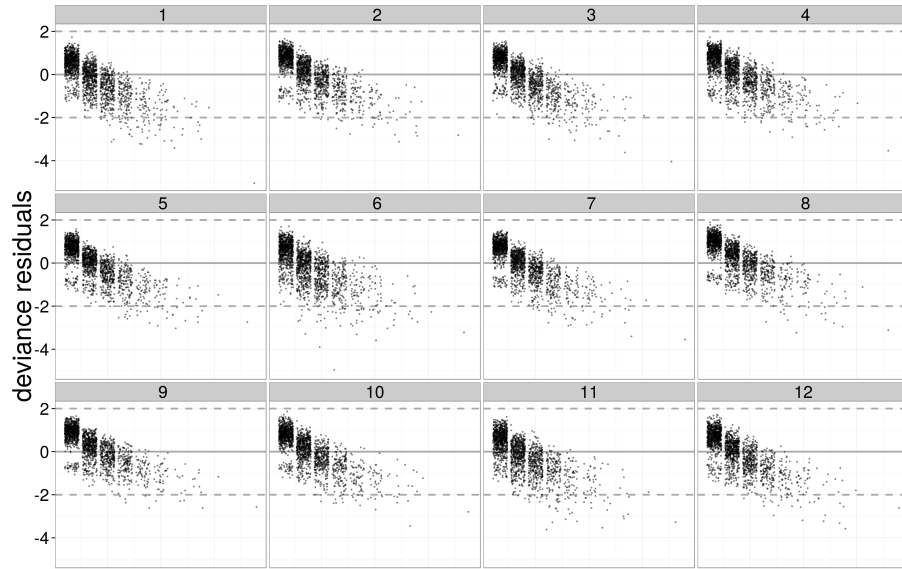


Figure S1: Deviance residuals from the fitted survival model compared to observed durations. Each graph depicts the residuals from single draws from the posterior distributions of all estimated parameters. Positive values indicate an underestimate of the observed duration, while negative values indicate an overestimate of the observed duration. A small amount of noise is added to each point to increase clarity. Twelve different examples are provided here to indicate consistency across multiple realizations.

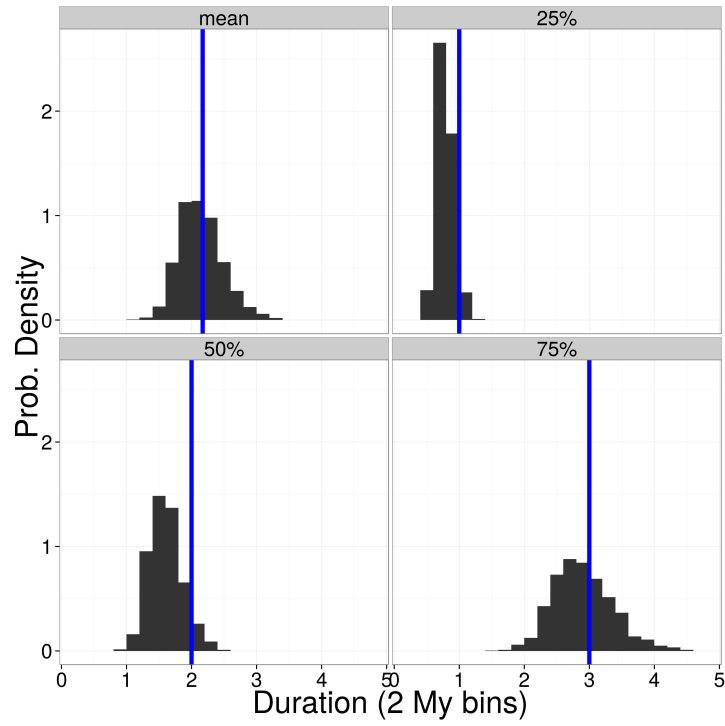


Figure S2: The results of additional posterior predictive checks for four summaries of the observed durations, as labeled. Blue vertical lines indicate the observed value. None of the observed values are significantly different from the posterior predictive distributions.

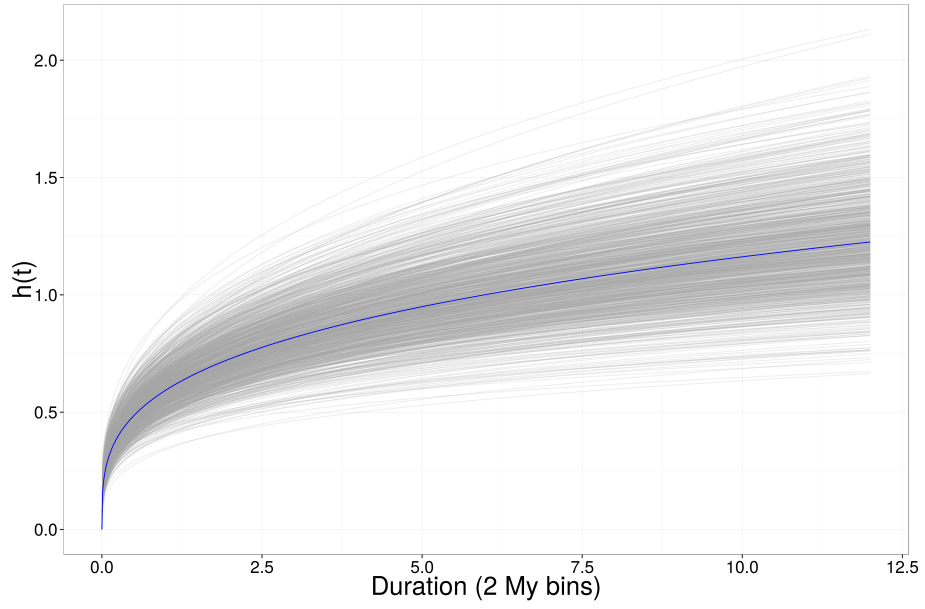


Figure S3: 100 estimates of the hazard function ( $h(t)$ ) for the observed species mean (grey), along with the median estimated hazard function.  $h(t)$  is an estimate of the rate at which a species of age  $t$  is expected to go extinct. Hazard functions were estimated from random draws from the estimated posterior distributions and evaluated with all covariate information set to 0, which corresponds to the expected duration of the mean species.

<sup>346</sup> **5**   **Supplementary tables**

Table S1: Marginal posterior estimates for the parameters of interest based on 1000 posterior samples. The intercept can be interpreted as the estimate for the mean observed species. The other values are the effect of a trait on the expected species duration as expressed as deviation from the mean. The categorical variables are binary index variables where an observation is of that category or not.  $\hat{R}$  values of less than 1.1 indicate approximate chain convergence for the posterior samples.

	mean	sd	2.5%	25%	50%	75%	97.5%	$\hat{R}$
alpha	1.29	0.03	1.23	1.27	1.29	1.31	1.36	1.00
intercept	-0.78	0.14	-1.05	-0.87	-0.78	-0.68	-0.51	1.00
logit(occupancy)	-0.53	0.08	-0.69	-0.59	-0.53	-0.48	-0.38	1.00
log(size)	-0.05	0.05	-0.14	-0.08	-0.05	-0.01	0.05	1.00
ground dwelling	-0.28	0.10	-0.47	-0.34	-0.28	-0.21	-0.09	1.00
scansorial	-0.22	0.11	-0.43	-0.29	-0.22	-0.14	-0.00	1.00
herbivore	0.09	0.09	-0.09	0.03	0.09	0.14	0.27	1.00
insectivore	0.10	0.11	-0.11	0.03	0.10	0.17	0.31	1.00
omnivore	-0.12	0.11	-0.33	-0.19	-0.12	-0.05	0.09	1.00
sd cohort	0.33	0.06	0.23	0.29	0.33	0.37	0.48	1.00
sd phylogeny	0.11	0.05	0.03	0.07	0.10	0.14	0.23	1.03



Table S2: Species trait assignments in this study are a coarser version of the information available in the PBDB. Information was coarsened to improve per category sample size and uniformity and followed this table.

This study		PBDB categories
Diet	Carnivore	Carnivore
	Herbivore	Browser, folivore, granivore, grazer, herbivore.
	Insectivore	Insectivore.
	Omnivore	Frugivore, omnivore.
Locomotor	Arboreal	Arboreal.
	Ground dwelling	Fossorial, ground dwelling, semifossorial, saltatorial.
	Scansorial	Scansorial.

Table S3: Regression equations used in this study for estimating body size. Equations are presented with reference to taxonomic grouping, part name, and reference.

Group	Equation	log(Measurement)	Source
General	$\log(m) = 1.827x + 1.81$	lower m1 area	(49)
General	$\log(m) = 2.9677x - 5.6712$	mandible length	(50)
General	$\log(m) = 3.68x - 3.83$	skull length	(51)
Carnivores	$\log(m) = 2.97x + 1.681$	lower m1 length	(52)
Insectivores	$\log(m) = 1.628x + 1.726$	lower m1 area	(53)
Insectivores	$\log(m) = 1.714x + 0.886$	upper M1 area	(53)
Lagomorph	$\log(m) = 2.671x - 2.671$	lower toothrow area	(12)
Lagomorph	$\log(m) = 4.468x - 3.002$	lower m1 length	(12)
Marsupials	$\log(m) = 3.284x + 1.83$	upper M1 length	(54)
Marsupials	$\log(m) = 1.733x + 1.571$	upper M1 area	(54)
Rodentia	$\log(m) = 1.767x + 2.172$	lower m1 area	(49)
Ungulates	$\log(m) = 1.516x + 3.757$	lower m1 area	(55)
Ungulates	$\log(m) = 3.076x + 2.366$	lower m2 length	(55)
Ungulates	$\log(m) = 1.518x + 2.792$	lower m2 area	(55)
Ungulates	$\log(m) = 3.113x - 1.374$	lower toothrow length	(55)

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