

Species occurrence as a function of both emergent biological traits  
and environmental context

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## Introduction

- 2 How do species pools change over time as species are recruited or go extinct? When are ecotypes enriched or depleted? How does global and regional environmental context affect the distribution of
- 4 species ecotypes (e.g. guilds) in a regional species pool?

A regional species pool is the set of species which form communities in a specific region; local communities are subsets of the regional pool. The composition of a regional species pool changes over time due to speciation, migration, extinction. Local scale processes like resource competition

6  
8 only affect the regional species pool if all communities are affected.

Valentine and Bambach how they presented guilds in paleobiology which is taxa united by similarity of their macroecology (Bambach, 1977; Valentine, 1969). Bush and Bambach presented an ecocube to describe what how marine invertebrates partition space and resources (Bambach et al., 2007; Bush and Bambach, 2011; Bush et al., 2007). Unique combinations represent what possible ecotypes are observable. The distribution of ecocube occupancy is then normally analyzed as raw counts of unique combinations or using ordination methods and the change in disparity over time is estimated (Bambach et al., 2007; Bush and Bambach, 2011; Bush et al., 2007).

16 Analysis of mammal diversity and hypotheses as to the processes that have shaped it tend to fall under a few categories: diversity of the whole system (Alroy, 1996; Alroy et al., 2000; Figueirido et al., 2012; Liow et al., 2008), guild based (Janis et al., 2004; Janis, 2008; Janis et al., 2000; Janis and Wilhelm, 1993; Jernvall and Fortelius, 2004; Pires et al., 2015), clade based (Quental and Marshall, 2013; Silvestro et al., 2015; Slater, 2015), climate based (Blois and Hadly, 2009; Janis, 1993; Janis and Wilhelm, 1993), and location based (Badgley and Finarelli, 2013; Eronen et al., 2015). Rarely are more than two of these categories considered simultaneously, and instead integration of these diverse observations and hypotheses tends to be based on coincidence. The goal 18 of this study is to pool information from multiple levels of organization by integrating both species and climate data into a single analysis in order to provide a more holistic interpretation of the 20 processes which may have shaped mammal species diversity.

Fourth-corner modeling is an approach to explaining the patterns of either species abundance or  
28 presence/absence as a product of species traits, environmental factors, and the interaction between  
traits and environment (Brown et al., 2014; Jamil et al., 2013; Pollock et al., 2012; Warton et al.,  
30 2015) CITATION. In modern ecological studies, what is being modeled is species occurrences at  
localities distributed across a region (Jamil et al., 2013; Pollock et al., 2012). In this study, what is  
32 being modeled is the pattern of species occurrence over time for most of the Cenozoic in North  
America (Fig. 1). These two approaches, modern and paleontological, are different views of the same  
34 three-dimensional pattern: species at localities over time. The temporal limitations of modern  
ecological studies and difficulties with uneven spatial occurrences of fossils in paleontological studies  
36 means that these approaches are complimentary but reveal different patterns of how species are  
distributed in time and space.

38 One of the greatest challenges with analyzing species occurrence data is the inherent incompleteness  
of any sample (Foote, 2001; Foote and Sepkoski, 1999; Lloyd et al., 2011; Royle and Dorazio, 2008;  
40 Royle et al., 2014; Wang and Marshall, 2016). In the modern, only presences are certain as an  
absence can be caused by both the species being truly absent or the species never having been  
42 sampled (Royle and Dorazio, 2008; Royle et al., 2014). For paleontological data in the context of  
this study, the incomplete preservation of fossil communities combined with the incomplete  
44 sampling of what fossils there are means that the true times of origination or extinction may not be  
observed (Foote, 2001; Foote and Sepkoski, 1999; Wang et al., 2016; Wang and Marshall, 2016).

46 In the analyses done here, a few key covariates which describe species' macroecology and  
environmental context are considered. Because of the complexity of fourth-corner analyses in terms  
48 of both number of covariates considered and structure of each model, it is possible to consider and  
test a large number of possible hypotheses. Presented here are the species traits and related  
50 hypotheses, followed by the environmental factors and related hypotheses.

The principle species trait considered in this study is a species' ecotype, defined here as the unique  
52 combination of species dietary category and locomotor category (e.g. arboreal omnivore versus  
unguligrade herbivore). This classification is analogous to the marine invertebrate ecocube discussed

54 above (Bush and Bambach, 2011; Bush et al., 2007; ?). Species mass was also included as a species trait, but is mostly included in order to control for that effect on species observation and occurrence.

56 Translating previous work into hypotheses applicable to this analysis is difficult. Taxonomic grouping is frequently invoked in many proposed hypotheses for how mammal diversity is  
58 structured (Janis, 2008; Janis and Wilhelm, 1993; Pires et al., 2015; Quental and Marshall, 2013;  
60 Slater, 2015). However, this practice is problematic because taxonomic grouping conflates shared evolutionary history and similarities in species macroecology which means that whatever aspects of species biology are important for the processes underlying species diversity are obscured.

62 Jernvall and Fortelius (2004) found that for the Neogene of Europe the relative abundance of mammal guilds was stable over time even in the face of high turnover rates.

64 Many discussions of the effects or associates of species ecology and diversity have focused on ungulate herbivores (Janis et al., 2004; Janis, 2008; Janis et al., 2000; Janis and Wilhelm, 1993) and  
66 carnivores (Janis and Wilhelm, 1993; Pires et al., 2015; Silvestro et al., 2015; Slater, 2015).

The diversity history of ungulate herbivores is characterized by younger originating taxa having  
68 longer legs, higher crowned teeth, and a preference for grazing over browsing than their earlier originating counterparts (Janis et al., 2004; Janis, 2008; Janis et al., 2000; Janis and Wilhelm,  
70 1993); all of which have all been attributed to environmental change or tectonic activity driving climate and environmental change (Blois and Hadly, 2009; Eronen et al., 2015; Janis, 2008).

72 Additionally, it has been observed that ungulate cursorial forms arose before carnivore cursorial forms, an observation attributed to the reorganization of plant communities towards the end of the  
74 Cenozoic (Janis and Wilhelm, 1993).

Within the canid guild of North America (e.g. plantigrade and digitigrade carnivores) there is  
76 evidence that their diversity, or at least the structure of that diversity, is self-regulating in the sense that species from different clades are “competing” for niche or guild space in the North American  
78 regional species pool (Silvestro et al., 2015).

A pattern of generally constant diversity through time is also observed within the canid carnivore

80 subguilds of hypercarnivore, hypocarnivore, and mesocarnivores though there was no evidence of  
diversity-dependence in trait (e.g. body size) evolution (Slater, 2015). The general pattern of  
82 constant diversity in the face of turnover is however consistent with a possibly self-regulating  
system.

84 There is some uncertainty as to the effect of species body size on mammal diversity and aspects of  
the diversification processes, specifically extinction (Liow et al., 2008, 2009; Smits, 2015; Tomiya,  
86 2013).

88 Smits (2015) found several systematic differences in mammal species durations associated with  
various species traits. Omnivorous taxa were found to have, on average, a greater duration than  
other dietary categories. Additionally, arboreal taxa were found to have a shorter duration than  
90 other locomotor categories.

92 An unresolved question from Smits (2015) is whether the greater extinction risk faced by arboreal is  
constant over time or if there was a change in extinction risk at the Paleogene/Neogene boundary.  
Specifically, the question is whether the extinction risk arboreal taxa increased in the Neogene,  
94 driving the loss of arboreal taxa and average extinction risk of arboreal taxa down.

96 There are no observed massive cross-taxonomic turnover events in the North American record,  
unlike the Neogene record Europe (Alroy, 1996, 2009; Alroy et al., 2000; Eronen et al., 2015; Janis,  
1993).

98 Fundamentally, all species respond differently to climate and environmental change (Blois and  
Hadly, 2009). Macroecological patterns are the similarities across species, the emergent properties  
100 of how species react to a similar “stimulus.”

102 The Cenozoic is generally characterized by a global cooling trend and the development of polar  
ice-caps during the Neogene, with a few notable exceptions (Cramer et al., 2011; Zachos et al., 2008,  
2001). The Cenozoic of North America is additionally characterized by an environmental transition  
104 from the closed, partially forested environments of the Paleogene to the savannah and grasslands  
environments of the Neogene (Blois and Hadly, 2009; Janis, 1993; Janis et al., 2000; Strömborg,

<sup>106</sup> 2005).

With respect to North America specifically, much of regional climatic and environmental change has  
<sup>108</sup> been attributed to tectonic activity and uplift (Badgley and Finarelli, 2013; Blois and Hadly, 2009;  
Eronen et al., 2015; Janis, 2008) CITATIONS. Additionally, tectonic activity and uplift is  
<sup>110</sup> considered the driving causal mechanism behind both changes to diversity and trait evolution  
(Badgley and Finarelli, 2013; Blois and Hadly, 2009) CITATIONS.

<sup>112</sup> The Eocene-Oligocene transition is associated with high extinction amongst ungulate taxa (Janis,  
2008). This period is also the transition from the Paleogene to the Neogene and from herbivores  
<sup>114</sup> being browsing dominated to grazing dominated CITATION.

There is an observed stability in estimates of global temperature from the E/O transition till the  
<sup>116</sup> end of the Miocene; this is called the Mid-Miocene climatic optimum (Zachos et al., 2008, 2001).  
The Mid-Miocene climatic optimum is bookended by periods of temperature decline.

<sup>118</sup> The environmental factors included in this study include estimates of global tempreature and the  
changing floral groups present in North America across the Cenozoic. These covariates were chosen  
<sup>120</sup> because they provide high level characterizations of the environmental context of the entire North  
American regional species pool for most of the Cenozoic. Importantly, the effects of a species  
<sup>122</sup> ecotype on diversity are themselves modeled as functions of environmental factors (Fig. 1) allowing  
for inference as to how species ecology mediates environmental context.

<sup>124</sup> The effect of climate on diversity and the diversification process has been the focus of considerable  
research with many analyses favoring diversification being more biologically-mediated than  
<sup>126</sup> climate-mediated (Alroy, 1996; Alroy et al., 2000; Clyde and Gingerich, 1998; Figueirido et al.,  
2012). Scale of analysis makes a big difference in interpretation of results, both temporal and  
<sup>128</sup> geographic. For example when the mammal fossil record analyzed at small temporal and geographic  
scales a correlation between diversity and climate are observable (Clyde and Gingerich, 1998).

<sup>130</sup> However, when the record is analyzed at the scale of the continent and the Cenozoic there is no  
correlation with diversity and climate (Alroy et al., 2000). This results, however, does not go  
<sup>132</sup> against the idea that there may be short periods of correlation and that this correlation change or

reverse direction over time; instead this result means that there is no single direction of correlation  
134 between diversity and climate (Figueirido et al., 2012).

In the case of a fluctuating correlation between diversity and climate it is hard to make the  
136 argument of an actual causal link between the two without understanding the ecological differences  
in mammalian fauna over time; when this analysis is based on diversity or taxonomy alone no  
138 mechanisms are possible to infer. After all, taxonomy conflates many potential factors that could  
affect diversification into a single variable; by separating the effects of shared common ancestry (i.e.  
140 phylogeny) from species ecology the subtle differences in the diversification process can be observed  
(Smits, 2015).

142 Ultimately, the goal of this analysis are to understand when are unique ecotypes enriched or  
depleted in the North American mammal regional species pool and how changes in ecotypic  
144 diversity are related to changes in species' environmental context.

## Materials and Methods

### 146 Taxon occurrences and species-level information

All fossil occurrence information was downloaded from the Paleobiology Database.  
148 Occurrences (PBDB) were restricted to all Mammalia sampled in North America between the  
Maastrichtian and Gelasian stages. Taxonomic, stratigraphic, and ecological metadata for each  
150 occurrence was included. The raw data is available for download at <http://goo.gl/2s1geU>.

This raw data was then sorted, cleaned, and manipulated programmatically prior to analysis.  
152 Species taxonomic assignments given by the PBDB were updated for accuracy and consistency. For  
example, species classified in the order Artiodactyla were reclassified as Cetartiodactyla. These  
154 re-assignments follow Smits (2015) and were Janis et al. (2008, 1998) and the Encyclopedia of Life  
WEBSITE. Additionally, Taxa who's life habit was classified as either volant (i.e. Chiroptera) or  
156 aquatic (e.g. Cetacea) were excluded from this analysis because of both differences in fossilization

potential and applicability to the study of terrestrial species pools.

158 The life habit and dietary categories provided through the PBDB were coarsened to increase per  
 159 ecotype sample size; this coarsening follows the same procedure as Smits (2015). Additionally, life  
 160 habit category was further modified to break-up the vague “ground-dwelling” category;  
 161 re-classifying these species by ankle posture gives more precise information about that species’  
 162 environmental context. Ground-dwelling taxa were reassigned following ? by species taxonomic  
 163 context. Species ecotype is defined as the interaction between life habit and diet categories. Ecotype  
 164 categories with less than 10 species having ever been in that combination were excluded, yielding a  
 total of 18 of 24 possible ecotypes.

Table 1: 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 2: Posture assignment based on taxonomy

Order	Family	Stance
	Ailuridae	plantigrade
	Allomyidae	plantigrade
	Amphicyonidae	plantigrade
	Amphilemuridae	plantigrade
	Anthracotheriidae	digitigrade
	Antilocapridae	unguligrade
	Apheliscidae	plantigrade

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**Table 2 – continued from previous page**

Order	Family	Stance
	Aplodontidae	plantigrade
	Apternodontidae	scansorial
	Arctocyonidae	unguligrade
	Barbourofelidae	digitigrade
	Barylambdidae	plantigrade
	Bovidae	unguligrade
	Camelidae	unguligrade
	Canidae	digitigrade
	Cervidae	unguligrade
	Cimolodontidae	scansorial
	Coryphodontidae	plantigrade
	Cricetidae	plantigrade
	Cylindrodontidae	plantigrade
	Cyriacotheriidae	plantigrade
	Dichobunidae	unguligrade
Dinocerata		unguligrade
	Dipodidae	digitigrade
	Elephantidae	digitigrade
	Entelodontidae	unguligrade
	Eomyidae	plantigrade
	Erethizontidae	plantigrade
	Erinaceidae	plantigrade
	Esthonychidae	plantigrade
	Eutypomyidae	plantigrade
	Felidae	digitigrade

Continued on next page

**Table 2 – continued from previous page**

Order	Family	Stance
	<i>Florentiamyidae</i>	plantigrade
	<i>Gelocidae</i>	unguligrade
	<i>Geolabididae</i>	plantigrade
	<i>Glyptodontidae</i>	plantigrade
	<i>Gomphotheriidae</i>	unguligrade
	<i>Hapalodectidae</i>	plantigrade
	<i>Heteromyidae</i>	digitigrade
	<i>Hyaenidae</i>	digitigrade
	<i>Hyaenodontidae</i>	digitigrade
	<i>Hypertragulidae</i>	unguligrade
	<i>Ischyromyidae</i>	plantigrade
	<i>Jimomyidae</i>	plantigrade
Lagomorpha		digitigrade
	<i>Leptictidae</i>	plantigrade
	<i>Leptochoeridae</i>	unguligrade
	<i>Leptomerycidae</i>	unguligrade
	<i>Mammutidae</i>	unguligrade
	<i>Megalonychidae</i>	plantigrade
	<i>Megatheriidae</i>	plantigrade
	<i>Mephitidae</i>	plantigrade
	<i>Merycoidodontidae</i>	digitigrade
Mesonychia		unguligrade
	<i>Mesonychidae</i>	digitigrade
	<i>Micropternodontidae</i>	plantigrade
	<i>Mixodectidae</i>	plantigrade

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**Table 2 – continued from previous page**

Order	Family	Stance
	Moschidae	unguligrade
	Muridae	plantigrade
	Mustelidae	plantigrade
	Mylagaulidae	fossorial
	Mylodontidae	plantigrade
	Nimravidae	digitigrade
	Nothrotheriidae	plantigrade
Notoungulata		unguligrade
	Oromerycidae	unguligrade
	Oxyaenidae	digitigrade
	Palaeomerycidae	unguligrade
	Palaeoryctidae	plantigrade
	Pampatheriidae	plantigrade
	Pantolambdidae	plantigrade
	Peritychidae	digitigrade
Perissodactyla		unguligrade
	Phenacodontidae	unguligrade
Primates		plantigrade
	Procyonidae	plantigrade
	Proscalopidae	plantigrade
	Protoceratidae	unguligrade
	Reithroparamyidae	plantigrade
	Sciuravidae	plantigrade
	Sciuridae	plantigrade
	Simimyidae	plantigrade

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**Table 2 – continued from previous page**

Order	Family	Stance
	Soricidae	plantigrade
	Suidae	digitigrade
	Talpidae	fossorial
	Tayassuidae	unguligrade
	Tenrecidae	plantigrade
	Titanoideidae	plantigrade
	Ursidae	plantigrade
	Viverravidae	plantigrade
	Zapodidae	plantigrade

166

Species mass information was gathered from multiple different sources where a plurality of the body  
168 size estimates are from the PBDB. Body part measurements for many species are also available  
through the PBDB. Just as with Smits (2015), these measurements and corresponding regression  
170 equations were used to get mass estimates for more species. Additional mass estimates and body  
part measurements were sourced from numerous publications and the Neogene Old World Database;  
172 see the supplementary material to Smits (2015) for details. Mass was log-transformed and then  
mean-centered and rescaled by dividing by two-times its standard deviation; this insures that the  
174 magnitude of effects for both continuous and discrete covariates are comparable (Gelman, 2008;  
Gelman and Hill, 2007).

176 All fossil occurrences from 64 to 2 million years ago (Mya) were binned into 31 2 million year (My)  
bins. This temporal length was chosen because it is approximately the resolution of the North  
178 American mammal fossil record.

Table 3: 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	Legendre (1986)
General	$\log(m) = 2.9677x - 5.6712$	mandible length	?
General	$\log(m) = 3.68x - 3.83$	skull length	?
Carnivores	$\log(m) = 2.97x + 1.681$	lower m1 length	?
Insectivores	$\log(m) = 1.628x + 1.726$	lower m1 area	?
Insectivores	$\log(m) = 1.714x + 0.886$	upper M1 area	?
Lagomorph	$\log(m) = 2.671x - 2.671$	lower toothrow area	Tomiya (2013)
Lagomorph	$\log(m) = 4.468x - 3.002$	lower m1 length	Tomiya (2013)
Marsupials	$\log(m) = 3.284x + 1.83$	upper M1 length	?
Marsupials	$\log(m) = 1.733x + 1.571$	upper M1 area	?
Rodentia	$\log(m) = 1.767x + 2.172$	lower m1 area	Legendre (1986)
Ungulates	$\log(m) = 1.516x + 3.757$	lower m1 area	?
Ungulates	$\log(m) = 3.076x + 2.366$	lower m2 length	?
Ungulates	$\log(m) = 1.518x + 2.792$	lower m2 area	?
Ungulates	$\log(m) = 3.113x - 1.374$	lower toothrow length	?

## Environmental and temporal covariates

- 180 The group-level covariates in this study are descriptors of species' environmental context,  
 specifically global temperature estimates and Graham's floral intervals CITATION. Global  
 182 temperature across most of the Cenozoic was calculated from Mg/Ca isotope record from deep sea  
 carbonates (Cramer et al., 2011). Mg/Ca based temperature estimates are preferable to the  
 184 frequently used  $\delta^{18}\text{O}$  temperature proxy (Alroy et al., 2000; Figueirido et al., 2012; Zachos et al.,  
 2008, 2001) because Mg/Ca estimates do not conflate temperature with ice sheet volume and  
 186 depth/stratification changes; this makes it preferable as an estimate of global temperature for  
 macroevolutionary and macroecological studies (Ezard et al., 2016).
- 188 Two aspects of the Mg/Ca-based temperature curve were included in this analysis: mean and range.  
 Both were calculated as the mean of all respective estimates for each 2 My temporal bins. Both  
 190 mean and range were then rescaled as above: subtract mean, divide by twice the standard deviation.
- The other major set of environmental factors included in this study are Graham's Cenozoic plant  
 192 phases CITATION. Graham's plant phases are holistic descriptors of the taxonomic composition of

		State at $t + 1$		
		$0_{never}$	1	$0_{extinct}$
State at $t$	$0_{never}$	$1 - \theta$	$\theta$	0
	1	0	$\theta$	$1 - \theta$
	$0_{extinct}$	0	0	1

(a) Pure-presence

		State at $t + 1$		
		$0_{never}$	1	$0_{extinct}$
State at $t$	$0_{never}$	$1 - \phi$	$\phi$	0
	1	0	$\pi$	$1 - \pi$
	$0_{extinct}$	0	0	1

(b) Birth-death

Table 4: Transition matrices for the pure-presence (4a) and birth-death (4b) models. Both of these models share the core machinery of discrete-time birth-death processes but make distinct assumptions about the equality of originating and surviving (Eq. 2, and 3). Note also that while there are only two state “codes” (0, 1), there are in fact three states: never having originated  $0_{never}$ , present 1, extinct  $0_{extinct}$  (Allen, 2011).

12 ecosystem types, which plants are present at a given time, and the relative modernity of those  
 194 plant groups with younger phases representing increasingly modern taxa CITATION. Graham  
 CITATION defines four intervals from the Cretaceous to the Pliocene, though only three of these  
 196 intervals are included in this analysis. Graham’s plant phases CITATION was included as a series  
 of “dummy variables” encoding the three phases included in this analysis. This means that the first  
 198 phase is synonymous with the intercept and phases

## Modelling species occurrence

200 Two different models were used in this study: a pure-presence model and a birth-death model. Both  
 models at their core are hidden Markov model where the latent aspect of the process has an  
 202 absorbing state (Allen, 2011). The difference between these two models is if the probability of a  
 species origination and survival are considered equal or different (Table 4). Something that is  
 204 important to realize is that while there are only two state “codes” in a presence-absence matrix (i.e.  
 0/1), there are in fact three states in a birth-death model: never having originated, extant, and  
 206 extinct. The last of these is the absorbing state, as once a species has gone extinct it cannot  
 re-originate (Allen, 2011); this is made obvious in the transition matrices as the probability of an  
 208 extinct species changing states is 0 (Table 4). See below for parameter explanations (Tables 6, and  
 7).

210 **Data augmentation**

All presence/absence observations are incomplete. The hidden Markov model at the core of this  
212 analysis allows for observed absences to be used meaningfully to estimate the number of unobserved  
species. Of specific concern in this analysis is the unknown “true” size of the dataset; how many  
214 species could have actually been observed? While many species have been observed, the natural  
incompleteness of all observations, especially in the case of paleontological data, there are obviously  
216 many species which were never sampled (Royle and Dorazio, 2008; Royle et al., 2007).

Let  $N$  by the total number of observed species,  $M$  be the upper limit of possible species that could  
218 have existed given a model of species presence, and  $N^*$  is the all-zero histories where  $N^* = M - N$ .  
This approach assumes that  $\hat{N} \sim \text{Binomial}(M, \psi)$  where  $\hat{N}$  is the estimated “true” number of  
220 species and  $\psi$  is the probability that any augmented species should actually be “present.” Because  
 $M$  is user defined, this approach effectively gives  $\psi$  a uniform prior over  $N$  to  $M$  (Royle and  
222 Dorazio, 2008). For this study,  $M = N + \lfloor N/4 \rfloor$ .

Data imputation is the process of estimating missing data for partially observed covariates (Gelman  
224 and Hill, 2007; Rubin, 1996), this is simple in a Bayesian context because data are also parameters  
(Gelman et al., 2013). Augmented species also have no known mass so a mass estimate must be  
226 imputed for each possible species (Royle and Dorazio, 2012). This procedure assumes that mass  
values for augmented species are from the same distribution as observed species. The distribution of  
228 observed mass values is estimated as part of the model, and new mass values are then generated  
from this distribution. This approach is an example of imputing data missing completely at random  
230 (Gelman and Hill, 2007; Royle and Dorazio, 2012). Because log mass values are rescaled as a part of  
this study, the body mass distribution is already known ( $\mathcal{N}(0, 0.5)$ ); augmented species body mass  
232 just simply drawn from this distribution.

In addition to body mass information, the augmented species need an ecotype classification. Because  
234 these species are completely unknown, they were all classified as “augmented,” an additional  
grouping indicating their unknown biology. This classification has no biological interpretation.

Table 5: Observation parameters

Parameter	dimensions	explanation
$y$	$N \times T$	observed species presence/absence
$z$	$N \times T$	“true” species presence/absence
$p$	$T$	probability of observing a species that is present at time $t$
$m$	$N$	species log mass, rescaled
$\alpha_0$	1	average log-odds of $p$
$\alpha_1$	1	change in average log-odds of $p$ per change mass
$r$	$T$	difference from $\alpha_0$ associated with time $t$
$\sigma$	1	standard deviation of $r$

### 236 Observation process

- The type of hidden Markov model used in this study has three characteristic probabilities:
- 238 probability  $p$  of observing a species given that it is present, probability  $\phi$  of a species surviving from one time to another, and probability  $\pi$  of a species first appearing (Royle and Dorazio, 2008). In  
240 this formulation, the probability of a species going extinct is  $1 - \pi$ . For the pure-presence model  
 $\phi = \pi$ , while for the birth-death model  $\phi \neq \pi$ .
- 242 The probability of observing a species that is present  $p$  is modeled as a logistic regression was a time-varying intercept and species mass as a covariate. The effect of species mass on  $p$  was assumed  
244 linear and constant over time and given a prior reflecting a possible positive relationship; these assumptions are reflected in the structure of the model Equation 1. The parameters associated with  
246 this part of the model are described in Table 5.

$$\begin{aligned}
y_{i,t} &\sim \text{Bernoulli}(p_{i,t} z_{i,t}) \\
p_{i,t} &= \text{logit}^{-1}(\alpha_0 + \alpha_1 m_i + r_t) \\
r_t &\sim \mathcal{N}(0, \sigma)
\end{aligned} \tag{1}$$

### Pure-presence process

- 248 For the pure-presence model there is only a single probability dealing with the presence of a species  $\theta$  (Table 4a). This probability was modeled as multi-level logistic regression with both species-level

Table 6: Parameters for the model of presence in the pure-presence model

Parameter	dimensions	explanation
$z$	$N \times T$	“true” species presence/absence
$\theta$	$N \times T - 1$	probability of $z = 1$
$a$	$T - 1 \times D$	ecotype-varying intercept; mean value of log-odds of $\theta$
$m$	$N$	species log mass, rescaled
$b_1$	1	effect of species mass on log-odds of $\theta$
$b_2$	1	effect of species mass, squared, on log-odds of $\theta$
$U$	$T \times D$	matrix of group-level covariates
$\gamma$	$U \times D$	matrix of group-level regression coefficients
$\Sigma$	$D \times D$	covariance matrix of $a$
$\Omega$	$D \times D$	correlation matrix of $a$
$\tau$	$D$	vector of standard deviations for each ecotype $a_d$

250 and group-level covariates (Gelman et al., 2013; Gelman and Hill, 2007). The parameters associated  
with pure-presence model are presented in Table 6 and the full sampling statement in Equation 2.

252 The species-level of the model (Eq. 2) is a logistic regression with varying-intercept that varies by  
ecotype. Additionally, species mass was included as a covariate associated with two regression  
254 coefficients allowing a quadratic relationship with log-odds of occurrence. This assumption is based  
on the known distribution of mammal body masses where species with intermediate mass values are  
256 more common than either small or large bodied species. These assumptions are also reflected in the  
choice of priors for these regression coefficients.

258 The values of each ecotype’s intercept are themselves modeled as regressions using the group-level  
covariates associated with environmental context. Each of these regressions has an associated  
260 variance of possible values of each ecotype’s intercept (Gelman and Hill, 2007). In addition, the  
covariances between ecotype intercepts, given this group-level regression, are modeled (Gelman and  
262 Hill, 2007).

All parameters not modeled elsewhere were given weakly informative priors (Gelman et al., 2013)  
264 CITATION STAN MANUAL STATISTICAL RETHINKING. Weakly informative means that  
priors do not necessarily encode actual prior information but instead help regularize or weakly  
266 constrain posterior estimates. These priors have a concentrated probability density around and near  
zero; this has the effect of tempering our estimates and help prevent overfitting the model to the

268 data (Gelman et al., 2013) CITATION STAN MANUAL STATISTICAL RETHINKING.

$$\begin{aligned} y_{i,t} &\sim \text{Bernoulli}(p_{i,t} z_{i,t}) & \alpha_0 &\sim \mathcal{N}(0, 1) \\ p_{i,t} &= \text{logit}^{-1}(\alpha_0 + \alpha_1 m_i + r_t) & \alpha_1 &\sim \mathcal{N}(1, 1) \\ r_t &\sim \mathcal{N}(0, \sigma) & \sigma &\sim \mathcal{N}^+(1) \\ z_{i,1} &\sim \text{Bernoulli}(\rho) & b_1 &\sim \mathcal{N}(0, 1) \\ z_{i,t} &\sim \text{Bernoulli}(\theta_{i,t}) & b_2 &\sim \mathcal{N}(-1, 1) \\ \theta_{i,t} &= \text{logit}^{-1}(a_{t,j[i]} + b_1 m_i + b_2 m_i^2) & \gamma &\sim \mathcal{N}(0, 1) \\ a &\sim \text{MVN}(u\gamma, \Sigma) & \tau &\sim \mathcal{N}^+(1) \\ \Sigma &= \text{diag}(\tau)\Omega\text{diag}(\tau) & \Omega &\sim \text{LKJ}(2) \end{aligned} \tag{2}$$

### Birth-death process

- 270 In the birth-death model,  $\phi \neq \pi$  and so each of these probabilities are modeled separately but in a  
similar manner to how  $\theta$  is modeled in the pure-presence model (Eq. 2, Table 4b). The parameters  
272 associated with the birth-death presence model are presented in Table 7 and the full sampling  
statement, including observation (Eq. 1), is described in Equation 3.
- 274 Similar to the pure-presence model, both  $\phi$  and  $\pi$  are modeled as logistic regressions with  
varying-intercept and one covariate associated with two parameters. The possible relationships  
276 between mass and both  $\phi$  and  $\pi$  are reflected in the parameterization of the model and choice of  
priors (Eq. 3).
- 278 The intercepts of  $\phi$  and  $\pi$  both vary by species ecotype and those values are themselves the product  
of group-level regression using environmental factors as covariates (Eq. 3); this is identical to the

Table 7: Parameters for the model of presence in the pure-presence model

Parameter	dimensions	explanation
$z$	$N \times T$	“true” species presence/absence
$\phi$	$N \times T$	probability of $z_{-,t} = 1   z_{-,t-1} = 0$
$\pi$	$N \times T - 1$	probability of $z_{-,t} = 1   z_{-,t-1} = 1$
$a^\phi$	$T - 1 \times D$	ecotype-varying intercept; mean value of log-odds of $\theta$
$a^\pi$	$T - 1 \times D$	ecotype-varying intercept; mean value of log-odds of $\theta$
$m$	$N$	species log mass, rescaled
$b_1^\phi$	1	effect of species mass on log-odds of $\phi$
$b_1^\pi$	1	effect of species mass on log-odds of $\pi$
$b_2^\phi$	1	effect of species mass, squared, on log-odds of $\phi$
$b_2^\pi$	1	effect of species mass, squared, on log-odds of $\pi$
$U$	$T \times D$	matrix of group-level covariates
$\gamma^\phi$	$U \times D$	matrix of group-level regression coefficients
$\gamma^\pi$	$U \times D$	matrix of group-level regression coefficients
$\Sigma^\phi$	$D \times D$	covariance matrix of $a^\phi$
$\Sigma^\pi$	$D \times D$	covariance matrix of $a^\pi$
$\Omega^\phi$	$D \times D$	correlation matrix of $a^\phi$
$\Omega^\pi$	$D \times D$	correlation matrix of $a^\pi$
$\tau^\phi$	$D$	vector of standard deviations for each ecotype $a_d^\phi$
$\tau^\pi$	$D$	vector of standard deviations for each ecotype $a_d^\pi$

280 pure presence model (Eq. 2).

$$\begin{aligned}
 y_{i,t} &\sim \text{Bernoulli}(p_{i,t} z_{i,t}) & \Sigma^\phi &= \text{diag}(\tau^\phi) \Omega^\phi \text{diag}(\tau^\phi) \\
 p_{i,t} &= \text{logit}^{-1}(\alpha_0 + \alpha_1 m_i + r_t) & \Sigma^\pi &= \text{diag}(\tau^\pi) \Omega^\pi \text{diag}(\tau^\pi) \\
 r_t &\sim \mathcal{N}(0, \sigma) & \rho &\sim U(0, 1) \\
 \alpha_0 &\sim \mathcal{N}(0, 1) & b_1^\phi &\sim \mathcal{N}(0, 1) \\
 \alpha_1 &\sim \mathcal{N}(1, 1) & b_1^\pi &\sim \mathcal{N}(0, 1) \\
 \sigma &\sim \mathcal{N}^+(1) & b_2^\phi &\sim \mathcal{N}(-1, 1) \\
 z_{i,1} &\sim \text{Bernoulli}(\phi_{i,1}) & b_2^\pi &\sim \mathcal{N}(-1, 1) \\
 z_{i,t} &\sim \text{Bernoulli} \left( z_{i,t-1} \pi_{i,t} + \sum_{x=1}^t (1 - z_{i,x}) \phi_{i,t} \right) & \gamma^\phi &\sim \mathcal{N}(0, 1) \\
 && \gamma^\pi &\sim \mathcal{N}(0, 1) \\
 \phi_{i,t} &= \text{logit}^{-1}(a_{t,j[i]}^\phi + b_1^\phi m_i + b_2^\phi m_i^2) & \tau^\phi &\sim \mathcal{N}^+(1) \\
 \pi_{i,t} &= \text{logit}^{-1}(a_{t,j[i]}^\pi + b_1^\pi m_i + b_2^\pi m_i^2) & \tau^\pi &\sim \mathcal{N}^+(1) \\
 a^\phi &\sim \text{MVN}(U\gamma^\phi, \Sigma^\phi) & \Omega^\phi &\sim \text{LKJ}(2) \\
 a^\pi &\sim \text{MVN}(U\gamma^\pi, \Sigma^\pi) & \Omega^\pi &\sim \text{LKJ}(2)
 \end{aligned} \tag{3}$$

## Posterior inference and model adequacy

282 Programs that implement joint posterior inference for the above models (Eqs. 2, 3) were  
283 implemented in the probabilistic programming language Stan CITATION. The models used here  
284 both feature latent discrete parameters in the large matrix  $z$  (Tables 5, 6, 7; Eqs. 1, 2, 3). All  
285 methods for posterior inference implemented in Stan are derivative based which causes  
286 complications for actually implementing the above models because integers do not have derivatives.  
287 Instead of implementing a latent discrete parameterization, the posterior probabilities of all possible  
288 states of the latent parameters  $z$  were estimated (i.e. marginalized).

Species durations at minimum range-through from the FAD to the LAD, but the incompleteness of  
290 all observations means that the actual time of origination or extinction is unknown. The  
marginalization approach used here means that the probabilities all possible histories for a species  
292 are calculated, from the end members of the species having existed for the entire study interval and  
the species having only existed between the directly observed FAD and LAD to all possible  
294 intermediaries CITATION STAN MANUAL.

The combined size of the dataset and large number of parameters in both models (Eqs. 2, 3),  
296 specifically the total number of latent parameters that are the matrix  $z$ , means that stochastic  
approximate posterior inference is computationally very slow even using HMC. Instead, an  
298 approximate Bayesian approach was used: variational inference. A recently developed automatic  
variational inference algorithm called “automatic differentiation variational inference” (ADVI) is  
300 implemented in Stan and was used here CITATION. ADVI assumes that the posterior is Gaussian  
but still yields a true Bayesian posterior; this assumption is similar to quadratic approximation of  
302 the likelihood function used in maximum likelihood inference CITATION. The principal limitation  
of assuming the joint posterior is Gaussian is that the true topology of the log-posterior isn’t  
304 estimated; this is a particular burden for scale parameters which are bound to be positive (e.g.  
standard deviation).

306 After fitting both models (Eqs. 2, 3) using ADVI, model adequacy and quality of fit was assessed  
using a series of posterior predictive checks CITATION CITATION. Because all Bayesian models

308 are inherently generative, simulations of new data sets is “free” CITATION. By simulating many  
 310 theoretical data sets using the observed covariate information the congruence between predictions  
 311 made by the model and the observed empirical data can be assessed. By combining multiple  
 312 posterior predictive tests of congruence between empirical and simulated values of interest, the  
 holistic adequacy of the model can be analyzed CITATION.

An example posterior predictive check used in this study was comparing the observed average  
 314 number of observations per species to a distribution of simulated averages; if the empirically  
 observed value sits in the middle of the distribution than the model is adequate in reproducing the  
 316 observed number of occurrences per species.

Posterior simulations for time series are start with the values at  $t = 1$  and then just simulating  
 318 forward.

Given parameter estimates, diversity and diversification rates are estimated through posterior  
 320 predictive simulations. Given the observed presence-absence matrix  $y$ , estimates of the true  
 presence-absence matrix  $z$  can be simulated and the distribution of possible occurrence histories  
 322 can be analyzed. This is conceptually similar to marginalization where the probability of each  
 possible occurrence history is estimated (Fig. 2).

324 The posterior distribution of  $z$  gives the estimate of standing diversity  $N_t^{stand}$  for all time points as

$$N_t^{stand} = \sum_{i=1}^M z_{i,t}. \quad (4)$$

Given estimates of  $N^{stand}$  for all time points, the estimated number of originations  $O_t$  are be  
 326 estimated as

$$O_t = \sum_{i=1}^M z_{i,t} = 1 | z_{i,t-1} = 0 \quad (5)$$

and number of extinctions  $E_t$  estimated as

$$E_t = \sum_{i=1}^M z_{i,t} = 0 | z_{i,t-1} = 1. \quad (6)$$

<sup>328</sup> Per-capita growth  $D^{rate}$ , origination  $O^{rate}$  and extinction  $E^{rate}$  rates are then calculated as

$$\begin{aligned} O_t^{rate} &= \frac{O_t}{N_{t-1}^{stand}} \\ E_t^{rate} &= \frac{E_t}{N_{t-1}^{stand}} \\ D_t^{rate} &= O_t^{rate} - E_t^{rate}. \end{aligned} \tag{7}$$

## Results

<sup>330</sup> Posterior results take one of two forms: direct inspection of parameter estimates, and downstream  
estimates of diversity and diversification rates. For the former, both the pure-presence and  
<sup>332</sup> birth-death models (Eq. 2, and 3 are inspected. For the latter, only posterior estimates from the  
birth-death model are considered; the reason for this is explained below in the comparison of the  
<sup>334</sup> models' posterior predictive check results.

### Comparing parameter estimates from the pure-presence and birth-death models

Comparison of the posterior predictive performance of the pure-presence and birth-death models  
<sup>338</sup> reveals a striking difference in quality of the models' fits to the data (Fig. 3a and 3b). The  
birth-death model is clearly able to reproduce the observed average number of occurrence, in  
<sup>340</sup> contrast to the pure-birth model which greatly underestimates the ovserved average number of  
occurrences. The interpretation of these results is that the results of the birth-death model are  
<sup>342</sup> more representative of the data than the pure-presence model, though further inspection of the  
posterior parameter estimates can provide further insight into why these models give different  
<sup>344</sup> posterior predictive results (Gelman et al., 2013). However, it is expected that downstream analyses  
from the birth-death model will be more reliable than that from the pure-presence model.  
<sup>346</sup> Occurrence probabilities estimated from the pure-presence model (Fig. 4) are much more similar to  
the origination estimates from the birth-death model (Fig. 5) than the estimates of survival

<sup>348</sup> probability (Fig. 6).

In general, both occurrence probabilities estimated from the pure-presence model (Fig. 4) and  
<sup>350</sup> origination probabilities estimated from the birth-death model (fig. 5) increase with time. Notable,  
ecotypes with arboreal components do not follow this average; instead, occurrence and origination  
<sup>352</sup> probabilities appear relatively flat for most of the Cenozoic.

The dramatic differences between origination and survival probabilities indicate how different these  
<sup>354</sup> processes are, and may be responsible for the better posterior predictive performance of the  
birth-death model over the pure-presence model (Fig. 3a, and 3b). While the estimates of both time  
<sup>356</sup> series have high variance, what is striking is how mean origination probability changes over time  
while in general survival probabilities have relatively stable means (Fig. 5, and 6).

<sup>358</sup> Estimates of origination probabilities appear to have less uncertainty than for survival (Fig. 5, and  
6).

<sup>360</sup> The pure-presence and birth-death models differ in estimated effect of mass on the probability of  
observing a species that is present (Fig. 7). For the pure-presence model, mass is estimated to have  
<sup>362</sup> no effect on the probability of observing a species that is present (Fig. 7a). Contrastingly, for the  
birth-death model mass is found to have a negative relationship with observation such that larger  
<sup>364</sup> species are less likely to be observed if present than smaller species (Fig. 7b).

The result from the birth-death model is unexpected given that it is generally assumed that larger  
<sup>366</sup> mammals are more likely to have been collected than smaller mammals CITATION. However,  
collection is not preservation; similarities in preservation rate indicate similarities in how gap-filled  
<sup>368</sup> species records are. What this result means is that the record of large bodied species is expected on  
average to be more gap-filled and less consistent from time point to time point than smaller bodied  
<sup>370</sup> species. Additionally, this is presence/absence data, so higher preservation and collection in terms  
of individual specimens at a location or a single temporal horizon does not necessarily translate to  
<sup>372</sup> high preservation over time.

The effect of species mass on probability of occurrence as estimated from the pure-presence (Fig. 8)

<sup>374</sup> is most similar to the effect of species mass on probability of origination as estimates from the  
<sup>375</sup> birth-death model (Fig. 9). The striking pattern observable in both sets of estimates is the higher  
<sup>376</sup> probability of occurrence for species with body sizes closer to the mean than either extremes. This  
<sup>377</sup> result is consistent with the canonically normal distribution of mammal body sizes CITATION; it is  
<sup>378</sup> then expected that the most likely to occur species would be those from the middle of the  
<sup>379</sup> distribution, and that species originating will on average be of average mass, especially considering  
<sup>380</sup> species shared common ancestry CITATION.

In contrast, the effect of species mass on probability of survival as estimated from the birth-death  
<sup>382</sup> model (Fig. 10) indicates little effect of mass on extinction; this is consistent with previous findings  
from the North American mammal fossil record (Smits, 2015; Tomiya, 2013). Note that all variation  
<sup>384</sup> between ecotypes is due to differences in ecotype-specific survival probability and the associated  
effects of plant phase.

<sup>386</sup> Similarities in parameters estimates between ecotypes may be due to similar response to  
environmental factors. Some of the obvious patterns from inspection of the individual-level  
<sup>388</sup> estimates of occurrence (Fig. 4), origination (Fig. 5), and survival probabilities (Fig. 6) that are of  
note are the similarities between arboreal taxa and the differences between arboreal and all other  
<sup>390</sup> taxa.

Inspection of parameter estimates for the group-level covariates

## <sup>392</sup> Analysis of diversity

All analyses of diversification and macroevolutionary rates has been done using only the birth-death  
<sup>394</sup> model; this is because of the models better posterior predictive check performance (Fig. 3a, and 3b).

For the first half of the Cenozoic there appears to be a very slow decline and then plateau in total  
<sup>396</sup> diversity until the WHEN? (Fig. 14a).

When viewed through the lens of diversification rate the structure behind this pattern begins to  
<sup>398</sup> take shape (Fig. 14b). For approximately the first third of the Cenozoic, diversification rate is

frequently below zero species gained per species present per two million years; this is broken up by  
400 few inferred spikes in diversification WHEN?. During the observed period of possible stability in

The comparison between per capita origination and extinction rate estimates reveals how  
402 diversification rate is formed (Fig. 14c, 14d). Origination rate seems most closely mimic  
diversification rate while extinction rate has a saw-toothed pattern for the Cenozoic with no  
404 obvious emergent structure; inferred spikes in origination rate do not correspond to any spikes in  
extinction rate.

406 Diversity partitioned by ecotype reveals a lot of the complexity behind the pattern of mammal  
diversity for the Cenozoic (Fig. 15).

408 An impressive commonality across multiple ecotype-specific diversity time series are two spikes in  
diversity, either up or down (Fig. 15). Spikes of increased diversity are seen this is seen in all  
410 arboreal ecotypes, plantigrade insectivores, scansorial insectivores, and scansorial omnivores. The  
converse pattern, spikes of decreased diversity, are strongly observed in the diversity history of  
412 digitigrade herbivores, with weaker decreases observed in the histories of digitigrade carnivores, and  
unguligrade herbivores.

414 Arboreal ecotypes are estimated to have disappeared and reappeared as short bursts over the last  
65 million years in North America, with arboreal carnivores and insectivores being most often rarer  
416 than arboreal herbivores and omnivores.

Fossorial ecotypes, whether herbivorous and insectivorous appear rare or possibly absent for most  
418 the Cenozoic, which maximum estimated diversity being obtained in the latter half of the time  
series (Fig. 15).

420 Plantigrade ecotypes appear most variable, plantigrade herbivores having a very different diversity  
history than plantigrade carnivores and omnivores and plantigrade insectivores.

422 Unguligrade and plantigrade herbivores have relatively stable standing diversities throughout the  
Cenozoic of North America (Fig. 15). Similarly, digitigrade carnivorous taxa appear to have a  
424 relatively stable diversity for the Cenozoic.

## Discussion

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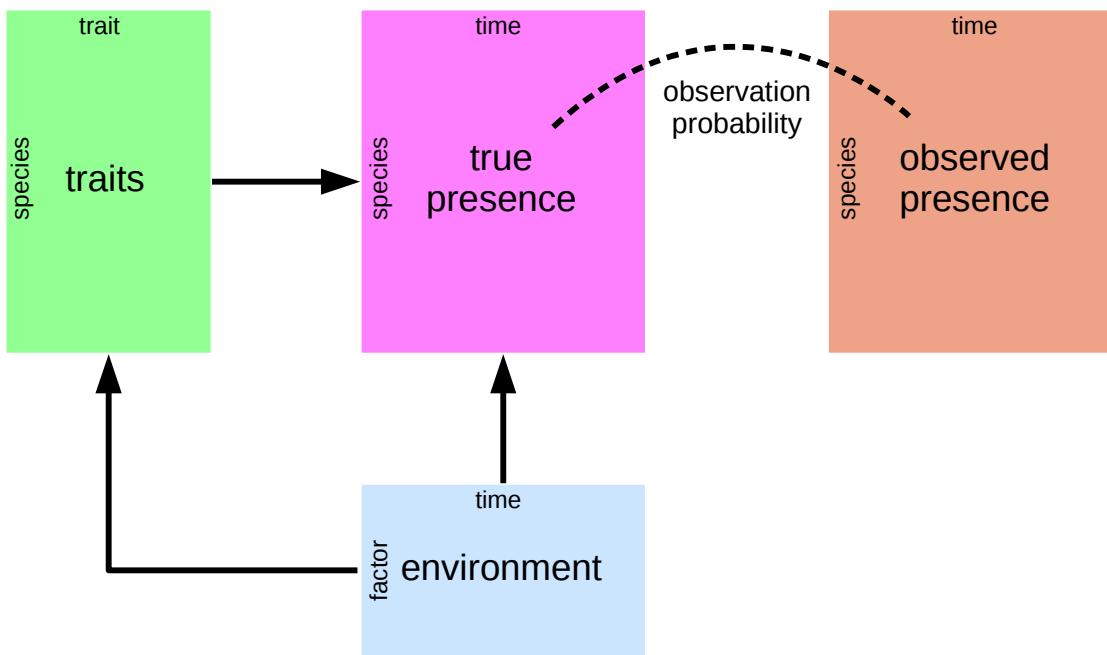


Figure 1: Conceptual diagram of the paleontological fourth corner problem. The observed presence matrix (orange) is the empirical presence/absence pattern for all species for all time points; this matrix is an incomplete observation of the “true” presence/absence pattern (purple). The estimated true presence matrix is modeled as a function of both environmental factors over time (blue) and multiple species traits (green). Additionally, the effect of environmental factors on species traits are also modeled as traits are expected to mediate the effects of a species environmental context. This diagram is based partially on material presented in Brown et al. (2014) and Warton et al. (2015).

	Time Bin							
	1	2	3	4	5	6	7	8
Observed	0	0	0	1	0	1	1	0
Certain	?	?	?	1	1	1	1	?
Potential	0	0	0	1	1	1	1	0
Potential	0	0	1	1	1	1	1	0
Potential	0	1	1	1	1	1	1	0
Potential	1	1	1	1	1	1	1	0
Potential	0	0	0	1	1	1	1	1
Potential	0	0	1	1	1	1	1	1
Potential	0	1	1	1	1	1	1	1
Potential	1	1	1	1	1	1	1	1

Figure 2: Conceptual figure of all possible occurrence histories for an observed species. The first row represents the observed presence/absence pattern for a single species at eight time points. The second row corresponds to the known aspects of the “true” occurrence history of that species. The remaining rows correspond to all possible occurrence histories that are consistent with the observed data. The process of parameter marginalization described in the text

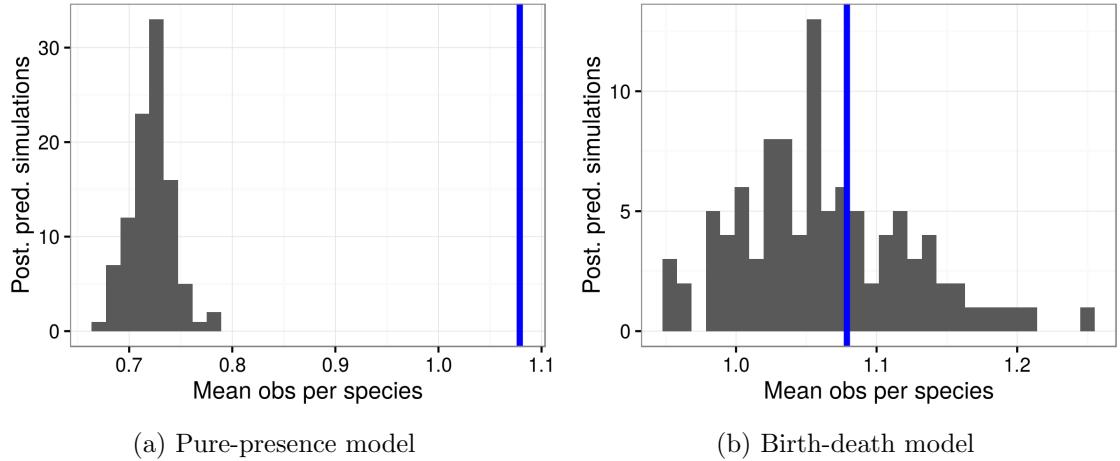


Figure 3: Comparison of the average observed number of occurrences per species (blue line) to the average number of occurrences from 100 posterior predictive datasets using the posterior estimates from the pure-presence and birth-death models.

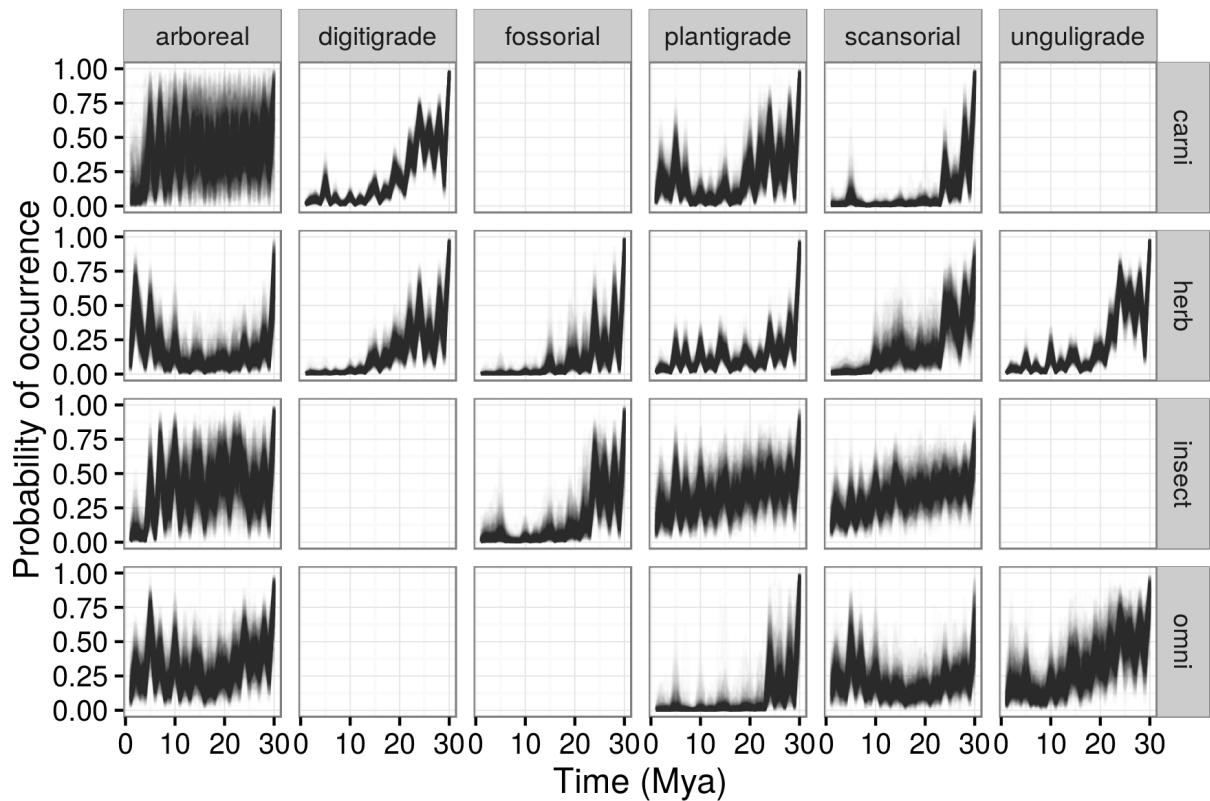


Figure 4: Probability of a mammal ecotype occurring over time as estimated from the pure-presence model. Each panel depicts 100 random samples from the model's posterior. The columns are by locomotor category and rows by dietary category; their intersections are the observed and analyzed ecotypes. Panels with no lines are ecotypes not observed in the dataset.

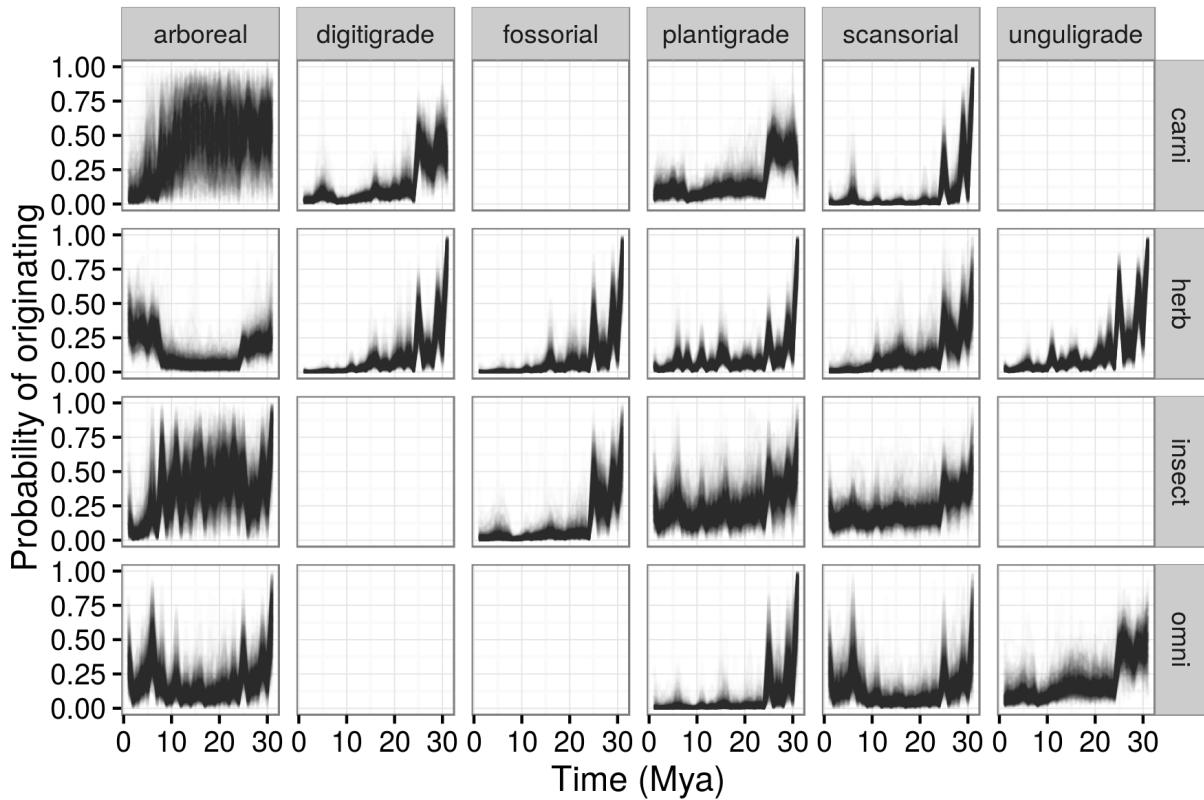


Figure 5: Probability of a mammal ecotype origination probabilities at each time point as estimated from the birth-death model. Each panel depicts 100 random samples from the model's posterior. The columns are by locomotor category and rows by dietary category; their intersections are the observed and analyzed ecotypes. Panels with no lines are ecotypes not observed in the dataset.

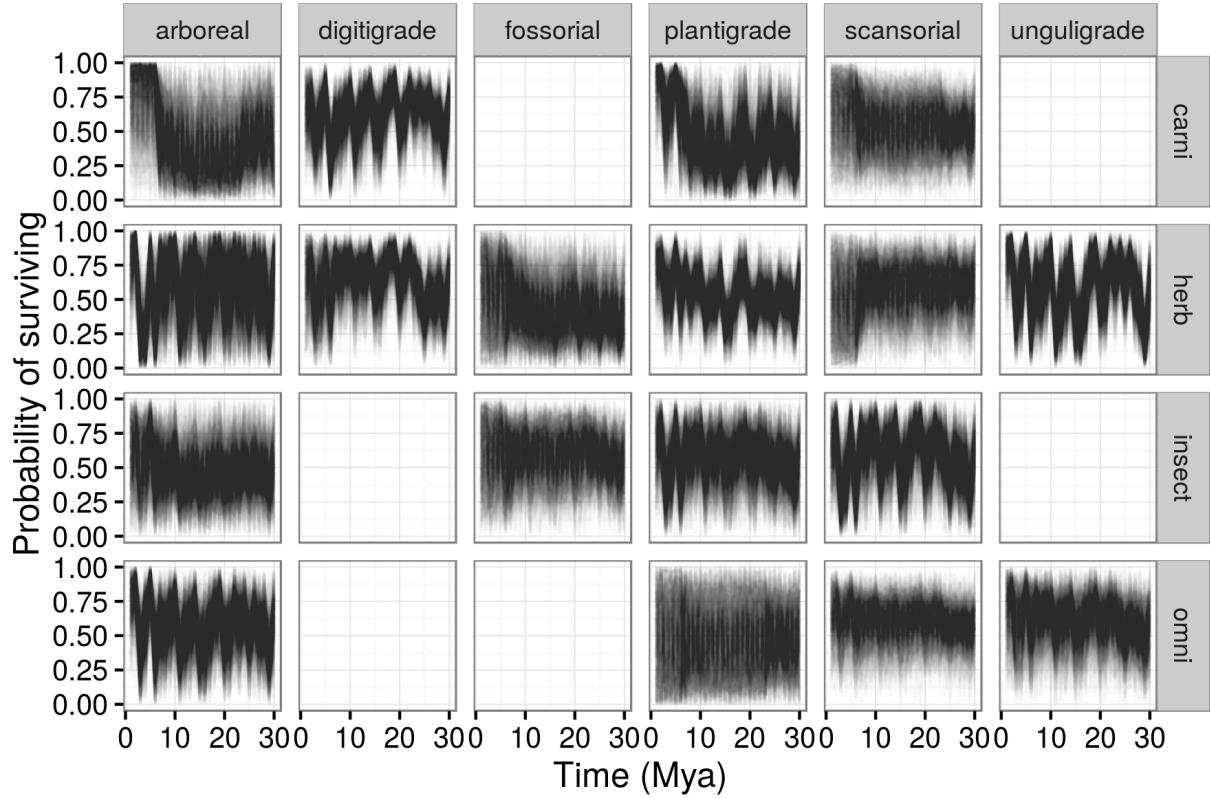


Figure 6: Probability of a mammal ecotype survival probabilities at each time point as estimated from the birth-death model. Each panel depicts 100 random samples from the model’s posterior. The columns are by locomotor category and rows by dietary category; their intersections are the observed and analyzed ecotypes. Panels with no lines are ecotypes not observed in the dataset.

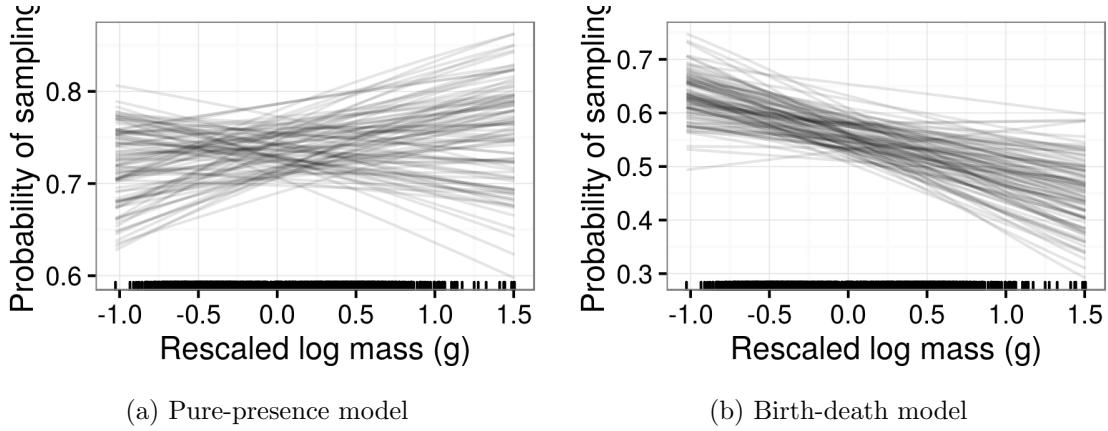


Figure 7: Estimates of the effect of species mass on probability of observing a present species ( $p$ ). Mass has been log-transformed, centered, and rescaled; this means that a mass of 0 corresponds to the mean of log-mass of all observed species and that mass is in standard deviation units. Estimates are from both the pure-presence and birth-death models.

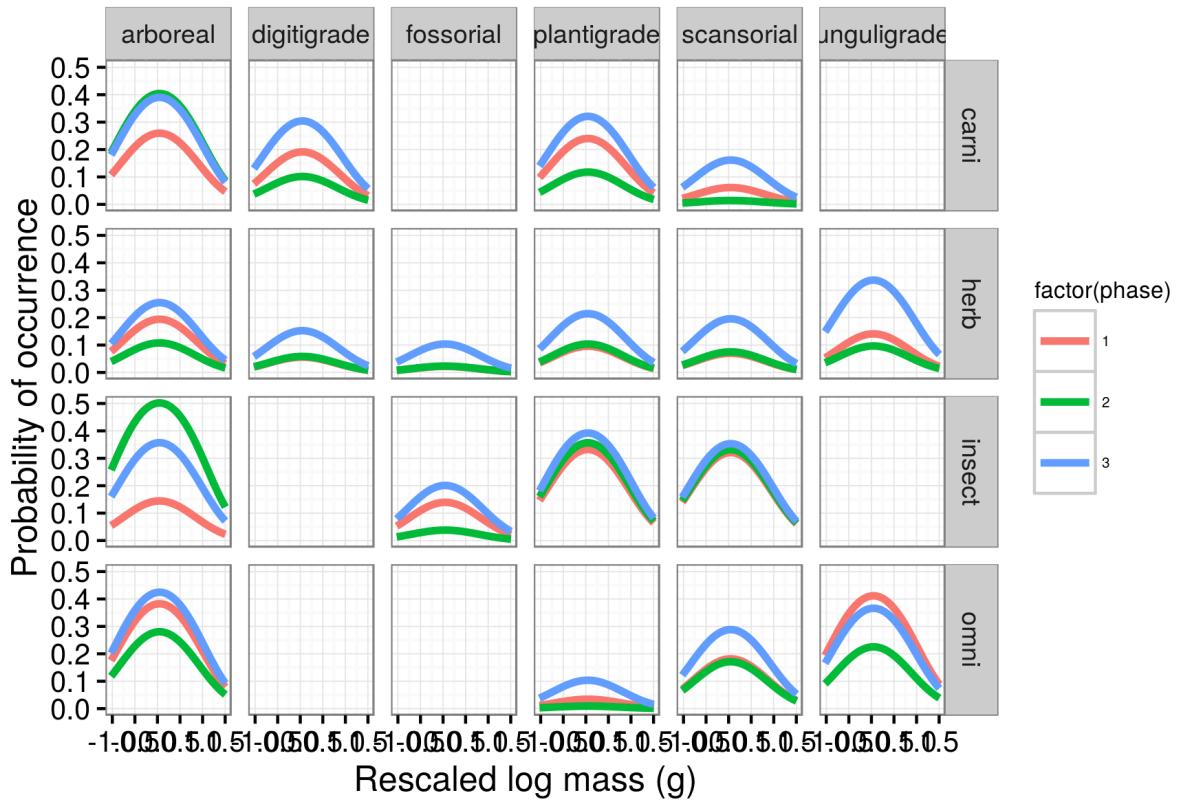


Figure 8: Mean estimate of the effect of species mass on the probability of a species occurrence for each of the three plant phases. The effect of mass is considered constant over time and that the only aspect of the model that changes with plant phase is the intercept of the relationship between mass and occurrence. The three plant phases are indicated by the color of the line. Mass has been log-transformed, centered, and rescaled; this means that a mass of 0 corresponds to the mean of log-mass of all observed species and that mass is in standard deviation units. Only the mean estimates of the effects of both mass and plant phase are plotted for clarity; these estimates are obviously made with uncertainty.

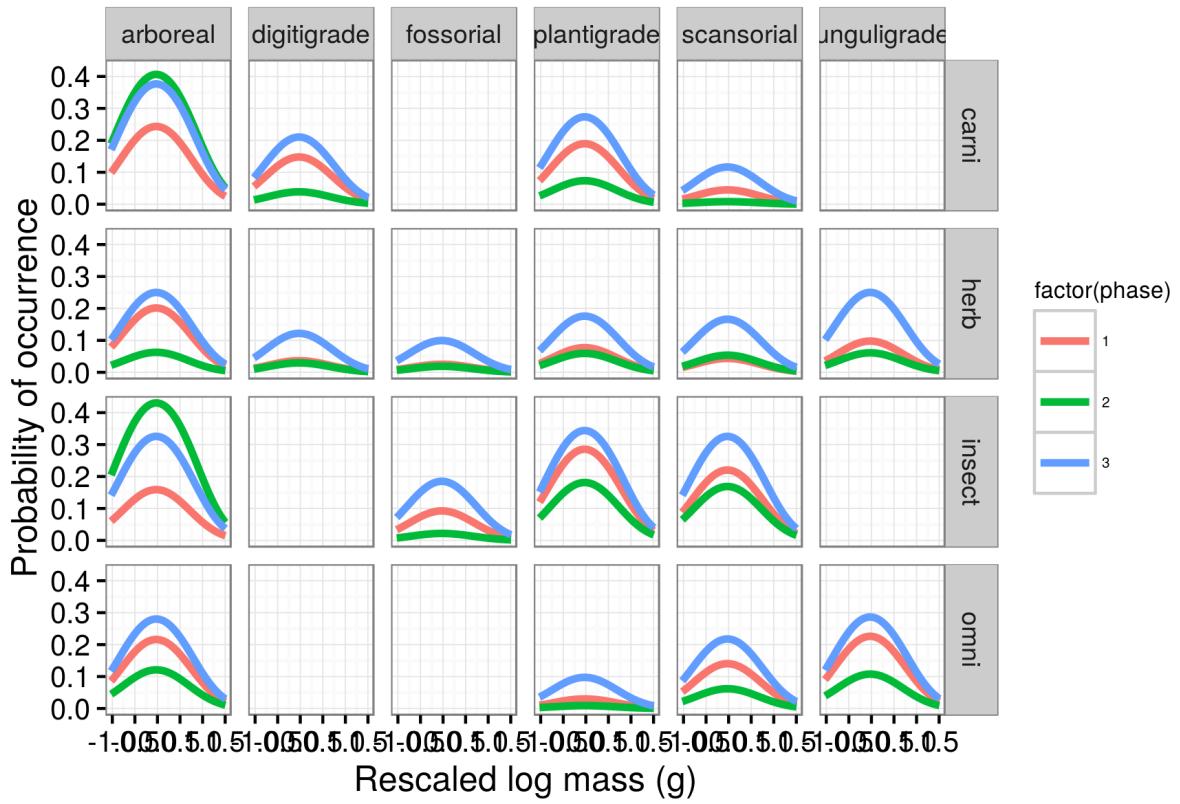


Figure 9: Mean estimate of the effect of species mass on the probability of a species originating for each of the three plant phases. The effect of mass is considered constant over time and that the only aspect of the model that changes with plant phase is the intercept of the relationship between mass and origination. The three plant phases are indicated by the color of the line. Mass has been log-transformed, centered, and rescaled; this means that a mass of 0 corresponds to the mean of log-mass of all observed species and that mass is in standard deviation units. Only the mean estimates of the effects of both mass and plant phase are plotted for clarity; these estimates are obviously made with uncertainty.

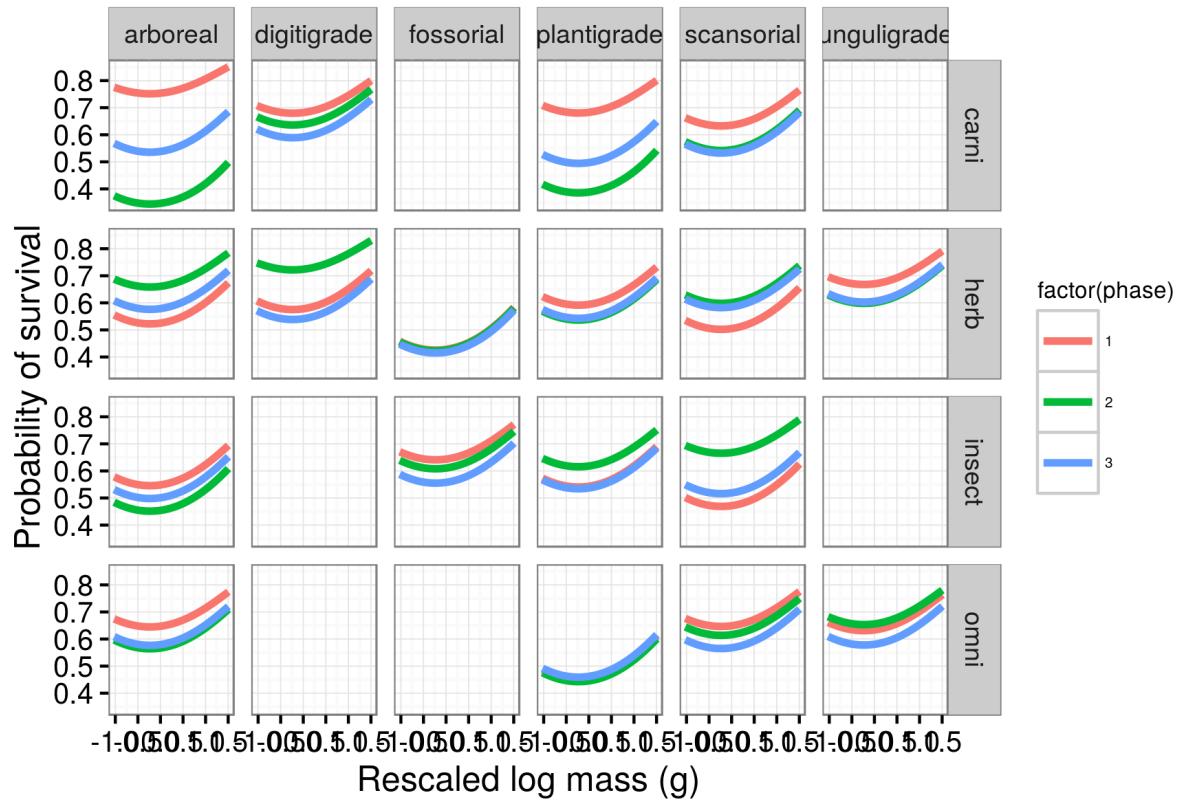


Figure 10: Mean estimate of the effect of species mass on the probability of a species survival for each of the three plant phases. The effect of mass is considered constant over time and that the only aspect of the model that changes with plant phase is the intercept of the relationship between mass and survival. The three plant phases are indicated by the color of the line. Mass has been log-transformed, centered, and rescaled; this means that a mass of 0 corresponds to the mean of log-mass of all observed species and that mass is in standard deviation units. Only the mean estimates of the effects of both mass and plant plant are plotted for clarity; these estimates are obviously made with uncertainty.

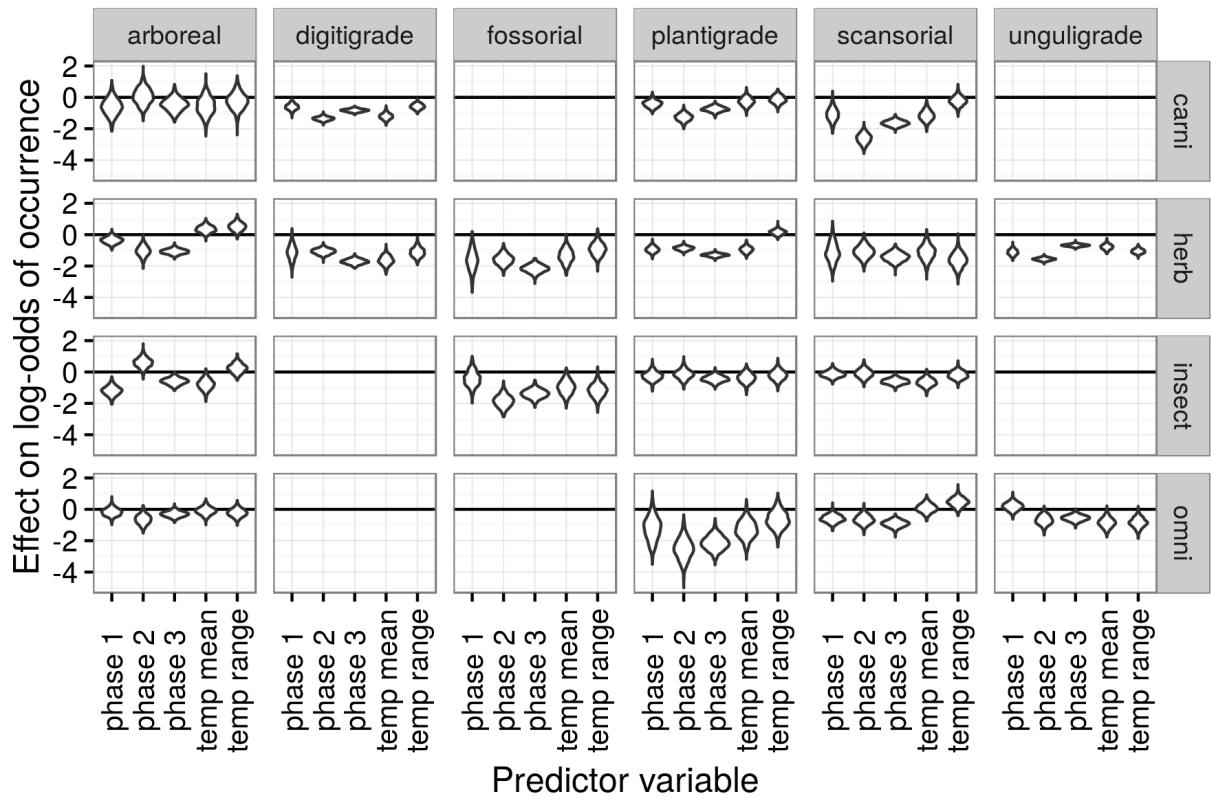


Figure 11: Estimated effects of the group-level covariates describing environmental context on log-odds of species occurrence. These estimates are from the pure-presence model.

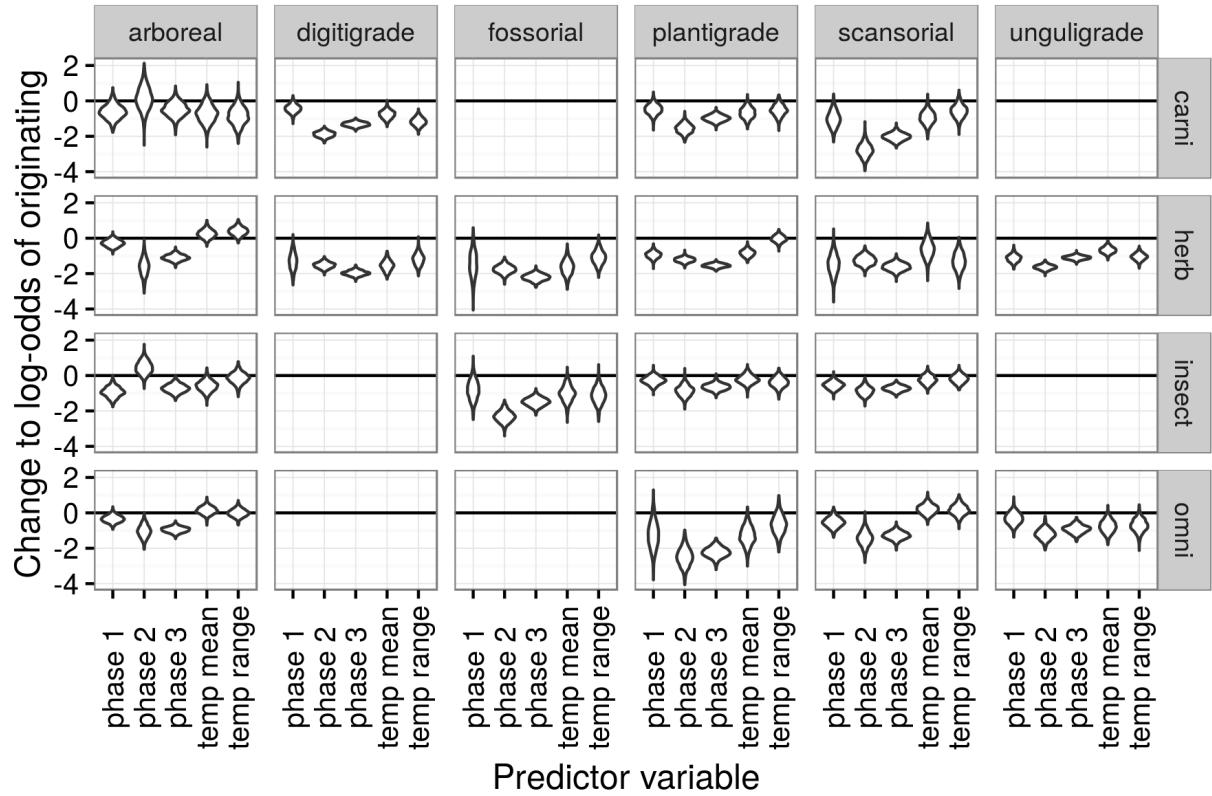


Figure 12: Estimated effects of the group-level covariates describing environmental context on log-odds of species origination. These estimates are from the birth-death model.

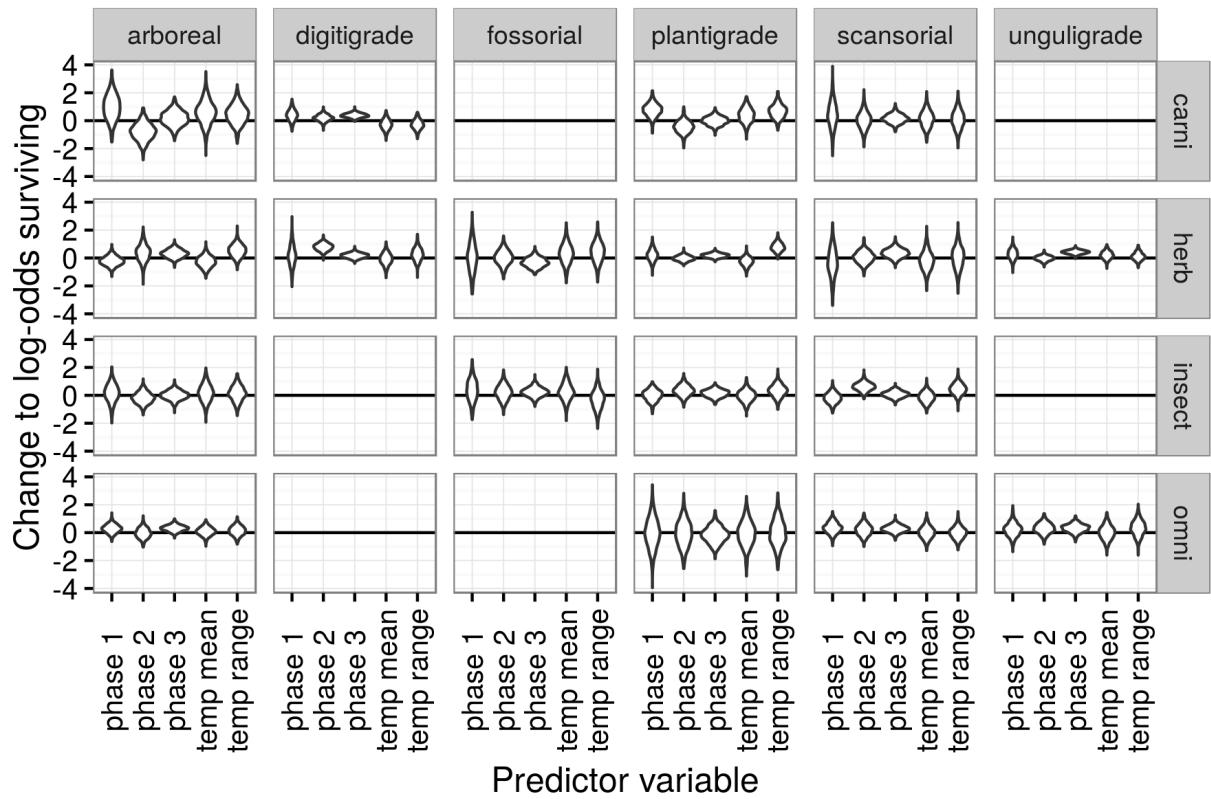


Figure 13: Estimated effects of the group-level covariates describing environmental context on log-odds of species survival. These estimates are from the birth-death model.

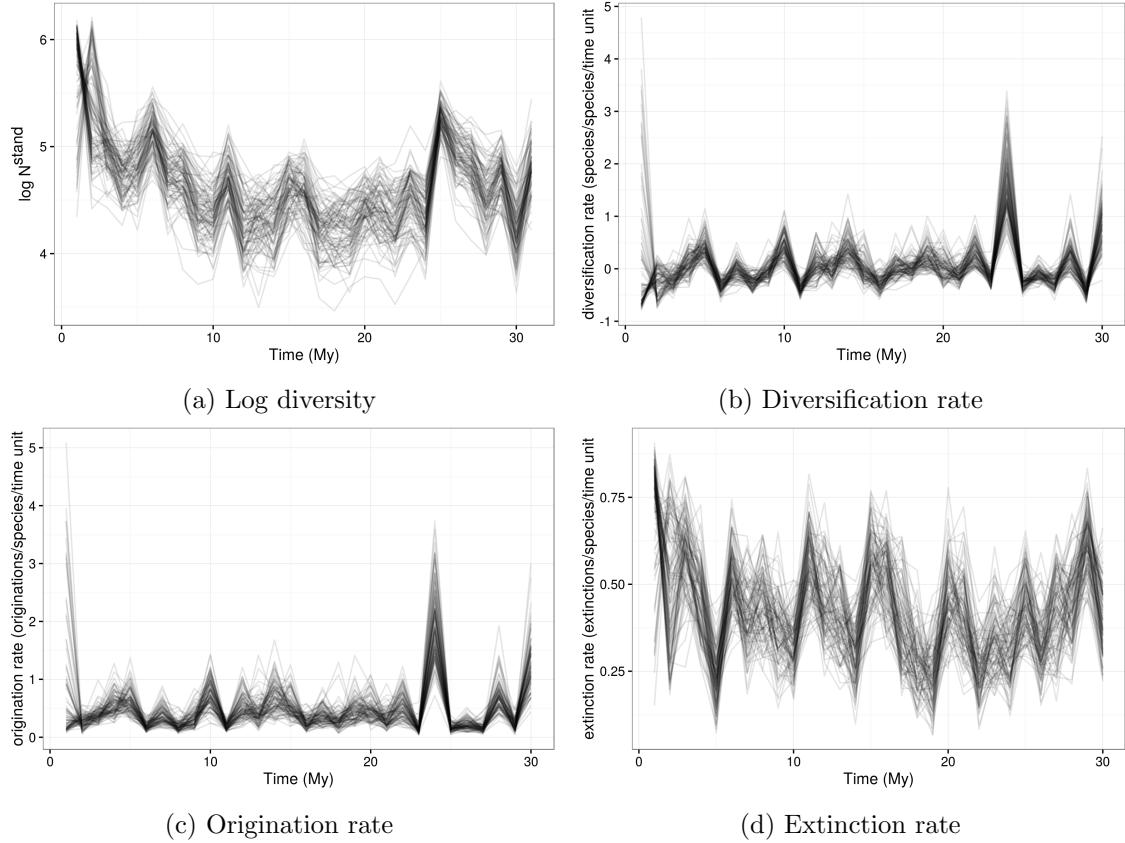


Figure 14: Posterior estimates of the time series of Cenozoic North American mammal diversity and its characteristic macroevolutionary rates; all estimates are from the birth-death model and 100 posterior draws are plotted to indicate the uncertainty in these estimates. The dramatic differences between diversity estimates at the first and second time points and the penultimate and last time points in this series are caused by well known edge effects in discrete-time birth-death models caused by  $p_{-,t=1}$  and  $p_{-,t=T}$  being partially unidentifiable (Royle and Dorazio, 2008); the hierarchical modeling strategy used here helps mitigate these effects but they are still present (Gelman et al., 2013; Royle and Dorazio, 2008). Diversification rate is in units of species gained per species present per time unit (2 My), origination rate is in units of species originating per species present per time unit, and extinction rate is in units of species becoming extinct per species present per time unit.

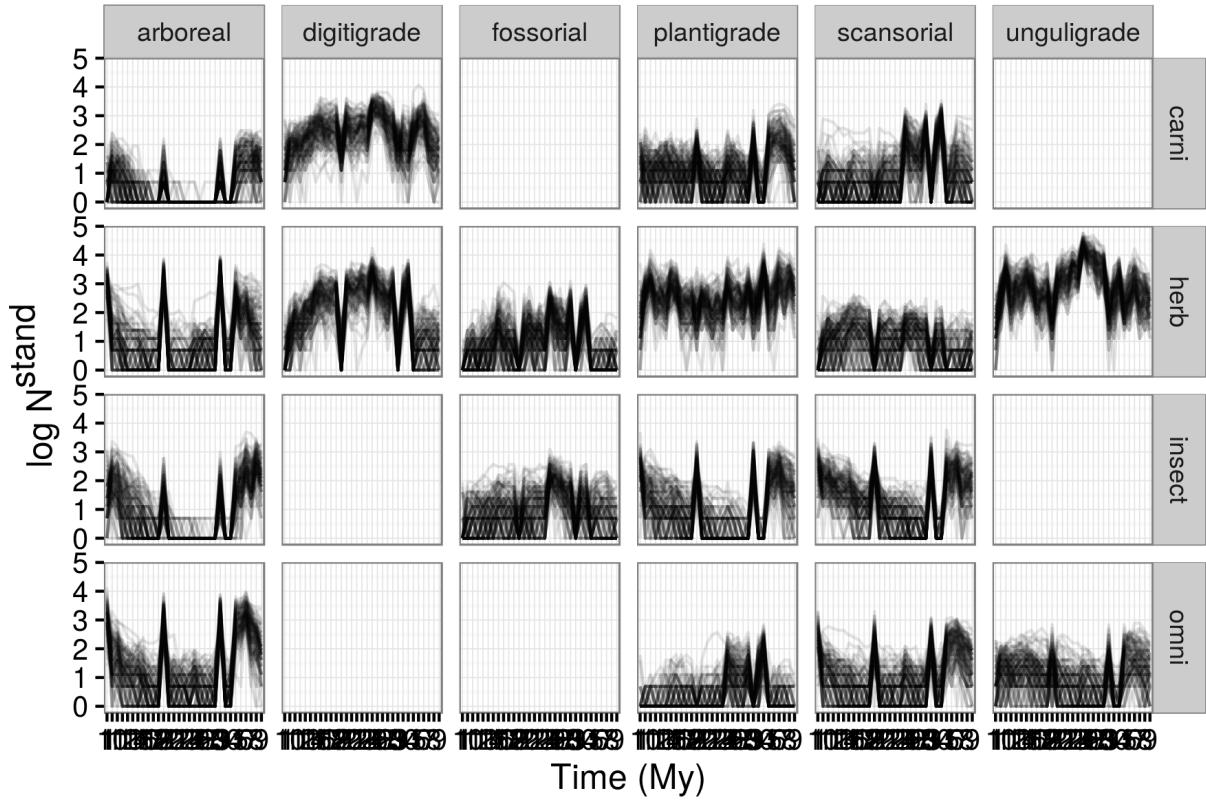


Figure 15: Posterior of standing log-diversity of North American mammals by ecotype for the Cenozoic as estimated from the birth-death model; 100 posterior draws are plotted to indicate the uncertainty in these estimates and what is technically plotted is log of diversity plus 1. The dramatic differences between diversity estimates at the first and second time points and the penultimate and last time points in this series are caused by well known edge effects in discrete-time birth-death models caused by  $p_{-,t=1}$  and  $p_{-,t=T}$  being partially unidentifiable (Royle and Dorazio, 2008); the hierarchical modeling strategy used here helps mitigate these effects but they are still present (Gelman et al., 2013; Royle and Dorazio, 2008).