

**Title:** How macroecology affects macroevolution: the interplay  
2 between extinction intensity and trait-dependent extinction in  
brachiopods.

4 **Running title:** Trait-dependent extinction in brachiopods

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## Abstract

As extinction intensity increases, how do the effects of traits on taxonomic survival change? Does the extinction rate associated with certain traits increase while that of others decreases? Using a hierarchical Bayesian approach, I develop a model of how the effects of biological traits on extinction risk can vary with respect to extinction intensity, origination cohort (i.e. time of origination), and in relation to each other. The emergent traits I analyze in relation to their patterns of Paleozoic brachiopod genus durations are geographic range, affinity for epicontinental seas versus open ocean environments, and body size. Additionally, I estimate the effects of environmental generalization versus specialization on taxonomic survival by allowing environmental preference to have a nonlinear effect on duration. My analytical framework eschews the traditional distinction between background and mass extinction, and instead considers extinction intensity as a continuum. I find that the cohort-specific effects of geographic range and environmental preference are negatively correlated with baseline extinction intensity. Additionally, I find support for greater survival of environmental generalists versus specialists in all origination cohorts. These results support the conclusion that for Paleozoic brachiopods, as extinction intensity increases overall extinction selectivity increases.

## 1 Introduction

Extinction is one half of the diversification process (Raup, 1994, Stanley, 1975, 1979), second only to speciation or origination; it can also be the ultimate manifestation of selection as a taxon with a beneficial trait should persist for longer on average than a taxon without that beneficial trait (Jablonski, 2008, Rabosky and McCune, 2010, Raup, 1994, Stanley, 1975).

While estimation of both trait-dependent speciation and extinction rates from  
40 phylogenies of extant taxa has grown dramatically (Fitzjohn, 2010, Goldberg  
et al., 2011, 2005, Maddison et al., 2007, Rabosky et al., 2013, Stadler, 2011,  
42 2013, Stadler and Bokma, 2013), there are two major ways to estimate  
trait-dependent extinction: analysis of phylogenies, and analysis of the fossil  
44 record. These two directions, phylogenetic comparative and paleobiological, are  
complementary and intertwined in the field of macroevolution (Hunt and  
46 Rabosky, 2014, Jablonski, 2008, Rabosky and McCune, 2010). In the case of  
extinction, analysis of the fossil record has the distinct advantage over  
48 phylogenies of only extant taxa because extinction is observable; this means  
that extinction rate is possible to estimate (Liow et al., 2010, Quental and  
50 Marshall, 2009, Rabosky, 2010). The approach used here is thus complementary  
to the analysis of trait-dependent extinction based on a phylogeny.

52 Jablonski (1986) observed that for bivalves at the end Cretaceous mass  
extinction event, the effects of some biological traits on taxonomic survival  
54 decreased. However, this pattern was not the case for the effect of geographic  
range on survival (Jablonski, 1986, Payne and Finnegan, 2007). There are  
56 multiple possible macroevolutionary mechanisms which may underlie this  
pattern: the effect of geographic range on survival remains constant and those of  
58 other biological traits decrease, the effect of geographic range on survival  
increases and those of other biological traits stay constant, or the effects of all  
60 traits decrease potentially by different degrees.

While Jablonski (1986) phrased his conclusions in terms of background versus  
62 mass extinction, these states are not distinguishable in terms of extinction rate  
alone; my analysis treats the time period analyzed as part of the same  
64 continuum (Payne and Finnegan, 2007, Simpson and Harnik, 2009, Wang, 2003).  
Additionally, in order to test the proposed macroevolutionary mechanism behind

the Jablonski (1986) scenario; not only do the taxon trait effects need to be modeled, but the correlation between trait effects need to be modeled as well.

Here I model brachiopod taxon durations because trait based differences in extinction risk should manifest as differences in taxon durations. Brachiopods are an ideal group for this study as they are well known for having an exceptionally complete fossil record (Foote, 2000b, Foote and Raup, 1996). I focus on the brachiopod record from the post-Cambrian Paleozoic, from the start of the Ordovician (approximately 485 My) through the end Permian (approximately 252 My) as this represents the time of greatest global brachiopod diversity (Alroy, 2010) meaning a large sample size for this analysis.

The analysis of taxon durations, or time from origination to extinction, falls under the purview of survival analysis, a field of applied statistics commonly used in health care and engineering (Klein and Moeschberger, 2003) but has a long history in paleontology (Crampton et al., 2016, Simpson, 1944, 1953, Smits, 2015, Van Valen, 1973, 1979). I adopt a hierarchical modeling approach (Gelman et al., 2013, Gelman and Hill, 2007), which represents both a conceptual and statistical unification of the paleontological dynamic and cohort survival analytic approaches (Baumiller, 1993, Crampton et al., 2016, Ezard et al., 2012, Foote, 1988, Raup, 1975, 1978, Simpson, 2006, Smits, 2015, Van Valen, 1973, 1979).

## 1.1 Factors affecting brachiopod survival

Conceptually, taxon survival can be considered an aspect of “taxon fitness” (Cooper, 1984, Palmer and Feldman, 2012). Traits associated with taxon survival are thus examples of species (or higher-level) selection, as differences in survival are analogous to differences in fitness. The traits analyzed here are all examples of emergent and aggregate traits (Jablonski, 2008, Rabosky and

McCune, 2010); specifically I analyze genus-level traits. Emergent traits are  
92 those which are not measurable at a lower level (e.g. species versus individual  
organism) such as geographic range, or even fossil sampling rate. Aggregate  
94 traits, like body size or environmental preference, are the average of a shared  
trait across all members of a lower level.

96 Geographic range is widely considered the most important biological trait for  
estimating differences in extinction risk at nearly all times, with large  
98 geographic range associated with low extinction risk (Finnegan et al., 2012,  
Harnik et al., 2012, Jablonski, 1986, 1987, 2008, Jablonski and Roy, 2003, Payne  
100 and Finnegan, 2007). This stands to reason even if extinction is completely at  
random; a taxon with an unrestricted range is less likely to go extinct at  
102 random than a taxon with a restricted range.

Epicontinental seas are a shallow-marine environment where the ocean has  
104 spread over the continental interior or craton with a depth typically less than  
100m. In contrast, open-ocean coastline environments have much greater  
106 variance in depth, do not cover the continental craton, and can persist during  
periods of low sea level (Miller and Foote, 2009). Because of this, a simple  
108 hypothesis that taxa which favor epicontinental seas would be at great risk  
during periods of low sea levels, such as during glacial periods, when  
110 epicontinental seas are drained. During the Paleozoic (approximately 541–252  
My), epicontinental seas were widely spread globally but declined over the  
112 Mesozoic (approximately 252–66 My) and have nearly disappeared during the  
Cenozoic (approximately 66–0 My) as open-ocean coastlines became the  
114 dominant shallow-marine setting (Johnson, 1974, Miller and Foote, 2009, Peters,  
2008, Sheehan, 2001). Taxa in epicontinental environments could also have a  
116 greater extinction susceptibility than taxa in open-ocean environments due to  
anoxic events due to enhanced water stratification or poor water circulation

118 (Peters, 2007).

Miller and Foote (2009) demonstrated that during several mass extinctions taxa  
120 associated with open-ocean environments tend to have a greater extinction risk  
than those taxa associated with epicontinental seas. During periods of  
122 background extinction, however, they found no consistent difference between  
taxa favoring either environment. Miller and Foote (2009) hypothesize that  
124 open-ocean taxa may have a greater extinction rate because these environments  
would be more strongly affected by waterborne hazards such as fallout from  
126 impacts or volcanic events which would propagate more quickly than in  
epicontinental environments with sluggish circulation. These two environment  
128 types represent the primary identifiable environmental dichotomy observed in  
ancient marine systems (Miller and Foote, 2009, Sheehan, 2001). Given these  
130 findings, I would hypothesize that as extinction risk increases, the extinction  
risk associated with open-ocean environments should generally increase.

132 Because environmental preference is defined here as the continuum between  
occurring exclusively in open-ocean environments versus epicontinental  
134 environments, intermediate values are considered “generalists” in the sense that  
they favor neither end member. A long-standing hypothesis is that generalists or  
136 unspecialized taxa will have greater survival than specialists (Baumiller, 1993,  
Liow, 2004, 2007, Nürnberg and Aberhan, 2013, 2015, Simpson, 1944, Smits,  
138 2015). Because of this, the effect of environmental preference was modeled as a  
quadratic function where a concave down relationship between preference and  
140 expected duration indicates that generalists are favored over specialists  
end-members.

142 Body size, measured as shell length, is also considered as a trait that may  
potentially influence extinction risk (Harnik, 2011, Payne et al., 2014). Body  
144 size is a proxy for metabolic activity and other correlated life history traits

(Payne et al., 2014). Harnik et al. (2014) analyzed the effect of body size  
146 selectivity in Devonian brachiopods in both a phylogenetic and  
non-phylogenetic context; finding that body size was not found to be associated  
148 with differences in taxonomic duration. It has also been found that, at least in  
the case of some bivalve subclades, body size can be as important a factor as  
150 geographic range size in determining extinction risk (Harnik, 2011). Given these  
results, I expect that if body size has any effect on brachiopod taxonomic  
152 survival it is very small.

It is well known that, given the incompleteness of the fossil record, the observed  
154 duration of a taxon is an underestimate of that taxon's true duration (Alroy,  
2014, Foote and Raup, 1996, Liow and Nichols, 2010, Solow and Smith, 1997,  
156 Wagner and Marcot, 2013, Wang and Marshall, 2004). Because of this, the  
concern is that a taxon's observed duration may reflect its relative chance of  
158 being sampled and not any of the effects of the covariates of interest. In this  
case, for sampling to be a confounding factor there must be consistent  
160 relationship between the quality of sampling of a taxon and its apparent  
duration (e.g. greater sampling, longer duration). If there is no relationship  
162 between sampling and duration then interpretation can be made clearly; while  
observed durations are obviously truncated true durations, a lack of a  
164 relationship would indicate that the amount and form of this truncation is not a  
major determinant of the taxon's apparent duration. By including sampling as a  
166 covariate in the model, this effect can be quantified and can be taken into  
account when interpreting the estimates of the effects of the other covariates.

## 168 2 Materials and Methods

### 2.1 Fossil occurrence information

170 The brachiopod dataset analyzed here was sourced from the Paleobiology  
Database (<http://www.paleodb.org>) which was then filtered based on  
172 taxonomic (Rhychonelliformea: Rhynchonellata, Chileata, Obolellida,  
Kutorginida, Strophomenida, Spiriferida), temporal (post-Cambrian Paleozoic),  
174 stratigraphic, and other occurrence information used in this analysis. Analyzed  
occurrences were restricted to those with paleolatitude and paleolongitude  
176 coordinates, assignment to either epicontinental or open-ocean environment,  
and belonging to a genus present in the body size dataset (Payne et al., 2014).  
178 Epicontinental versus open-ocean assignments for each fossil occurrence are  
partially based on those from Miller and Foote (2009), with additional  
180 occurrences assigned similarly (Miller and Foote, personal communication).  
These filtering criteria are very similar to those from Foote and Miller (2013)  
182 with an additional constraint of being present in the body size data set from  
Payne et al. (2014). In total, there 1130 were genera included in the dataset.  
184 Fossil occurrences were analyzed at the genus level which is common for  
paleobiological, macroevolutionary and macroecological studies of marine  
186 invertebrates (Alroy, 2010, Foote and Miller, 2013, Harnik et al., 2012, Kiessling  
and Aberhan, 2007, Miller and Foote, 2009, Nürnberg and Aberhan, 2013, 2015,  
188 Payne and Finnegan, 2007, Simpson and Harnik, 2009, Vilhena et al., 2013).  
While species diversity dynamics are frequently of much greater interest than  
190 those of higher taxa (though see Foote 2014, Hoehn et al. 2015), the nature of  
the fossil record makes accurate, precise, and consistent taxonomic assignments  
192 at the species level difficult for all occurrences. As such, the choice to analyze  
genera as opposed to species was in order to assure a minimum level of



194 confidence and accuracy in the data analyzed here.

Genus duration was calculated as the number of geologic stages from first  
196 appearance to last appearance, inclusive. Durations were based on geologic  
stages as opposed to millions of years because of the inherently discrete nature  
198 of the fossil record; dates are not assigned to individual fossils themselves but  
instead fossils are assigned to a geological interval which represents some  
temporal range. In this analysis, stages are effectively irreducible temporal  
200 intervals in which taxa may occur. Genera with a last occurrence in or after  
Changhsingian stage (e.g. the final stage of the study interval) were right  
202 censored at the Changhsingian; genera with a duration of only one stage were  
left censored (Klein and Moeschberger, 2003). How the likelihood of censored  
204 observations is calculated is detailed in section 2.2.

206 The covariates of duration included in this analysis are geographic range size  
( $r$ ), environmental preference ( $v, v^2$ ), body size ( $m$ ), and sampling ( $s$ ).

208 Geographic range was calculated as relative occupancy corrected for incomplete  
sampling. First, the paleolatitude-paleolongitude coordinates for all occurrences  
210 were projected onto an equal-area cylindrical map projection. Each occurrence  
was then assigned to one of the cells from a  $70 \times 34$  regular raster grid placed  
212 on the map. Each grid cell represents approximately 250,000 km<sup>2</sup>. The map  
projection and regular lattice were made using shape files from  
214 <http://www.natureearthdata.com/> and the **raster** package for R (Hijmans,  
2015). For each stage, the total number of occupied grid cells was calculated.  
216 Then, for each temporal bin, the relative occurrence probability of the observed  
taxa was calculated using the JADE method developed by Chao et al. (2015).  
218 This method accounts for the fact that taxa with an occupancy of 0 cannot be  
observed which means that occupancy follows a truncated Binomial distribution.  
220 This correction is critical when comparing occupancies from different times with

different geographic sampling. Finally, for each genus, the mean relative  
 222 occurrence probability was calculated as the average of that genus' occurrence  
 probabilities for all stages it was sampled to yield relative occupancy, my proxy  
 224 for geographic range.

Environmental preference was defined as probability of observing the ratio of  
 226 epicontinental occurrences to total occurrences ( $\theta_i = e_i/E_i$ ) or greater given the  
 background occurrence probability  $\theta'_i$  as estimated from all other taxa occurring  
 228 at the same time ( $e'_i/E'_i$ ). This measure of environmental preference is  
 expressed.

$$\begin{aligned} p(\theta'_i|e'_i, E'_i) &\propto \text{Beta}(e'_i, E'_i - e'_i)\text{Beta}(1, 1) \\ &= \text{Beta}(e'_i + 1, E'_i - e'_i + 1), \end{aligned} \tag{1}$$

230 where  $v$  is the percent of the distribution defined in equation 1 less than or  
 equal to  $\theta_i$ . The Beta distribution is used here because it is a continuous  
 232 distribution bounded at 0 and 1, which is idea for modeling percentages.

Body size, measured as shell length, was sourced directly from Payne et al.  
 234 (2014). These measurements were made from brachiopod taxa figured in the  
*Treatise on Invertebrate Paleontology* (Williams et al., 2007).

236 The sampling probability for individual taxa was calculated using the standard  
 gap statistic (Foote, 2000a, Foote and Raup, 1996). The gap statistic is  
 238 calculated as the number of stages in which the taxon was sampled minus two  
 divided by the duration of the taxon minus two. Subtracting two from both the  
 240 numerator and denominator is because the first and last appearance stages are  
 by definition sampled. Because taxa that were right censored only include a first  
 242 appearance, one was subtracted from the numerator and denominator instead of  
 two.

244 The minimum duration for which a gap statistic can be calculated is three

stages, so I chose to impute the gap statistic for all observations with a  
 246 duration less than 3. Imputation is the “filling in” of missing observations based  
 on the observed values (Gelman and Hill, 2007, Rubin, 1996). This is fairly  
 248 straight forward in a Bayesian framework because both covariates and  
 parameters are considered random variables, meaning that the missing values of  
 sampling can be modeled as coming from some probability distribution. The  
 250 model for imputing sampling probability is described in section 2.3.  
  
 252 Prior to analysis, geographic range was logit transformed and body size was  
 natural-log transformed; both of these transformations make these variables  
 254 defined for the entire real line. Sampling probability was transformed as  
 $(s(n - 1) + 0.5)/n$  where  $n$  is the sample size as recommended by Smithson and  
 256 Verkuilen (2006); this serves to slightly shrink the range of the data so that  
 there are no values of 0 or 1. All covariates except for sampling were  
 258 standardized by subtracting the mean from all values and dividing by twice its  
 standard deviation, which follows Gelman and Hill (2007). This standardization  
 260 means that the associated regression coefficients are comparable as the expected  
 change per 1-unit change in the rescaled covariates. Finally,  $D$  is defined as the  
 262 total number of covariates, excluding sampling, plus one for the intercept term.

## 2.2 Details of model

264 Hierarchical modelling is a statistical approach which explicitly takes into  
 account the structure of the observed data in order to model both the within  
 266 and between group variance (Gelman et al., 2013, Gelman and Hill, 2007). The  
 units of study (e.g. genera) each belong to a single group (e.g. origination  
 268 cohort). Each group is considered a draw from a shared probability distribution  
 (e.g. prior) of all cohorts, observed and unobserved. The group-level parameters,

270 or the hyperparameters of this shared prior, are themselves given (hyper)prior  
 distributions and are also estimated like the other parameters of interest (e.g.  
 272 covariate effects) (Gelman et al., 2013). The subsequent estimates are partially  
 pooled together, where parameters from groups with large samples or effects  
 274 remain large while those of groups with small samples or effects are pulled  
 towards the overall group mean. All covariate effects (regression coefficients), as  
 276 well as the intercept term (baseline extinction risk), were allowed to vary by  
 group (origination cohort). The covariance between covariate effects was also  
 278 modeled.

Genus durations were assumed to follow a Weibull distribution which allows for  
 280 age-dependent extinction (Klein and Moeschberger, 2003):  $y \sim \text{Weibull}(\alpha, \sigma)$ .  
 The Weibull distribution has two parameters: scale  $\sigma$ , and shape  $\alpha$ . When  
 282  $\alpha = 1$ ,  $\sigma$  is equal to the expected duration of any taxon.  $\alpha$  is a measure of the  
 effect of age on extinction risk where values greater than 1 indicate that  
 284 extinction risk increases with age, and values less than 1 indicate that  
 extinction risk decreases with age. Note that the Weibull distribution is  
 286 equivalent to the exponential distribution when  $\alpha = 1$ .

In the case of the right- and left-censored observations mentioned above, the  
 288 probability of those observations has a different calculation (Klein and  
 Moeschberger, 2003). For right-censored observations, the likelihood is  
 290 calculated  $p(y|\theta) = 1 - F(y) = S(y)$  where  $F(y)$  is the cumulative distribution  
 function. In contrast, the likelihood of a left-censored observation is calculated  
 292  $p(y|\theta) = F(y)$ .

The scale parameter  $\sigma$  was modeled as a regression following Kleinbaum and  
 294 Klein (2005) with both varying intercept and varying slopes and the effect of

sampling; this is expressed

$$\sigma_i = \exp \left( \frac{-\mathbf{X}_i B_{j[i]} + \delta s_i}{\alpha} \right) \quad (2)$$

where  $i$  indexes across all observations where  $i = 1, \dots, n$  where  $n$  is the total number of observations,  $j[i]$  is the cohort membership of the  $i$ th observation where  $j = 1, \dots, J$  where  $J$  is the total number of cohorts,  $X$  is a  $N \times D$  matrix of covariates along with a column of 1's for the intercept term,  $B$  is a  $J \times D$  matrix of cohort-specific regression coefficients, and  $\delta$  is the regression coefficient for the effect of sampling  $s$ .  $\delta$  does not vary by cohort.

Each of the rows of matrix  $B$  are modeled as realizations from a multivariate normal distribution with length  $D$  location vector  $\mu$  and  $J \times J$  covariance matrix  $\Sigma$ :  $B_j \sim \text{MVN}(\mu, \Sigma)$ . The covariance matrix was then decomposed into a length  $J$  vector of scales  $\tau$  and a  $J \times J$  correlation matrix  $\Omega$ , defined  $\Sigma = \text{diag}(\tau)\Omega\text{diag}(\tau)$  where “diag” indicates a diagonal matrix.

The elements of  $\mu$  were given independent normally distributed priors. The effects of geographic range size and the breadth of environmental preference were given informative priors reflecting the previous findings while the others were given weakly informative favoring no effect. The correlation matrix  $\Omega$  was given an LKJ distributed prior (Lewandowski et al., 2009) that slightly favors an identity matrix as recommended by Stan Development Team (2014b). These

priors are defined

$$\begin{aligned}
\mu^0 &\sim \mathcal{N}(0, 5) \\
\mu^r &\sim \mathcal{N}(-1, 1) \\
\mu^v &\sim \mathcal{N}(0, 1) \\
\mu^{v^2} &\sim \mathcal{N}(1, 1) \\
\mu^m &\sim \mathcal{N}(0, 1) \\
\tau &\sim \text{C}^+(1) \\
\Omega &\sim \text{LKJ}(2).
\end{aligned} \tag{3}$$

314 The log of the shape parameter  $\alpha$  was given a weakly informative prior  
 $\log(\alpha) \sim \mathcal{N}(0, 1)$  centered at  $\alpha = 1$ , which corresponds to the Law of Constant  
316 Extinction (Van Valen, 1973).

## 2.3 Imputation of sampling probability

318 The vector sampling  $s$  has two parts: the observed part  $s^o$ , and the unobserved  
part  $s^u$ . Of the 1130 total observations, 539 have a duration of 3 or more and  
320 have an observed gap statistic. The gap statistic for the remaining 591  
observations was imputed. As stated above, the unobserved part is the imputed,  
322 or filled in, based on the observed part  $s^o$ . Because sampling varies between 0  
and 1, I chose to model it as a Beta regression with the other covariates  $X$  (e.g.  
324 geographic range size) as predictors of sampling; this assumes that the sampling  
value for all taxa come from the same distribution. Importantly, I make no  
326 assumptions of causal structure. Predicting sampling probability from the other  
covariate information and then using it as an additional covariate of duration is  
328 acceptable in the case of imputation where the sample goal is accurate  
prediction (Gelman and Hill, 2007, Rubin, 1996). Not including these covariates  
330 can lead to biased estimates where the correlation between terms is biased

towards 0, especially in the case of structured or hierarchical data (Rubin, 1996).

332 The Beta regression is defined

$$s^o \sim \text{Beta}(\phi = \text{logit}^{-1}(X^o\gamma), \lambda), \quad (4)$$

where  $\gamma$  is a length  $D$  vector of regression coefficients, and  $X$  defined as above.

334 The Beta distribution used in the regression is reparameterized in terms of a mean parameter

$$\phi = \frac{\alpha}{\alpha + \beta} \quad (5)$$

336 and total count parameter

$$\lambda = \alpha + \beta \quad (6)$$

where  $\alpha$  and  $\beta$  are the characteristic parameters of the Beta distribution.

338 The next step is to then estimate  $s^u | s^o, X^o, X^u, \gamma$ , the posterior distribution of which are folded back into  $s$  and used as a covariate of duration (Eq. 2). All the  
340 elements of  $\gamma$ , and both  $\delta$  (Eq. 2) and  $\lambda$  (Eq. 4) were given weakly informative priors where

$$\begin{aligned} \gamma &\sim \mathcal{N}(0, 1) \\ \delta &\sim \mathcal{N}(0, 1) \\ \lambda &\sim \text{Pareto}(0.1, 1.5). \end{aligned} \quad (7)$$

## 342 2.4 Posterior inference and posterior predictive checks

The joint posterior was approximated using a Markov-chain Monte Carlo  
344 routine that is a variant of Hamiltonian Monte Carlo called the No-U-Turn Sampler (Hoffman and Gelman, 2014) as implemented in the probabilistic  
346 programming language Stan (Stan Development Team, 2014a). The posterior distribution was approximated from four parallel chains run for 10,000 steps

each, split half warm-up and half sampling and thinned to every 10th sample for a total of 4000 posterior samples. Chain convergence was assessed via the scale reduction factor  $\hat{R}$  where values close to 1 ( $\hat{R} < 1.1$ ) indicate approximate convergence. Convergence means that the chains are approximately stationary and the samples are well mixed (Gelman et al., 2013).

Model adequacy was evaluated using a couple of posterior predictive checks. Posterior predictive checks are a means for understanding model fit or adequacy where the basic idea is that replicated data sets simulated from the fitted model should be similar to the original data and systematic differences between the simulations and observations indicate weaknesses of the model fit (Gelman et al., 2013). For both approaches used here, each posterior predictive datasets were generated from a unique draw from the posterior distribution of each parameter. The two posterior predictive checks used in this analysis are a comparison of a non-parametric estimate of the survival function  $S(t)$  from the empirical dataset to the non-parametric estimates of  $S(t)$  from the 100 posterior predictive datasets, and comparison of the observed genus durations to the average posterior predictive estimate of  $\log(\sigma)$  (Eq. 2). The former is to see if simulated data has a similar survival pattern to the observed, while the latter is to see if the model systematically over- or under- estimates taxon survival.

### 3 Results

Comparison of the posterior predictive estimates of  $S(t)$  to the empirical estimate reveal few obvious biases except for the case of values from the far right tail of observed durations (Fig. 1). This result is reinforced by the additional posterior predictive comparison where most estimates are not systematically biased except for a consistent under-estimate of  $\log(\sigma)$  for older



taxa (Fig. 2). The results of both posterior predictive checks indicate that, for  
 374 the majority of observations, model fit is generally not biased.

The cohort-level estimate of the effect of geographic range size indicates that as  
 376 a taxon's geographic range increases, that taxon's duration is expected to  
 increase (Table 1). Given the estimates of  $\mu^r$  and  $\tau^r$ , there is a less than 3.7%  
 378 ( $\pm 0.04\%$  SD) probability that this relationships would be reversed  
 ( $\Pr(\mathcal{N}(\mu^r, \tau^r) > 0)$ ). The between-cohort variance  $\tau^r$  is the lowest of all the  
 380 regression coefficients (Table 1).

Body size is estimated to have no effect on taxon duration, with the estimate  
 382 being nearly 0 (Table 1). The variance between the cohort-specific estimates of  
 the effect of body size  $\tau^m$  is estimated to be greater than the variance of  
 384 between-cohort estimates of the effect of geographic range size  $\tau^r$ .

The group-level estimate of the effect of environmental preference is estimated  
 386 from both  $\mu^v$  and  $\mu^{v^2}$ .

The estimate of  $\mu^v$  indicates that epicontinental favoring taxa are expected to  
 388 have a greater duration than open-ocean favoring taxa (Table 1). Additionally,  
 given the estimate of between-cohort variance  $\tau^v$ , there is approximately 18%  
 390 ( $\pm 7\%$  SD) probability that, for any given cohort, taxa favoring open-ocean  
 environments would have a greater expected duration than taxa favoring  
 392 epicontinental environments ( $\Pr(\mathcal{N}(\mu^v, \tau^v) > 0)$ ).

The estimate of  $\mu^{v^2}$  indicates that the overall relationship between  
 394 environmental preference and  $\log(\sigma)$  is concave down (Fig. 3), with only a 2.7%  
 ( $\pm 3\%$  SD) probability that any given cohort is convex up  
 396 ( $\Pr(\mathcal{N}(\mu^{v^2}, \tau^{v^2}) < 0)$ ).

The cohort-specific estimates of all the regression coefficients demonstrate a lot  
 398 of between cohort variance, with no obvious trends. As indicated in Table 1 and

detectable visually (Fig. 4), the between-cohort estimates for  $\beta^0$ ,  $\beta^r$ , and  $\beta^m$  all  
 400 have much lower variance than the between-cohort estimates of both  $\beta^v$  and  
 $\beta^{v^2}$ .

402 While most cohort-specific estimates are very similar to the overall cohort-level  
 estimate, there are a few notable excursions away from the overall mean (Fig.  
 404 4). There are simultaneous excursions in both  $\beta^0$  and  $\beta^v$  for cohorts originating  
 in the Givetian (387-382 My) and Frasnian (382-372 My) stages; both of which  
 406 directly precede the late Devonian mass extinction event at the  
 Frasnian/Famennian boundary. These cohorts are marked by both a high  
 408 extinction intensity and an increase in expected duration for taxa favoring  
 epicontinental environments over open-ocean ones; this is consistent with the  
 410 results of Miller and Foote (2009).

Cohorts originating from the Silurian through the Early Devonian have a  
 412 slightly lower extinction intensity than the overall mean; these cohorts are those  
 originating in the Llandovery (443-443 My) through the Emsian (407-393 My).  
 414 This is also a time period is also when there is the lowest overall probability  
 that epicontinental favoring taxa are expected to have greater duration than  
 416 open-ocean favoring taxa. Both the Silurian and Devonian periods are notable  
 for having been periods with a mostly “hothouse” climate, with no polar icecaps  
 418 and a high sea-level (Edwards and Fanning, 1985, Joachimski et al., 2009,  
 Munnecke et al., 2010).

420 The cohort-specific relationships between environmental preference and  $\log(\sigma)$   
 were calculated from the estimates of  $\beta^0$ ,  $\beta^v$ , and  $\beta^{v^2}$  (Fig. 5) and reflect how  
 422 these three parameters act in concert and not just individually (Fig. 4). Beyond  
 results already discussed above in the context of the parameters individually, it  
 424 is notable that the cohort originating in the Kungurian (279-272 My) is least  
 like the overall expected relationship and has the most sharply curved

426 appearance due to a high estimate  $\beta^{v^2}$  (Fig. 4). This cohort has the biggest  
 difference in extinction risk between environmental generalists and specialists.  
 428 The cohorts originating during the Emsian (407-393 My) and Frasnian (382 -  
 372 My) are tied for second in sharpness of curvature. The least sharply curved  
 430 cohorts include those originating during Tremadocian (484-477 My), Hirnantian  
 (445-443 My), Llandovery (443-433 My), and Ludlow (427-423 My). Except for  
 432 the Tremadocian cohort, most of these cohorts originate during the Silurian  
 through the Early Devonian range identified earlier as having lower expected  
 434 extinction intensity than what is expected from the group-level estimate.

The correlations of the cohort-specific estimates of the regression coefficients are  
 436 estimated as the off-diagonal elements of the correlation matrix  $\Omega$ . Only two of  
 the elements of  $\Omega$  are distinguishable from 0: the correlation of  $\beta^0$  (extinction  
 438 intensity) with both  $\beta^r$  and  $\beta^v$  (Fig. 6).

There is an approximate 90% probability that the cohort-specific estimates of  
 440 baseline extinction intensity  $\beta^0$  and the effect of geographic range  $\beta^r$  are  
 negatively correlated; this means that for cohorts experiencing a lower  
 442 extinction intensity ( $\beta^0$  decreases), the magnitude of the effect of geographic  
 range is expected to decrease as well, and *vice versa*; this is in contrast to the  
 444 observation made by Jablonski (1986) with regards to late Cretaceous bivalves.

Similarly, there is an approximate 97.4% probability that the cohort-specific  
 446 estimates of  $\beta^0$  and  $\beta^v$  are negatively correlated; this means that as extinction  
 intensity increases it is expected that epicontinental taxa become more favored  
 448 over open-ocean environments (i.e. as  $\beta^0$  increases,  $\beta^v$  decreases).

There is only an approximate 30% probability that  $\beta^r$  and  $\beta^v$  are positively  
 450 correlated. This lack of cross-correlation may be due in part to the much higher  
 between-cohort variance of the effect of environmental preference  $\tau^v$  than the

452 very small between-cohort variance in the effect of geographic range  $\tau^r$  (Table  
1); the effect of geographic range might simply not vary enough relative to the  
454 much noisier environmental preference.

Comparison of observed values of sampling, as measured by the gap statistic, to  
456 random draws from the posterior estimates of the imputed sampling values  
indicate that they are very similar (Fig. 7. This result is very encouraging as  
458 this is the ultimate goal of multiple imputation: to fill in missing data with  
values similar to the observed while taking into account the randomness of that  
460 variable (Gelman and Hill, 2007, Rubin, 1996). The estimates of  $\delta$  are based on  
the set of observed values and the entire posterior of imputed values.

462 Sampling was found to have a negative effect (positive  $\delta$ ) on duration: greater  
sampling, shorter duration (Table 1). While potentially counter intuitive, this  
464 result is most likely due to some long lived taxa only be sampled in the stages of  
the first and last appearance. Also, longer lived taxa have more opportunities to  
466 not be sampled than shorter lived taxa. These two factors will lead to this result.

While the effect of sampling appears large compared to the other regression  
468 coefficients, this is only because sampling was not standardized like the other  
covariates. To make the coefficients comparable,  $\delta$  is multiplied by twice the  
470 posterior mean of the standard deviation of sampling probability; the  
transformed value of  $\delta$  is then 0.642 ( $\pm 0.1$  SD). This effect is relatively small  
472 compared to the other covariate effects (Table 1). There is then a 98.6%  
probability that the effect of geographic range  $\mu^r$  has a greater magnitude than  
474  $\delta$ . Similarly,  $\mu^v$  has a 71.8% probability of having a greater magnitude of effect  
than  $\delta$ . Finally,  $\mu^{v^2}$  has a 100% probability of having a greater magnitude of  
476 effect than  $\delta$ .

The Weibull shape parameter  $\alpha$  was found to be approximately 1.36 ( $\pm 0.05$  SD)

with a 100% probability of being greater than 1. This result is not consistent with the Law of Constant Extinction (Van Valen, 1973) and is instead consistent with accelerating extinction risk with taxon age. This may indicate that older taxa are out-competed by younger taxa, a result consistent with some empirical results (Quental and Marshall, 2013, Smits, 2015, Wagner and Estabrook, 2014) and (ironically) with a recently proposed Red Queen-like model of evolution (Rosindell et al., 2015). This results, however, is not consistent with other empirical results (Crampton et al., 2016, Finnegan et al., 2008) and could potentially be caused by the minimum resolution of the fossil record (Sepkoski, 1975). It is thus unclear if a strong biological inference can be made from this result, which means that further work is necessary on the effect of taxon age on extinction risk.

## 4 Discussion

The generating observation behind this study was that for bivalves at the end Cretaceous mass extinction event, the only biological trait that was found to affect extinction risk was geographic range while traits that had previously been beneficial had no effect (Jablonski, 1986). This observation raises two linked questions: how does the effect of geographic range change with changing extinction intensity, and how does the effect of other biological traits change with changing extinction intensity?

I find that as intensity increases ( $\beta^0$  decreases), the magnitude of the effect of geographic range increases. I also find that as intensity increases, the effect of favoring epicontinental environments of open-ocean environments is expected to be increase; this is consistent with the results of Miller and Foote (2009). There is no evidence for a correlation between the effect of geographic range and

environmental preference. Additionally, the between-cohort variance in effect of  
504 geographic range is much less than the between-cohort variance of the effect of  
environmental preference which may underlie the lack of correlation between  
506 these two effects.

Additionally, the lower between-cohort variance in the effect of geographic range  
508 versus that higher between-cohort variance implies that for cohorts with a  
greater than average extinction intensity, the difference in the effect geographic  
510 range and the group-level effect of geographic range is expected to be smaller  
than the difference between the effect of environmental preference and the  
512 group-level effect of environmental preference.

I find consistent support for the “survival of the unspecialized,” with respect to  
514 epicontinental versus open-ocean environmental preference, as a time-invariant  
generalization of brachiopod survival; taxa with intermediate environmental  
516 preferences are expected to have lower extinction risk than taxa specializing in  
either epicontinental or open-ocean environments (Fig. 3), though the curvature  
518 of the relationship varies from rather shallow to very peaked (Fig. 5). However,  
this relationship is not symmetric about 0, as taxa favoring epicontinental  
520 environments are expected to have a greater duration than taxa favoring  
open-ocean environments. This description of environment only describes one  
522 major aspect of a taxon’s environmental context, with factors such as  
bathymetry and temperature being further descriptors of a taxon’s adaptive  
524 zone (Harnik, 2011, Harnik et al., 2012, Heim and Peters, 2011, Nürnberg and  
Aberhan, 2013); inclusion of these factors in future analyses would potentially  
526 improve our understanding of the “survival of the unspecialized” hypothesis  
(Simpson, 1944).

528 Hopkins et al. (2014), in their analysis of niche conservatism and substrate  
lithological preference in marine invertebrates, found that brachiopods were

530 among the least “conservative” groups; taxa were found to easily change  
 substrate preference on short time scales. While substrate preference is not the  
 532 same as environmental preference (as defined here), a question does arise: are  
 there three classes of environmental preference instead of two? These classes  
 534 would be taxa with broad tolerance (“true” generalists), inflexible specialists  
 (“true” specialists), and flexible but with a narrow tolerance. A flexible taxon is  
 536 one with a narrow habitat preference at one time, but with preference that  
 changes over time with changing environmental availability. My analysis  
 538 assumes that traits are constant over the duration of the taxon meaning that  
 this scenario is not detectable; taxa with broad tolerances and flexible taxa with  
 540 narrow per-stage preference end up being treated the same way. Future work  
 should explore how environmental preference changes over lineage duration in  
 542 relation to environmental availability to estimate if the generalists–specialists  
 continuum is actually ternary relationship.

544 An alternative approach for specifically modeling survival that can take into  
 account imperfect observation than the method used here is the  
 546 Cormack-Jolly-Seber (CJS) model (Liow et al., 2008, Liow and Nichols, 2010,  
 Royle and Dorazio, 2008, Tomiya, 2013). This model is a type of hidden Markov  
 548 model with an absorbing state (i.e. extinction). In this model, survival is defined  
 as the probability of surviving from time  $t$  to time  $t + 1$ . Additionally, the effect  
 550 of preservation and sighting is estimated as probability of observing a taxon that  
 is present; this can extend the duration of a taxon beyond its last occurrence.

552 This approach is a fundamentally different from the method used in my analysis:  
 I am estimating the biasing effect of sampling probability on taxon duration to  
 554 then compare with effects of other covariates, while the CJS model estimates the  
 pre-sampling fossil record and then estimates per-time unit survival probability.

556 The use of genera as the unit of the study and how to exactly interpret the

effects of the biological traits is an important question. For example, if any of  
558 the traits analyzed here are associated with increases in speciation rates, this  
might increase the duration of genera through self-renewal (Raup, 1991, 1994),  
560 which would be an example of the difference in biological pattern between  
species and genera (Jablonski, 1987, 2007, 2008). This could lead to a trait  
562 appearing to decrease generic level extinction risk by that trait increasing  
species level origination rate instead of decreasing species level extinction risk.

564 The model used here could be improved through either increasing the number of  
analyzed traits, expanding the hierarchical structure of the model to include  
566 other major taxonomic groups of interest, and the inclusion of explicit  
phylogenetic relationships between the taxa in the model as an additional  
568 hierarchical effect. An example trait that may be of particular interest is the  
affixing strategy or method of interaction with the substrate of the taxon, which  
570 has been found to be related to brachiopod survival where, for cosmopolitan  
taxa, taxa that are attached to the substrate are expected to have a greater  
572 duration than those that are not (Alexander, 1977).

It is theoretically possible to expand this model to allow for comparisons both  
574 within and between major taxonomic groups which would better constrain the  
brachiopod estimates while also allowing for estimation of similarities and  
576 differences in cross-taxonomic patterns. The major issue surrounding this  
particular expansion involves finding a similarly well sampled taxonomic group  
578 that is present during the Paleozoic. Potential groups include Crinoidea,  
Ostracoda, and other members of the “Paleozoic fauna” (Sepkoski, 1981).

580 With significant updates, it would also be possible to compare the brachiopod  
record with with Moden groups such as bivalves or gastropods (Sepkoski, 1981),  
582 though remembering that the groups may not necessarily share all cohorts with  
the brachiopods. This particular model expansion would act as a test of any



584 universal cross-taxonomic patterns in the effects of emergent traits on extinction  
such as has been proposed for geographic range (Payne and Finnegan, 2007).  
586 Additionally, this expanded model would also act as a test of the distinctness of  
the Sepkoski (1981) three-fauna hypothesis in terms of trait-dependent  
588 extinction.

Traits like environmental preference or geographic range (Hunt et al., 2005,  
590 Jablonski, 1987) are most likely heritable. Without phylogenetic context, this  
analysis assumes that differences in extinction risk between taxa are  
592 independent of the shared evolutionary history of those taxa (Felsenstein, 1985).  
In contrast, the origination cohorts only capture shared temporal context. For  
594 example, if taxon duration is phylogenetically heritable, then closely related  
taxa may have more similar durations as well as more similar biological traits.  
596 Without taking into account phylogenetic similarity the effects of these  
biological traits would be inflated solely due to inheritance. The inclusion of  
598 phylogenetic context as an additional individual-level hierarchical effect,  
independent of origination cohort, would allow for determining how much of the  
600 observed variability is due to shared evolutionary history versus shared temporal  
context versus actual differences associated with biological traits (Smits, 2015).  
602 The combination and integration of the phylogenetic comparative and  
paleontological approaches requires both sources of data, something which is not  
604 possible for this analysis because there is no phylogenetic hypothesis for all  
Paleozoic taxa, something that is frequently the case for marine invertebrates  
606 with a good fossil record. When both data sources are available has been  
possible, however, the analysis can more fully address the questions of interest  
608 in macroevolution (Fritz et al., 2013, Harnik et al., 2014, Raia et al., 2012a,b,  
Simpson et al., 2011, Slater et al., 2012, Slater, 2013, 2015, Smits, 2015, Tomiya,  
610 2013).

In summary, patterns of Paleozoic brachiopod survival were analyzed using a  
612 fully Bayesian hierarchical survival modelling approach while also eschewing the  
traditional separation between background and mass extinction. I find that  
614 cohort extinction intensity is negatively correlated with both the cohort-specific  
effects of geographic range and environmental preference. These results imply  
616 that as extinction intensity increases ( $\beta^0$ ) increases, it is expected that both  
effects will increase in magnitude. However, the change in effect of  
618 environmental preference is expected to be greater than the change in the effect  
of geographic range. Additionally, I find support for greater survival in  
620 environmental generalists over specialists in all origination cohorts analyzed;  
this is consistent with the long standing “survival of the unspecialized”  
622 hypothesis (Baumiller, 1993, Liow, 2004, 2007, Nürnberg and Aberhan, 2013,  
2015, Simpson, 1944, 1953, Smits, 2015). The results of this analysis support the  
624 conclusion that for Paleozoic brachiopods, as extinction intensity increases  
overall extinction selectivity is expected to increase as well.

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Table 1: Estimates of various parameters in the model used here. These include group-level estimates of the effects of biological traits on brachiopod generic survival, the standard deviation of the between-cohort effects, as well as the estimates of both the effect of sampling  $\delta$  and the Weibull shape parameter  $\alpha$ . The mean, standard deviation (SD), 10th, 50th, and 90th quantiles of the marginal posteriors are presented.

type	parameter	effect of	mean	SD	10%	50%	90%
Mean	$\mu^i$	intercept	-3.05	0.20	-3.30	-3.05	-2.80
	$\mu^r$	geographic range	-0.98	0.16	-1.18	-0.98	-0.79
	$\mu^v$	environmental preference	-0.76	0.19	-0.99	-0.76	-0.52
	$\mu^{v^2}$	environmental preference <sup>2</sup>	3.15	0.36	2.69	3.15	3.62
	$\mu^m$	body size	-0.01	0.13	-0.17	-0.01	0.15
Standard deviation	$\tau^i$	intercept	0.51	0.11	0.38	0.50	0.65
	$\tau^r$	geographic range	0.50	0.16	0.30	0.49	0.71
	$\tau^v$	environmental preference	0.84	0.17	0.63	0.82	1.05
	$\tau^{v^2}$	environmental preference <sup>2</sup>	1.51	0.36	1.08	1.48	1.97
	$\tau^m$	body size	0.47	0.13	0.32	0.46	0.64
Other	$\delta$	sampling	0.90	0.15	0.71	0.90	1.09
	$\alpha$	“time”	1.36	0.04	1.30	1.36	1.42

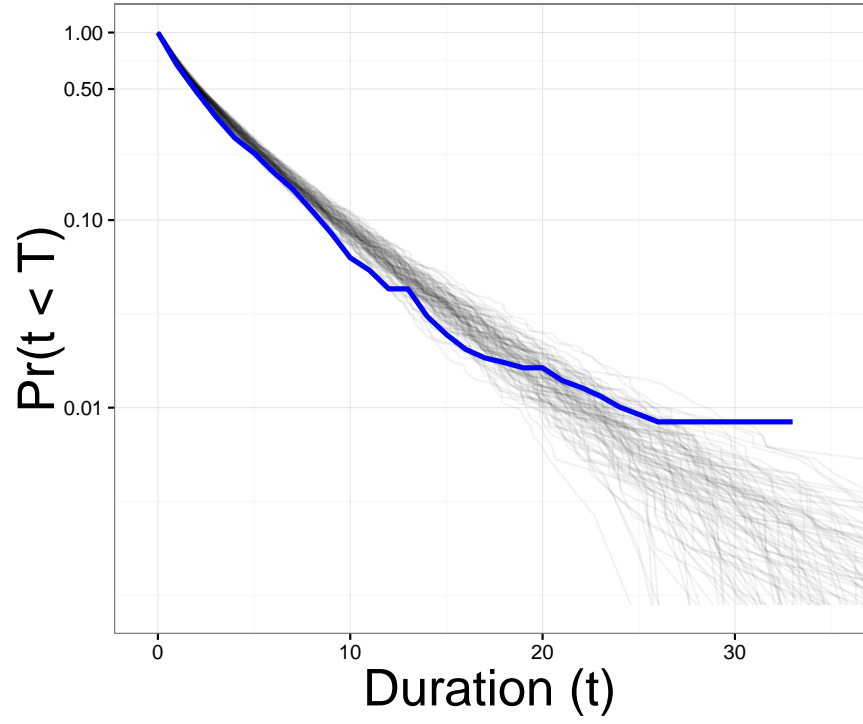


Figure 1: Comparison of the empirical estimate of  $S(t)$  (highlighted) versus estimates from 100 posterior predictive data sets (black).  $S(t)$  corresponds to the probability that the age of a genus  $t$  is less than the genus' ultimate duration  $T$ . The vertical axis is log10 transformed.



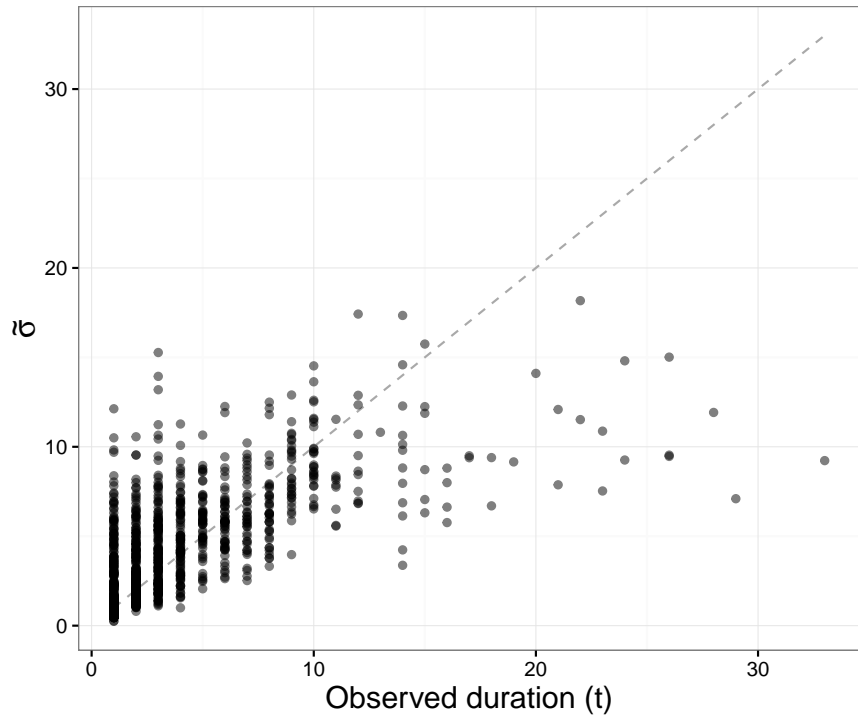


Figure 2: Comparison of all observed genus durations in number of geological stages to the average posterior predictive estimates of  $\log(\sigma)$ . The dashed, diagonal line corresponds to  $x = y$ .

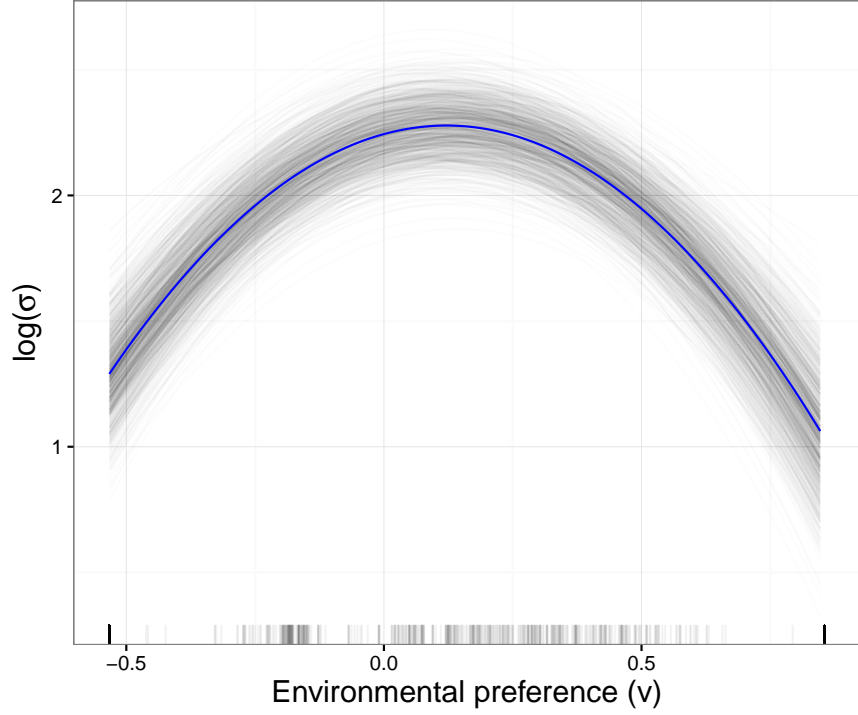


Figure 3: The overall expected relationship between environmental affinity  $v_i$  and a  $\log(\sigma)$  when  $r = 0$  and  $m = 0$ . The 1000 semi-transparent lines corresponds to a single draw from the posterior predictive distribution, while the highlighted line corresponds to the median of the posterior predictive distribution. The overall relationship is concave down with an optimum greater than 0, which means that taxa favoring epicontinental environments are expected to have longer durations than those favoring open-ocean environments. The tick marks along the bottom of the plot correspond to the (rescaled) observed values of environmental preference.

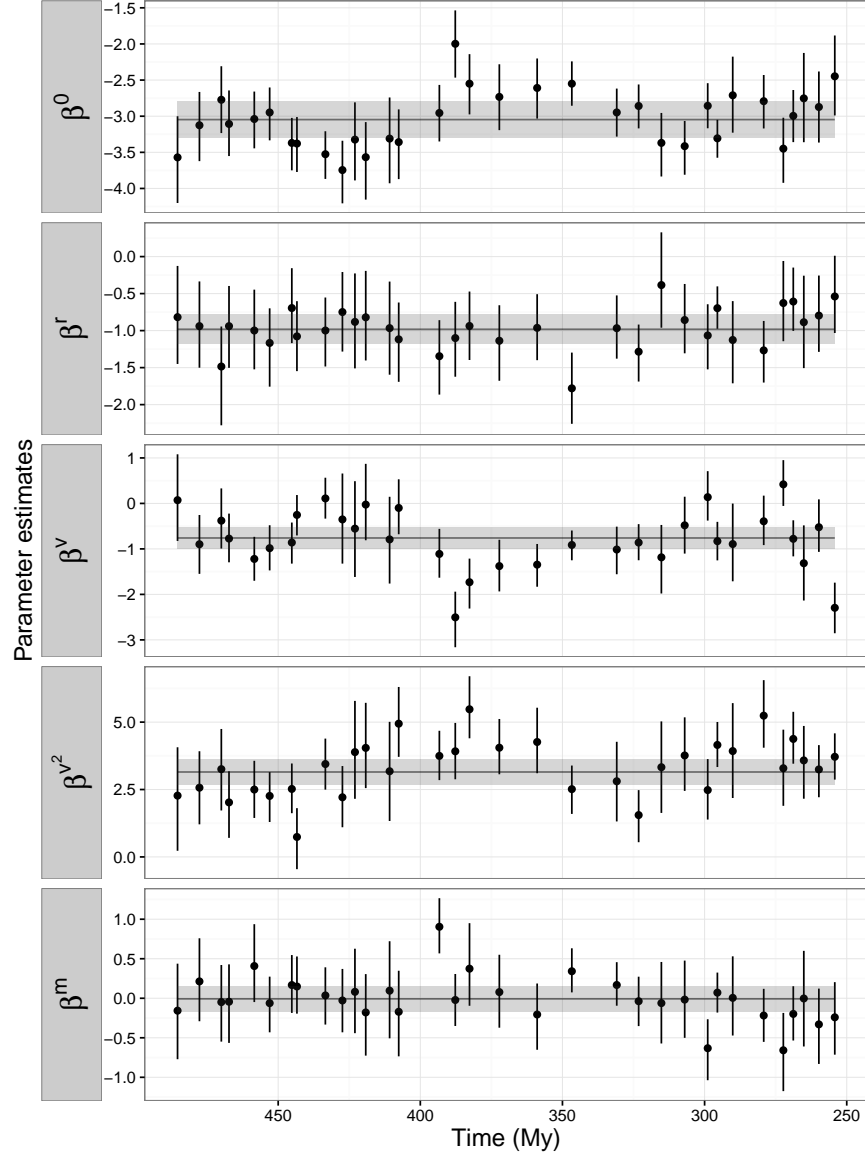


Figure 4: Comparison of cohort-specific estimates of  $\beta^0$ , the effect of geographic range on extinction risk  $\beta^r$ , the effect of environmental preference  $\beta^v$  and  $\beta^{v^2}$ , and body size  $\beta^m$ . Points correspond to the median of the cohort-specific estimate, along with 80% credible intervals. Points are plotted at the midpoint of the cohorts stage of origination in millions of years before present (My). Black, horizontal lines are the overall estimates of covariate effects along with 80% credible intervals (shaded).

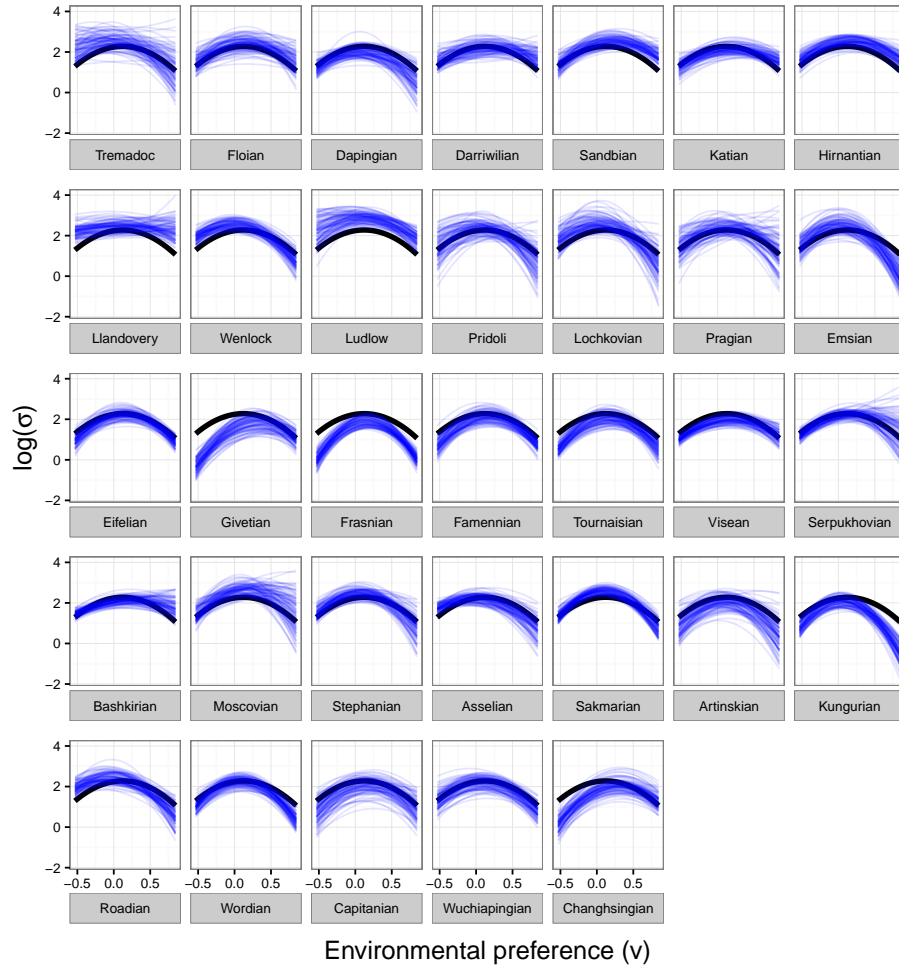


Figure 5: Comparison of origination cohort-specific (posterior predictive) estimates of the effect of environmental preference on  $\log(\sigma)$  to the mean overall estimate of the effect of environmental preference. Cohort-specific estimates are from 100 posterior predictive simulations across the range of (transformed and rescaled) observed values of environmental preference. The oldest cohort is in the top-right and younger cohorts proceed left to right, with the youngest cohort being the right-most facet of the last row. Panel names correspond to the name of the stage in which that cohort originated.

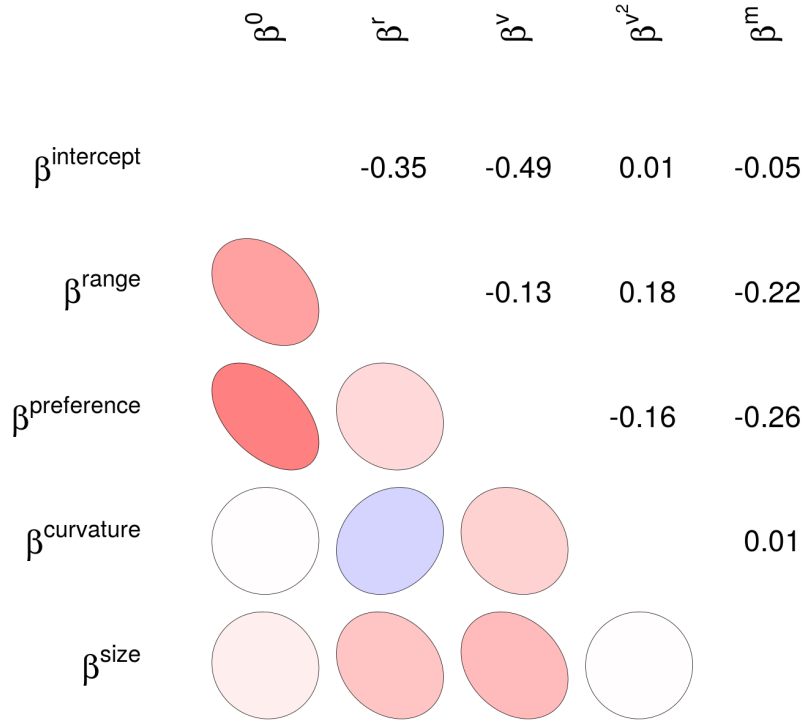


Figure 6: Mixed graphical and numerical representation of the correlation matrix  $\Omega$  of variation in cohort-specific covariate estimates. These correlations are between the estimates of the cohort-level effects of covariates, along with intercept/baseline extinction risk. The median estimates of the correlations are presented numerically (upper-triangle) and as idealized ellipses representing that much correlation (lower-triangle). The darkness of the ellipse corresponds to the magnitude of the correlation.

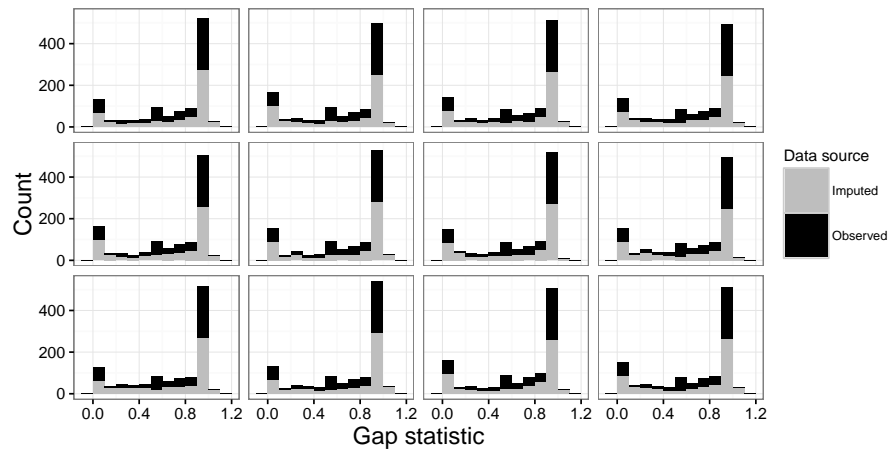


Figure 7: Histograms of the distribution of gap statistic values from both the observed values and the imputed values. For each panel the observed values are identical but the imputed values are from a single set of their posterior estimates.