

Title: The interplay between extinction intensity and selectivity:
2 correlation in trait effects on taxonomic survival

Running title: Variation in trait effects on taxonomic survival

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Abstract

While the effect of geographic range on extinction risk is well documented, how other traits may increase or decrease extinction risk is less well known. I analyze patterns of Paleozoic brachiopod genus durations and their relationship to geographic range, affinity for epicontinental seas versus open ocean environments, and body size. Additionally, I allow for environmental affinity to have a nonlinear effect on duration. Using a hierarchical Bayesian modeling approach, I also model the interaction between the effects of the biological traits and a taxon's time of origination. My analysis framework eschews the traditional distinction between background and mass extinction, instead the entire time period is analyzed where these "states" are part of a continuum. Contrary to previous work, I find evidence that as baseline extinction risk increases, the effects of biological traits (except body size) on extinction risk tend to increase. For parts of the Paleozoic I find support for a "survival of the generalists" scenario, there are times where this relationship is absent or even reversed. Importantly, I find that as baseline extinction risk increases, the steepness of this relationship is expected to increase as well.

1 Introduction

How do biological traits affect extinction risk? Jablonski (1986) observed that at a mass extinction event, the effects of biological traits on taxonomic survival decreased in size. However, this pattern was not the case for the effect of geographic range on survival (Jablonski, 1986). Biological traits are defined here as descriptors of a taxon's adaptive zone, which is the set of all biotic–biotic and biotic–abiotic interactions that a taxon can experience (Simpson, 1944). In effect, these are descriptors of a taxon's broad-sense ecology.

Jablonski (1986) phrased his conclusions in terms of background versus mass extinction, but this scenario is readily transferable to a continuous variation framework as there is no obvious distinction in terms of extinction rate between these two states (Wang, 2003). Additionally, the Jablonski (1986) scenario has strong model structure requirements in order to test its proposed macroevolutionary mechanism; not only do the taxon trait effects need to be modeled, but the correlation between trait effects need to be modeled as well.

There are two end-member macroevolutionary mechanisms which may underlie the pattern observed by Jablonski (1986): the effect of geographic range on predictive survival remains constant and those of other biological traits decrease, and the effect of geographic range in predicting survival increases and those of other biological traits stay constant. Reality, of course, may fall somewhere along this continuum.

I choose to model brachiopod taxon durations because trait based differences in extinction risk should manifest as differences in taxon durations. Namely, a taxon with a beneficial trait should persist for longer, on average, than a taxon without that beneficial trait. Conceptually, taxon survival can be considered an aspect of “taxon fitness” along with expected lineage specific branching/origination rate (Cooper, 1984, Palmer and Feldman, 2012).

Brachiopods are an ideal group for this study as they are well known for having an exceptionally complete fossil record (Foote, 2000). Specifically, I focus on the brachiopod record from most of the Paleozoic, from the start of the Ordovician (approximately 485 Mya) through the end Permian (approximately 252 Mya) as this represents the time of greatest global brachiopod diversity (Alroy, 2010).

The analysis of taxon durations, or time from origination to extinction, falls under the purview of survival analysis, a field of applied statistics commonly

- 66 used in health care (Klein and Moeschberger, 2003) but has a long history in
paleontology (Simpson, 1944, 1953, Van Valen, 1973, 1979).
- 68 Geographic range is widely considered the most important taxon trait for
estimating differences in extinction risk at nearly all times with large geographic
70 range associated with low extinction risk (Jablonski, 1986, 1987, Jablonski and
Roy, 2003, Payne and Finnegan, 2007), though Foote and Miller (2013) find
72 that this generalization does not hold in the Mesozoic. For the Paleozoic,
however, I expect this to hold true for the entire period analyzed.
- 74 Miller and Foote (2009) demonstrated that during several mass extinctions taxa
associated with open-ocean environments tend to have a greater extinction risk
76 than those taxa associated with epicontinental seas. During periods of
background extinction, however, they found no consistent difference between
78 taxa favoring either environment. These two environment types represent the
primary environmental dichotomy observed in ancient marine systems (Miller
80 and Foote, 2009, Peters, 2008, Sheehan, 2001).

Epicontinental seas are a shallow-marine environment where the ocean has
82 spread over the surface of a continental shelf with a depth typically less than
100m. In contrast, open-ocean coastline environments have much greater
84 variance in depth, do not cover the continental shelf, and can persist during
periods of low sea level. Because of this, it is strongly expected that taxa which
86 favor epicontinental seas would be at great risk during periods of low sea levels,
such as during glacial periods, where these seas are drained. During the
88 Paleozoic (approximately 541–252 My), epicontinental seas were widely spread
globally but declined over the Mesozoic (approximately 252–66 My) and
90 eventually nearly disappeared during the Cenozoic (approximately 66–0 My) as
open-ocean coastlines became the dominant shallow-marine setting (Johnson,
92 1974, Miller and Foote, 2009, Peters, 2008).

Given the above findings, I predict that as extinction risk increases, taxa
94 associated with open-ocean environments should generally increase in extinction
risk versus those that favor epicontinental seas. Additionally, there is a possible
96 nonlinear relationship between environmental preference and taxon duration. A
long standing hypothesis is that generalists or unspecialized taxa will have
98 greater survival than specialists (Baumiller, 1993, Liow, 2004, 2007, Nürnberg
and Aberhan, 2013, 2015, Simpson, 1944). In this analysis I allowed for
100 environmental preference to have a parabolic effect on taxon duration

Body size, measured as shell length (Payne et al., 2014), was also considered as
102 a potentially informative covariate. Body size is a proxy for metabolic activity
and other correlated life history traits (Payne et al., 2014). There is no strong
104 hypothesis of how body size effects extinction risk in brachiopods, such that a
positive, negative, or zero effect are all plausible.

106 I adopt a hierarchical Bayesian survival modeling approach, which represents
both a conceptual and statistical unification of the paleontological dynamic and
108 cohort survival analytic approaches (Baumiller, 1993, Foote, 1988, Raup, 1975,
1978, Simpson, 2006, Van Valen, 1973, 1979). By using a Bayesian framework I
110 am able to quantify the uncertainty inherent in the estimates of the effects of
biological traits on survival, especially in cases where the covariates of interest
112 (i.e. biological traits) are themselves known with error.

2 Materials and Methods

114 2.1 Fossil occurrence information

The dataset analyzed here was sourced from the Paleobiology Database
116 (<http://www.paleodb.org>) which was then filtered based on taxonomic,

temporal, stratigraphic, and other occurrence information that was necessary
118 for this analysis. These filtering criteria are very similar to those from Foote and
Miller (2013) with an additional constraint of being present in the body size
120 data set from Payne et al. (2014). Epicontinental versus open-ocean assignments
for each fossil occurrence are partially based on those from Miller and Foote
122 (2009), with additional occurrences assigned similarly (Miller and Foote,
personal communication).

124 Fossil occurrences were analyzed at the genus level which is common for
paleobiological, macroevolution, or macroecological studies of marine
126 invertebrates (Alroy, 2010, Foote and Miller, 2013, Harnik et al., 2013, Kiessling
and Aberhan, 2007, Miller and Foote, 2009, Nürnberg and Aberhan, 2013, 2015,
128 Payne and Finnegan, 2007, Simpson and Harnik, 2009, Vilhena et al., 2013).

While species diversity dynamics tend to be of much greater interest than those
130 of higher taxa, the nature of the fossil record makes accurate and precise
taxonomic assignments at the species level for all occurrences extremely difficult
132 if not impossible. Additionally, there is evidence of real differences in biological
patterns at the genus level versus the species level (Jablonski, 1987). As such,
134 the choice to analyze genera as opposed to species was in order to assure a
minimum level of confidence and accuracy in the data analyzed here.

136 Genus duration was calculated as the number of geologic stages from first
appearance to last appearance, inclusive. Durations were based on geologic
138 stages as opposed to millions of years because of the inherently discrete nature
of the fossil record; dates are not assigned to fossils themselves but instead
140 fossils are known from a geological interval which represents some temporal
range. Stages act as effectively irreducible globally consistent temporal intervals
142 in which taxa occur.

Genera with a last occurrence in or after Changhsingian stage were right

¹⁴⁴ censored at the Changhsingian. Genera with a duration of only one stage were
left censored (Appendix A). The covariates used to model genus duration were
¹⁴⁶ geographic range size (r), environmental preference (v, v^2), and body size (m).

¹⁴⁸ Geographic range was calculated using an occupancy approach. First, all
occurrences were projected onto an equal-area cylindrical map projection. Each
occurrence was then assigned to one of the cells from a 70×34 regular raster
¹⁵⁰ grid placed on the map. Each grid cell represents approximately $250,000 \text{ km}^2$.
The map projection and regular lattice were made using shape files from
¹⁵² <http://www.naturalearthdata.com/> and the **raster** package for R (Hijmans,
2015).

¹⁵⁴ For each stage, the total number of occupied grid cells, or cells in which a fossil
occurs, was calculated. Then, for each genus, the number of grid cells occupied
¹⁵⁶ by that genus was calculated. Dividing the genus occupancy by the total
occupancy gives the relative occupancy of that genus. Mean relative genus
¹⁵⁸ occupancy was then calculated as the mean of the per stage relative occupancies
of that genus.

¹⁶⁰ Body size data was sourced directly from Payne et al. (2014). Because those
measurements are presented without error, a measurement error model similar
¹⁶² to the one for environmental affinity could not be implemented (Appendix A).

Prior to analysis, geographic range and body size were transformed and
¹⁶⁴ standardized in order to improve interpretability of the results. Geographic
range, which can only vary between 0 and 1, was logit transformed. Body size,
¹⁶⁶ which is defined for all positive real values, was natural log transformed. These
covariates were then standardized by mean centering and dividing by two times
¹⁶⁸ their standard deviation following Gelman and Hill (2007).

2.2 Analytical approach

¹⁷⁰ Hierarchical modelling is a statistical approach which explicitly takes into account the structure of the observed data in order to model both the within and between group variance (Gelman et al., 2013, Gelman and Hill, 2007). The units of study (e.g. genera) each belong to a single grouping (e.g. origination cohort). These groups are considered separate draws from a shared probability distribution (e.g. all cohorts, observed and unobserved). The group-level parameters are then estimated simultaneously as the other parameters of interest (e.g. covariate effects) (Gelman et al., 2013). The subsequent estimates are partially pooled together, where parameters from groups with large samples or effects remain large while those of groups with small samples or effects are pulled towards the overall group mean.

This partial pooling is one of the greatest advantages of hierarchical modeling.
¹⁸² By letting the groups “support” each other, parameter estimates then better reflect our statistical uncertainty. Additionally, this partial pooling helps control for multiple comparisons and possibly spurious results as effects with little support are drawn towards the overall group mean (Gelman et al., 2013, Gelman and Hill, 2007).

All covariate effects (regression coefficients), as well as the intercept term
¹⁸⁸ (baseline extinction risk), were allowed to vary by group (origination cohort). The covariance/correlation between covariate effects was also modeled. This hierarchical structure allows inference for how covariates effects may change with respect to each other while simultaneously estimating the effects themselves, propagating our uncertainty through all estimates.

Additionally, instead of relying on point estimates of environmental affinity, I
¹⁹⁴ treat environmental affinity as a continuous measure of the difference between

the taxon's environmental occurrence pattern and the background occurrence
196 pattern (Appendix A).

2.3 Survival model

198 Genus durations were assumed to follow either an exponential or Weibull
distribution, both of which make different assumptions about how a taxon's
200 duration may effect its instantaneous extinction risk (Klein and Moeschberger,
2003). The exponential distribution assumes that extinction risk is independent
202 of duration. In contrast, the Weibull distribution allows for age dependent
extinction via the shape parameter α , though only as a monotonic function of
204 duration. Importantly, the Weibull distribution is equivalent to the exponential
distribution when $\alpha = 1$.

206 The following variables are here defined: y_i is the duration of genus i in geologic
stages, X is the matrix of covariates including a constant term, B_j is the vector
208 of regression coefficients for origination cohort j , Σ is the covariance matrix of
the regression coefficients, τ is the vector of scales the standard deviations of
210 the between-cohort variation in regression coefficient estimates, and Ω is the
correlation matrix of the regression coefficients.

²¹² The exponential model is defined

$$y_i \sim \text{Exponential}(\lambda)$$

$$\lambda_i = \exp(\mathbf{X}_i B_{j[i]})$$

$$B \sim \text{MVN}(\vec{\mu}, \Sigma)$$

$$\Sigma = \text{Diag}(\vec{\tau}) \Omega \text{Diag}(\vec{\tau})$$

$$\mu_k \sim \begin{cases} \mathcal{N}(0, \psi_k \nu) & \text{if } k \neq r, \text{ or} \\ \mathcal{N}(-1, 1) & \text{if } k = r \end{cases} \quad (1)$$

$$\tau_k \sim C^+(1)$$

$$\psi_k \sim C^+(1) \text{ if } k \neq r$$

$$\nu \sim C^+(1)$$

$$\Omega \sim \text{LKJ}(2).$$

Similarly, the Weibull model is defined

$$\begin{aligned}
y_i &\sim \text{Weibull}(\alpha_{j[i]}, \sigma) \\
\sigma_i &= \exp\left(\frac{-(\mathbf{X}_i B_{j[i]})}{\alpha_{j[i]}}\right) \\
B &\sim \text{MVN}(\vec{\mu}, \Sigma) \\
\Sigma &= \text{Diag}(\vec{\tau}) \Omega \text{Diag}(\vec{\tau}) \\
\log(\alpha) &\sim \mathcal{N}(a, \pi) \\
\mu_k &\sim \begin{cases} \mathcal{N}(0, \psi_k \nu) & \text{if } k \neq r, \text{ or} \\ \mathcal{N}(-1, 1) & \text{if } k = r \end{cases} \\
\tau_k &\sim \text{C}^+(1) \\
a &\sim \mathcal{N}(0, 1) \\
\pi &\sim \text{C}^+(1) \\
\psi_k &\sim \text{C}^+(1) \text{ if } k \neq r \\
\nu &\sim \text{C}^+(1) \\
\Omega &\sim \text{LKJ}(2).
\end{aligned} \tag{2}$$

²¹⁴ The principal difference between this model and the previous (Eq. 1) is the inclusion of the shape parameter α . Note that σ is approximately equivalent to ²¹⁶ $1/\lambda$.

²¹⁸ For an explanation of how this model was developed, parameter explanations, and choice of priors, please see Appendix B. Note that these models (Eq. 1, 2) do not include how the uncertainty in environmental affinity is included nor how ²²⁰ censored observations are included. For an explanation of both of these aspects, see Appendices A and C.

²²² **2.4 Parameter estimation**

The joint posterior was approximated using a Markov chain Monte Carlo
²²⁴ routine that is a variant of Hamiltonian Monte Carlo called the No-U-Turn
Sampler (Hoffman and Gelman, 2014) as implemented in the probabilistic
²²⁶ programming language Stan (Stan Development Team, 2014). The posterior
distribution was approximated from four parallel chains run for 10,000 draws
²²⁸ each, split half warm-up and half sampling and thinned to every 10th sample for
a total of 5000 posterior samples. Chain convergence was assessed via the scale
²³⁰ reduction factor \hat{R} where values close to 1 ($\hat{R} < 1.1$) indicate approximate
convergence, meaning that the chains are approximately stationary and the
²³² samples are well mixed (Gelman et al., 2013).

2.5 Model evaluation

²³⁴ Models were evaluated using both posterior predictive checks and an estimate of
out-of-sample predictive accuracy. The motivation behind posterior predictive
²³⁶ checks as tools for determining model adequacy is that replicated data sets
using the fitted model should be similar to the original data (Gelman et al.,
²³⁸ 2013). Systematic differences between the simulations and observations indicate
weaknesses of the model fit. An example of a technique that is very similar
²⁴⁰ would be inspecting the residuals from a linear regression.

The strategy behind posterior predictive checks is to draw simulated values
²⁴² from the joint posterior predictive distribution, $p(y^{rep}|y)$, and then compare
those draws to the empirically observed values (Gelman et al., 2013). To
²⁴⁴ accomplish this, for each replicate, a single value is drawn from the marginal
posterior distributions of each regression coefficient from the final model as well
²⁴⁶ as α for the Weibull model (Eq. 1, 2). Then, given the covariate information \mathbf{X} ,

a new set of n genus durations are generated giving a single replicated data set
248 y^{rep} . This is repeated 1000 times in order to provide a distribution of possible
values that could have been observed given the model.

250 In order to compare the fitted model to the observed data, various graphical
comparisons or test quantities need to be defined. The principal comparison
252 used here is a comparison between non-parameteric approximation of the
survival function $S(t)$ as estimated from both the observed data and each of the
254 replicated data sets. The purpose of this comparison is to determine if the
model approximates the same survival/extinction pattern as the original data.

256 The exponential and Weibull models were compared for out-of-sample predictive
accuracy using the widely-applicable information criterion (WAIC) (Watanabe,
258 2010). Out-of-sample predictive accuracy is a measure of the expected fit of the
model to new data. However, because the Weibull distribution reduces to the
260 exponential distribution when $\alpha = 1$, my interest is not in choosing between
these models. Instead, comparisons of WAIC values are useful for better
262 understanding the effect of model complexity on out-of-sample predictive
accuracy. The calculation of WAIC used here corresponds to the “WAIC 2”
264 formulation recommended by Gelman et al. (2013). For an explanation of how
WAIC is calculated, see Appendix D. Lower values of WAIC indicate greater
266 expected out-of-sample predictive accuracy than higher values.

3 Results

268 As stated above, posterior approximations for both the exponential and Weibull
models achieved approximate stationarity after 10,000 steps, as all parameter
270 estimates have an $\hat{R} < 1.1$.

Comparisons of the survival functions estimated from 1000 posterior predictive
272 data sets to the estimated survival function of the observed genera demonstrates
that both the exponential and Weibull models approximately capture the
274 observed pattern of extinction (Fig. 1). This is partially expected given that the
unit of analysis is genus species duration as opposed species level which can
276 alter the shape of $S(t)$ (Foote, 2001, Raup, 1975, 1978, 1985). The major
difference in fit between the two models is that the Weibull model has a slightly
278 better fit for longer lived taxa than the exponential model.

Additionally, the Weibull model is expected to have slightly better out-of-sample
280 predictive accuracy when compared to the exponential model (WAIC 4576
versus 4604, respectively). Because the difference in WAIC between these two
282 models is large, only those results from the Weibull model will be discussed.

Estimates of the overall mean covariate effects μ can be considered
284 time-invariant generalizations for brachiopod survival during the Paleozoic (Fig.
1). Consistent with prior expectations, geographic range size has a negative
286 effect on extinction risk, where genera with large ranges having greater
durations than genera with small ranges.

I infer that body size has no distinguishable effect on brachiopod taxonomic
288 survival. The mean estimate of the effect of body size on extinction risk is
290 negative, implying that increasing body size decreases extinction risk, however
this estimate is within 2 standard deviations of 0 (mean $\mu_m = -0.09$, standard
292 deviation 0.09; Fig. 1).

Interpretation of the effect of environmental preference v on duration is slightly
294 more involved. Because a quadratic term is the equivalent of an interaction
term, both μ_v and μ_{v^2} have to be interpreted together because it is illogical to
296 change values of v without also changing values v^2 . To determine the nature of

the effect of v on duration I calculated the multiplicative effect of environmental
298 preference on extinction risk.

Given mean estimated extinction risk $\tilde{\sigma}$, we can define the extinction risk
300 multiplier of an observation with environmental preference v_i as

$$f(v_i) = \exp\left(\frac{-(\mu_v v_i + \mu_{v^2} v^2)}{\alpha}\right). \quad (3)$$

This function $f(v_i)$ has a y-intercept of $\exp(0)$ or 1 because it does not have a
302 non-zero intercept term. Equation 3 can be either concave up or down. A
concave down $f(v_i)$ may indicate that genera of intermediate environmental
304 preference have greater durations than either extreme, and *vice versa* for
concave up function.

306 The expected effect of environmental preference as a multiplier of expected
extinction risk can then be visualized (Fig. 2). This figure depicts 1000 posterior
308 predictive estimates of Eq. 3 across all possible values of v . The number
indicates the posterior probability that the function is concave down, with
310 generalists having lower extinction risk/greater duration than either type of
specialist. Note that the inflection point of Fig. 2 is approximately $x = 0$,
312 something that is expected given the estimate of μ_v (Fig. 1).

The matrix Σ describing the covariance between the different coefficients
314 describes how these coefficients might vary together across the origination
cohorts. Similar to how this was modeled (Eq. 1, 2), for interpretation purposes
316 Σ is decomposed into a vector of standard deviations $\vec{\tau}$ and a correlation matrix
 Ω .

318 The estimates of the standard deviation of between-cohort coefficient estimates
 τ indicate that some effects can vary greatly between-cohorts (Fig. 1).
320 Coefficients with greater values of τ have greater between-cohort variation. The

covariate effects with the greatest between origination cohort variation are β_r ,
322 β_v , and β_{v^2} . Estimates of β_m have negligible between cohort variation, as there
is less between cohort variation than the between cohort variation in baseline
324 extinction risk β_0 . However the amount of between cohort variation in estimates
of β_{v^2} means that it is possible for the function describing the effect of
326 environmental affinity to be upward facing for some cohorts (Eq. 3), which
corresponds to environmental generalists being shorter lived than specialists in
328 that cohort.

The correlation terms of Ω (Fig. 3a) describe the relationship between the
330 coefficients and how their estimates may vary together across cohorts. The
correlations between the intercept term β_0 and the effects of the taxon traits are
332 of particular interest for evaluating the Jablonski (1986) scenario (Fig. 3a first
column/last row). Keep in mind that when β_0 is low, extinction risk is low; and
334 conversely, when β_0 is high, then extinction risk is high.

Marginal posterior probabilities of the correlations between the level of baseline
336 extinction risk β_0 and the effects of the taxon traits indicate that the correlation
between expected extinction risk and both geographic range β_r and β_{v^2} are of
338 particular note (Fig. 3b).

There is approximately a 98% probability that β_0 and β_r are negatively
340 correlated (Fig. 3b), meaning that as extinction risk increases, the
effect/importance of geographic range on genus duration increases. This means
342 that increases in baseline extinction rate are correlated with an increased
importance of geographic range size. There is a 93% probability that β_0 and β_{v^2}
344 are negatively correlated (Fig. 3b), meaning that as extinction risk increases,
the peakedness of $f(v_i)$ increases and the relationship tends towards concave
346 down. Additionally, there is a 97% probability that values of β_r and β_{v^2} are
positively correlated (Mean correlation 0.51, standard deviation 0.23).

³⁴⁸ While the overall group level estimates are of particular importance when
³⁵⁰ defining time-invariant differences in extinction risk, it is also important and
useful to analyze the individual level parameter estimates in order to better
understand how parameters actually vary across cohorts.

³⁵² In comparison to the overall mean extinction risk μ_0 , cohort level estimates β_0
³⁵⁴ show some amount of variation through time as expected by estimates of τ_0
(Fig. 4a). A similar, if slightly greater, amount of variation is also observable in
³⁵⁶ cohort estimates of the effect of geographic range β_r (Fig. 4b). Again, smaller
values of β_0 correspond to lower expected extinction risk. Similarly, smaller
³⁵⁸ values of β_r correspond to greater decrease in extinction risk with increasing
geographic range

How the effect of environmental affinity varies between cohorts can be observed
³⁶⁰ by using the cohort specific coefficients estimates. Following the same procedure
used earlier (Fig. 1), but substituting cohort specific estimates of β_v and β_{v^2} for
³⁶² μ_v and μ_{v^2} , the cohort specific effect of environmental preference as a multiplier
of mean extinction risk can be calculated. This was done only for the Weibull
³⁶⁴ model, though the observed pattern should be similar for the exponential model.

As expected based on the estimates of τ_v and τ_{v^2} , there is greater variation in
³⁶⁶ the peakedness of $f(v_i)$ than there is variation between convave up and down
functions (Fig. 5). 12 of the 33 cohorts have less than 50% posterior probability
³⁶⁸ that generalists are potentially expected to be shorter lived than specialists,
though two of those cases have approximately a 50% probability of being either
³⁷⁰ concave up or down. This is congruent with the 0.72 posterior probability that
 μ_{v^2} is positive/ $f(v_i)$ is concave down.

³⁷² Additionally, for some cohorts there is a quite striking pattern where the effect
of environmental preference v has a nearly-linear relationship (Fig. 5). These are

³⁷⁴ primarily scenarios where one of the end member preferences is expected to
³⁷⁵ have a greater duration than either intermediate or the opposite end member
³⁷⁶ preference. Whatever curvature is present in these nearly-linear cases is due to
³⁷⁷ the definition of $f(v)$ as it is not defined for non-negative values of σ (Eq. 3). For
³⁷⁸ all stages between the Emsian through the Viséan, inclusive, intermediate
³⁷⁹ preferences are of intermediate extinction risk when compared with
³⁸⁰ epicontinental specialists (lowest risk) or open-ocean specialists (highest risk).
This time period represents most of the Devonian through the early
³⁸² Carboniferous.

4 Discussion

³⁸⁴ My results demonstrate that both the effects of geographic range and the
³⁸⁵ peakedness/concavity of environmental preference are both negatively correlated
³⁸⁶ with baseline extinction risk, meaning that as baseline extinction risk increases
³⁸⁷ the effect sizes of both these traits are expected to increase (Fig. 3b). This
³⁸⁸ result supports neither of the two proposed end-member macroevolutionary
³⁸⁹ mechanisms for how biological traits should correlate with extinction risk. The
³⁹⁰ observed correlation between the two effects as well as between the effects and
³⁹¹ baseline extinction risk instead implies that as baseline extinction risk increases,
³⁹² the strength of the total selection gradient on biological traits (except body size)
³⁹³ increases. This manifests as greater differences in extinction risk for each unit
³⁹⁴ difference in the biological covariates during periods of high extinction risk,
while a relatively flatter selection gradient during periods of low extinction risk.
³⁹⁶ For the approximately 233 My period analyzed there is an approximate 75%
posterior probability that brachiopod genera with intermediate environmental
³⁹⁸ preferences are expected to have a lower extinction risk than either end

members. However, the over all curvature of $f(v_i)$ is not very peaked meaning
400 that when averaged over the entire Phanerozoic this relationship may not lead
to large differences in extinction risk (Fig. 2). Note that the duration of the
402 period analyzed is approximately four times then length of the Cenozoic (e.g.
time since the extinction of the non-avian dinosaurs). This result gives weak
404 support for the universality of the hypothesis that environmental generalists
have greater survival than environmental specialists (Liow, 2004, 2007,
406 Nürnberg and Aberhan, 2013, 2015, Simpson, 1944).

The posterior variance in the estimate of overall $f(v_i)$ reflects the large between
408 cohort variance in cohort specific estimates of $f(v_i)$ (Fig. 5). Given that there is
only a 75% posterior probability that the expected overall estimate of $f(v_i)$ is
410 concave down, it is not surprising that there are some stages where the
estimated relationship is in fact the reverse of the prior expectation.
412 Additionally, some of those same stages where $f(v_i)$ does not resemble the prior
expectation of a concave down nonlinear relation are instead is highly skewed
414 and effectively linear (Fig. 5). These results demonstrate that, while the
group-level estimate may only weakly support one hypothesis, the cohort-level
416 estimates may exhibit very different characteristics. These results are also
consistent with aspects of Miller and Foote (2009) who found that the effect of
418 environmental preference on extinction risk was quite variable and without
obvious patterning during times of background extinction.
420 There are two mass extinction events that are captured within the time frame
considered here: the Ordovician-Silurian and the Frasnian-Famennian. The
422 cohorts bracketing these events are worth considering in more detail.
The proposed mechanism for the end Ordovician mass extinction is a decrease
424 in sea level and the draining of epicontinental seas due to protracted glaciation
(Johnson, 1974, Sheehan, 2001). My results are broadly consistent with this

426 scenario with both epicontinental and open-ocean specialists having a much
lower expected duration than intermediate taxa (Fig. 5). All of the stages
428 between the Darriwillian and the Llandovery, except the Hirnantian, have a
high probability (90+) that $f(v)$ is concave down. The pattern for the
430 Darriwillian, which proceeds the supposed start of Ordovician glacial activity,
demonstrates that taxa tend to favor open-ocean environments are expected to
432 have a greater duration than either intermediate or epicontinental specialists, in
decreasing order.

434 For nearly the entire Devonian estimates of $f(v)$ indicate that one of the
environmental end members is favored over the other end member of
436 intermediate preference (Fig. 5). For almost the entirely the Givetian though
the end of the Devonian and into the Viséan, I find that epicontinental favoring
438 taxa are expected to have a greater duration than either intermediate or
open-ocean specialists. Additionally, for nearly the entire Devonian and through
440 to the Visean, the cohort-specific estimates of $f(v)$ are concave-up. This is the
opposite pattern than what is expected (Fig. 2). This result, however, seems to
442 reflect the intensity of the seemingly nearly-linear difference in expected
duration across the range of v as opposed to an inversion of the weakly expected
444 curvilinear pattern.

The use of genera as the unit of the study and how to exactly interpret the
446 effects of the biological traits is a remaining concern. For example, if any of the
traits analyzed here are associated with increases in speciation rates, this might
448 increase the duration of genera through self-renewal (Raup, 1991, 1994), which
would be an example of the difference in biological pattern between species and
450 genera (Jablonski, 1987, 2007, 2008). This could lead to a trait appearing to
decrease generic level extinction risk by increasing species level origination rate
452 instead of decreasing species level extinction risk. However, given the nature of

the brachiopod fossil record and the difficulty of identifying individual
454 specimens to the species level, there is no simple solution to decreasing this
uncertainty in the interpretations of how the biological traits studied here
456 actually affect extinction risk.

This model could be improved through either increasing the number of analyzed
458 taxon traits, expanding the hierarchical structure of the model to include other
major taxonomic groups of interest, and the inclusion of explicit phylogenetic
460 relationships between the taxa in the model as an additional hierarchical effect.

An example taxon trait that may be of particular interest is the affixing
462 strategy or method of interaction with the substrate of the taxon. This trait has
been found to be related to brachiopod survival (Alexander, 1977) so its
464 inclusion may be of particular interest.

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

472 Taxon traits like environmental preference or geographic range (Hunt et al.,
2005, Jablonski, 1987) are most likely heritable, at least phylogenetically
474 (Housworth et al., 2004, Lynch, 1991). Without phylogenetic context, this
analysis assumes that differences in extinction risk between taxa are
476 independent of those taxa's shared evolutionary history (Felsenstein, 1985). In
contrast, the origination cohorts only capture shared temporal context. The
478 inclusion of phylogenetic context as an addition individual level hierarchical

structure independent of origination cohort would allow for determining how
480 much of the observed variability is due to shared evolutionary history versus
actual differences associated with these taxonomic traits.

482 In summary, patterns of Paleozoic brachiopod survival were analyzed using a
fully Bayesian hierarchical survival modelling approach while also eschewing the
484 traditional separation between background and mass extinction. I modeled both
the overall mean effect of biological covariates on extinction risk while also
486 modeling the correlation between cohort-specific estimates of covariate effects. I
find that as baseline extinction risk increases, the strength of the selection
488 gradient on biological traits (except body size) increases. This manifests as
greater differences in extinction risk for each unit difference in the biological
490 covariates during periods of high extinction risk, while a much flatter total
selection gradient during periods of low extinction risk. I also find very weak for
492 “survival of the unspecialized” (Liow, 2004, 2007, Nürnberg and Aberhan, 2013,
2015, Simpson, 1944) as a general characterization of the effect of environmental
494 preference on extinction risk (Fig. 2), though there is heterogeneity between
origination cohorts with most periods of time conforming to this hypothesis
496 (Fig. 5).

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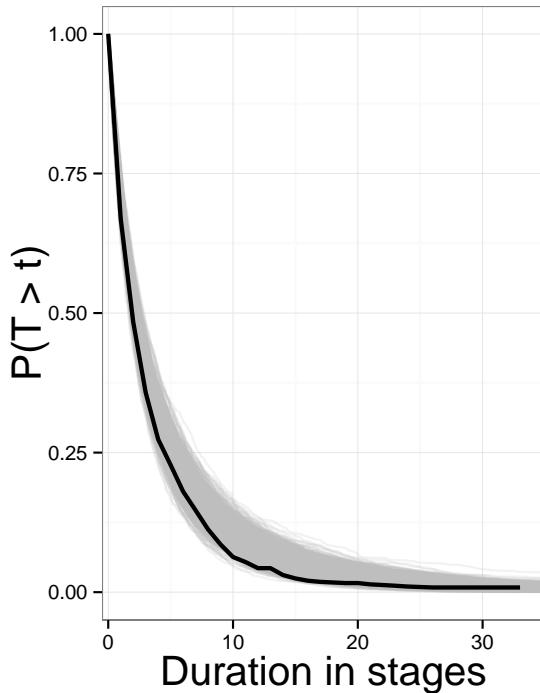


Figure 1: Comparison of empirical estimates of $S(t)$ versus estimates from 1000 posterior predictive data sets. $S(t)$ corresponds to $P(T > t)$ as it is the probability that a given genus observed at age t will continue to live. This is equivalent to the probability that t is less than the genus' ultimate duration T . Note that the Weibull (left) model has noticeably better fit to the data than the exponential (right).

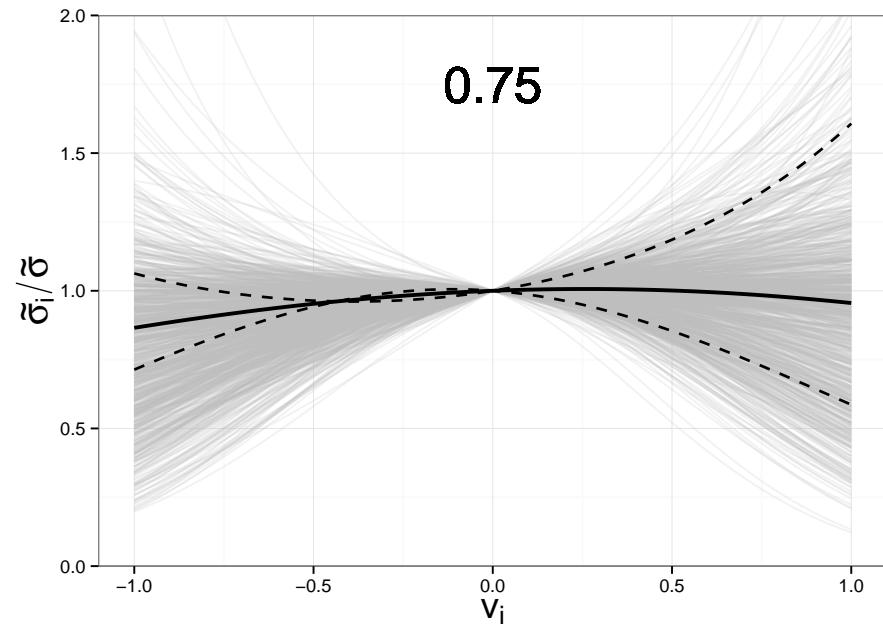


Figure 2: The overall expected relationship $f(v_i)$ between environmental affinity v_i and a multiplier of extinction risk (Eq. 3). Each grey line corresponds to a single draw from the posterior predictive distribution, the solid black line corresponds to the median of the posterior predictive distribution, and the dashed black lines correspond to the median relationship plus or minus one standard deviation. The overall shape of $f(v_i)$ is concave down with an optimum of close 0, which corresponds to affinity approximately equal to the expectation based on background environmental occurrence rates.

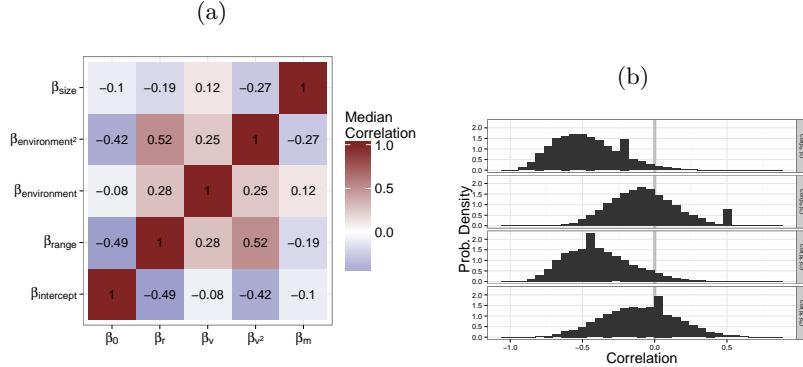


Figure 3: **A:** Heatmap for the median estimates of the terms of the correlation matrix Ω between cohort-level covariate effects. Both the exponential (left) and Weibull (right) models are presented. The off-diagonal terms are the correlation between the estimates of the cohort-level estimates of the effects of covariates, along with intercept/baseline extinction risk. **B:** Marginal posterior distributions of the correlations between intercept terms/baseline extinction risk and the effects of each of the covariates. These are presented for both the exponential (left) and Weibull (right) models.

parameter	mean	standard deviation
μ_i	-1.51	0.15
μ_r	-1.38	0.14
μ_v	-0.08	0.18
μ_{v^2}	0.25	0.43
μ_m	-0.09	0.09
τ_i	0.63	0.11
τ_r	0.48	0.12
τ_v	1.07	0.23
τ_{v^2}	1.88	0.66
τ_m	0.32	0.13

Table 1: Group-level estimates of the intercept terms the effects of biological traits on brachiopod generic survival from equations 1 and 2, presented as means and standard deviations. μ values are the location parameters of the effects, while τ values are the scale terms describing the variation between cohorts. The subscripts correspond to the following: i intercept, r geographic range, v environmental affinity, v^2 environmental affinity squared, m body size.

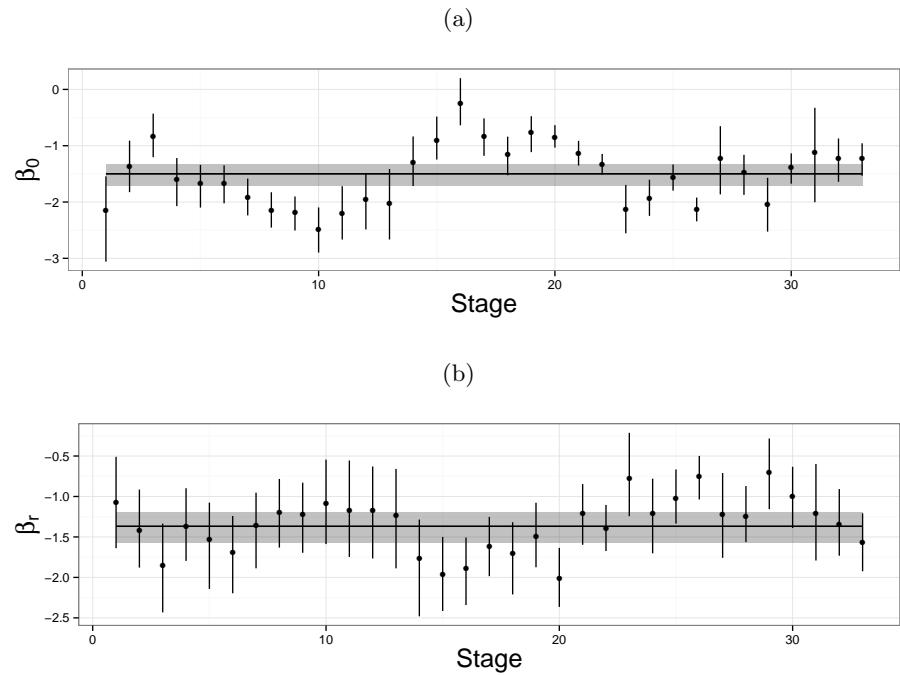


Figure 4: Comparison of cohort-specific estimates of β_0 presented along with the estimate for the overall baseline extinction risk. Points correspond to the median of the cohort-specific estimate, along with 80% credible intervals. The horizontal line is the median estimate of the overall baseline extinction risk along with 80% credible intervals. Results are presented for the exponential (top) and Weibull (bottom) models. Comparison of cohort-specific estimates of the effect of geographic range on extinction risk β_r presented along with the estimate for the overall effect of geographic range. Points correspond to the median of the cohort-specific estimate, along with 80% credible intervals. The horizontal line is the median estimate of the overall baseline extinction risk along with 80% credible intervals. Results are presented for the exponential (top) and Weibull (bottom) models.

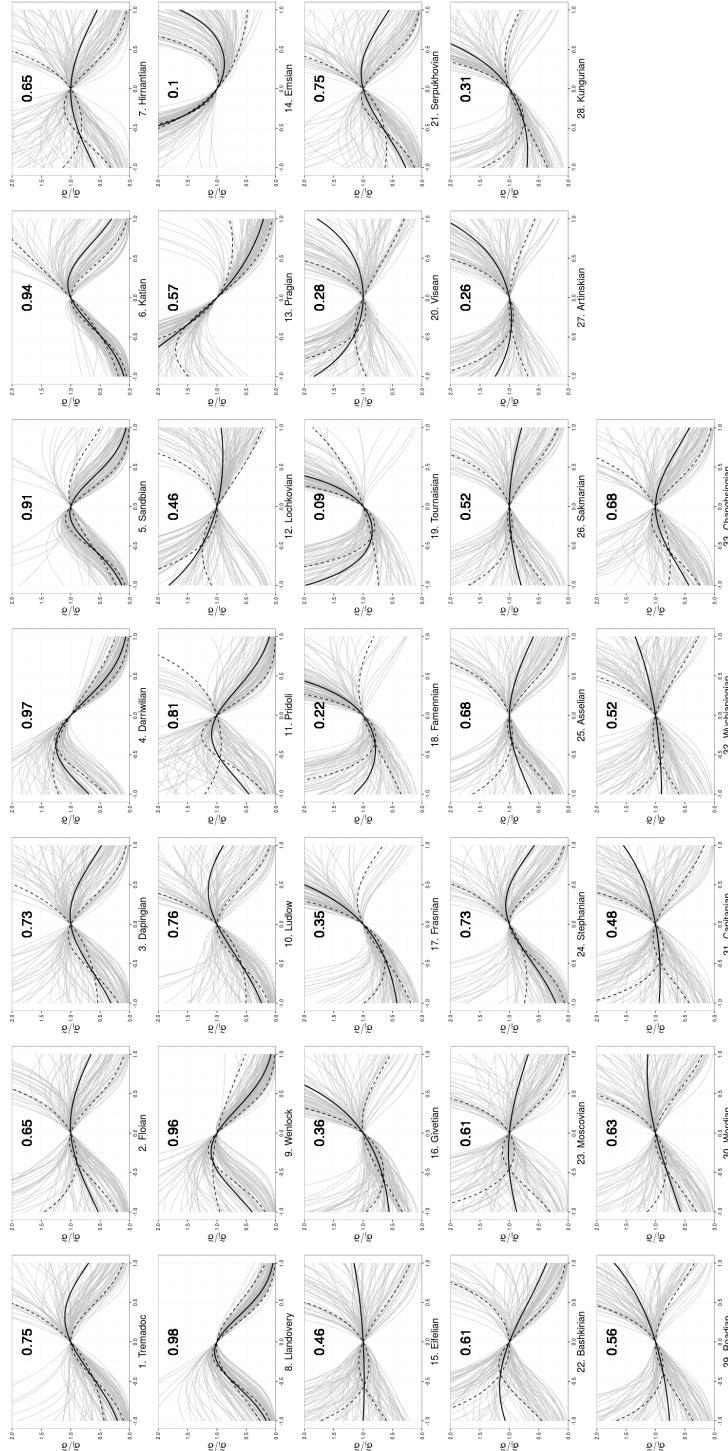


Figure 5: Comparison of the cohort-specific estimates of $f(v_i)$ (Eq. 3) for the 33 analyzed origination cohorts. The stage of origination is labeled on the x-axis of each panel. The oldest stage is in the upper left, while the youngest is in the lower left. The number in each panel corresponds to the posterior probability that $f(v_i)$ is concave down. Those that are highlighted in red have less than 51% posterior predictive probability that $f(v_i)$ is concave down. Each grey line corresponds to a single draw from the posterior predictive distribution, the solid black line corresponds to the median of the posterior predictive distribution, and the dashed black lines correspond to the median relationship plus or minus one standard deviation. Note that all estimates must pass through $y = 1$ when $x = 0$ (Eq. 3).