Title: How do biological traits affect brachiopod taxonomic survival? A hierarchical Bayesian approach.

Running title: How do biological traits affect taxonomic survival?

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Abstract

While the effect of geographic range on extinction risk is well documented, the effects of other traits are less well known. Here, 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 possible interaction between the effects of the biological traits and a taxon's time of origination. I find evidence that as extinction risk increases, the expected strength of the selection gradient on biological traits (except body size) increases. This manifests as greater expected differences in extinction risk for each unit change in geographic range and environmental preference during periods of high extinction risk, as opposed to a much flatter expected selection gradient during periods of low extinction risk. I find weak evidence for a nonlinear relationship between environmental preference and extinction risk such that "generalists" have a lower expected extinction risk than either "specialists". Interestingly, I find that as extinction risk increases, the peakedness of this relationship is expected to increases as well. These results demonstrate the importance of directly modeling the structure inherent in the observed data as a means to better understand which processes may have been driving the observed patterns of diversification.

1 Introduction

How do biological traits affect extinction risk? Jablonski (1986) observed that during periods of high expected extinction risk, the effects of biological traits on survival decreased in importance. However, this pattern was weakest/absent in 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 biotic–biotic and biotic–abiotic interactions that a taxon can experience. In effect, these are descriptors of a taxon's broad-sense ecology.

Jablonski (1986) phrased their 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). I adopt a continuous variation framework as this is more amenable for modeling the relationship between taxon traits and extinction risk. 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 relationships between these effects need to be modeled as well.

Two possible macroevolutionary mechanisms which may underly the pattern observed by Jablonski (1986) are: 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.

I model taxon durations because trait based differences in extinction risk should manifest as differences in taxon durations. Namely, a species with a beneficial trait should survive longer, on average, than a species without that beneficial trait. Conceptually, taxon survival can be considered an aspect of "taxon fitness" along with expected lineage branching/origination rate (Cooper, 1984, Palmer and Feldman, 2012). 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 (Klein and Moeschberger, 2003) but has a long history in paleontology (Simpson, 1944, 1953, Van Valen, 1973, 1979).

Geographic range is widely considered the most important taxon trait for estimating differences in extinction risk at nearly all times with large geographic range associated with low extinction risk (Jablonski, 1986, 1987, Jablonski and Roy, 2003, Payne and Finnegan, 2007). I expect this to hold true nearly always.

Miller and Foote (2009) demonstrated that during several mass extinctions taxa associated with open ocean environments tend to have a greater extinction risk than those taxa associated with epicontinental seas. During periods of background extinction, however, they found no consistent difference between taxa favoring either environment. Because of this study, the following prediction for survival patterns can be made: as extinction risk increases, taxa associated with open ocean environments should generally increase in extinction risk versus those that favor epicontinental seas.

There is also a possible nonlinear relationship between environmental preference and taxon duration. A long standing hypothesis is that generalists or unspecialized taxa will have greater survival than specialists (Baumiller, 1993, Liow, 2004, 2007, Nürnberg and Aberhan, 2013, 2015, Simpson, 1944) SMITS, IN PREP. I allowed for environmental preference to possibly have a parabolic effect on species duration

Body size, measured as shell length (Payne et al., 2014), was also considered as 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 hypothesis of how body size effects extinction risk in brachiopods, meaning a positive, negative, or null effect are all pluasible.

I adopt a hierarchical Bayesian survival modeling approach, which represents a conceptual and statistical unification of the paleontological dynamic and cohort survival analytic approaches (Baumiller, 1993, Foote, 1988, Raup, 1975, 1978,

Simpson, 2006, Van Valen, 1973, 1979). By using a Bayesian framework I 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 (biological traits) are themselves known with error.

2 Materials and Methods

2.1 Analytical approach

Hierarchical modelling, sometimes called "mixed-effects modeling," 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 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. 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 (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 treat environmental affinity as a continuous measure of the difference between the taxon's environmental occurrence pattern and the background occurrence pattern (Appendix A).

2.2 Fossil occurrence information

The dataset analyzed here is derived from the a combination of the occurrence information from Foote and Miller (2013) and the body size data from Payne et al. (2014). The Foote and Miller (2013) dataset is based on the Paleobiology Database (http://www.paleodb.org); see Foote and Miller (2013) for a full description of the inclusion criterion. Additionally, epicontinental versus open ocean assignemnts for occurrence information are based on Miller and Foote (2009). NOTE: I DON'T KNOW HOW THIS MAY NEED TO BE UPDATED.

Sampled occurrences were restricted to those with paleolatitude and paleolongitude coordinates, assignment to either epicontinental or open-ocean environment, and belonging to a genus present in the body size dataset (Payne et al., 2014). Genus duration was calculated as the number of geologic stages from first appearance to last appearance, inclusive. Genera with a last occurrence in or after Changhsingian stage were right censored at the Changhsingian. Genera with a duration of only one stage were left censored

(Appendix C). The covariates used to model genus duration were geographic range size (r), environmental preference (v, v^2), and body size (m).

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 grid placed on the map. Each grid cell represents approximately 250,000 km^2. The map projection and regular lattice were made using shape files from http://www.naturalearthdata.com/ and the `raster` package for R (Hijmans, 2015).

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

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

Prior to analysis, geographic range and body size were transformed and standardized in order to improve interpretability of the results. Geographic range, which can only vary between 0 and 1, was logit transformed. Body size, 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 their standard deviation following Gelman and Hill (2007).

2.3 Survival model

Genus durations were modeled as time-till-event data (Klein and Moeschberger, 2003), with covariate information used in estimates of extinction risk as a hierarchical regression model. Genus durations were assumed to follow either an exponential or Weibull distribution. Each of these distributions makes assumptions about how duration may effect extinction risk (Klein and Moeschberger, 2003). The exponential distribution assumes that extinction risk is independent of duration. In contrast, the Weibull distribution allows for age dependent extinction via the shape parameter α, though only as a monotonic function of duration. Importantly, the Weibull distribution is equivalent to the exponential distribution when $\alpha = 1$.

The following variables are 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 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 the between-cohort variation in regression coefficient estimates, and Ω is the correlation matrix of the regression coefficients.

The exponential model is defined

$$
\begin{aligned}
y_i &\sim \text{Exponential}(\lambda) \\
\lambda_i &= \exp(\mathbf{X}_i B_{j[i]}) \\
B &\sim \text{MVN}(\vec{\mu}, \Sigma) \\
\Sigma &= \text{Diag}(\vec{\tau})\Omega\text{Diag}(\vec{\tau}) \\
\mu_\kappa &\sim \begin{cases} \mathcal{N}(0,5) & \text{if } k \neq r, or \\ \mathcal{N}(-1,1) & \text{if } k = r \end{cases} \\
\tau_\kappa &\sim \text{C}^+(1) \text{ for } \kappa \in 1:k \\
\Omega &\sim \text{LKJ}(2).
\end{aligned}
\tag{1}
$$

Similarly, the Weibull model is defined

$$
\begin{aligned}
y_i &\sim \text{Weibull}(\alpha, \sigma) \\
\sigma_i &= \exp\left(\frac{-(\mathbf{X}_i B_{j[i]})}{\alpha}\right) \\
B &\sim \text{MVN}(\vec{\mu}, \Sigma) \\
\Sigma &= \text{Diag}(\vec{\tau})\Omega\text{Diag}(\vec{\tau}) \\
\alpha &\sim \text{C}^+(2) \\
\mu_k &\sim \begin{cases} \mathcal{N}(0,5) & \text{if } k \neq r, or \\ \mathcal{N}(-1,1) & \text{if } k = r \end{cases} \\
\tau_k &\sim \text{C}^+(1) \\
\Omega &\sim \text{LKJ}(2).
\end{aligned}
\tag{2}
$$

The principle difference between this model and the previous (Eq. 1) is the inclusion of the shape parameter α. Note that σ is approximately equivalent to

$1/\lambda$.

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

2.4 Parameter estimation

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

2.5 Model evaluation

Models were evaluated using both posterior predictive checks and an estimate of out-of-sample predictive accuracy. The motivation behind posterior predictive 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., 2013). Systematic differences between the simulations and observations indicate

weaknesses of the model fit. An example of a technique that is very similar would be inspecting the residuals from a linear regression.

The strategy behind posterior predictive checks is to draw simulated values 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 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 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 y^{rep}. This is repeated 1000 times in order to provide a distribution of possible values that could have been observed given the model.

In order to compare the fitted model to the observed data, various graphical comparisons or test quantities need to be defined. The principal comparison 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 replicated data sets. The purpose of this comparison is to determine if the model approximates the same survival/extinction pattern as the original data.

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

expected out-of-sample predictive accuracy than higher values.

3 Results

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

Comparisons of the survival functions estimated from 1000 posterior predictive data sets to the estimated survival function of the observed genera demonstrates that both the exponential and Weibull models approximately capture the observed pattern of extinction (Fig. 1). The major difference in fit between the two models is that the Weibull model has a slightly better fit for longer lived taxa than the exponential model.

Additionally, the Weibull model is expected to have slightly better out-of-sample predictive accuracy when compared to the exponential model (WAIC 4577 versus 4605, respectively). 1). Because the difference in WAIC between these two models is large, while results from both the exponential and Weibull models will be presented, only those from the Weibull model will be discussed.

Estimates of the overall mean covariate effects μ can be considered time-invariant generalizations for brachiopod survival during the Paleozoic SMITS IN PREP (Fig. 2). Consistent with prior expectations, geographic range size has a negative effect on extinction risk, where genera with large ranges having greater durations than genera with small ranges.

I find that there is an approximately 93% posterior probability that the overall effect of increasing body size decreases expected extinction risk. This parameter, however, is not very large and is within two standard deviations of 0 (mean

$\mu_m = -0.15$, standard deviation 0.1). Because of this, I interpret this as weak evidence for increases in body size to be associated with a decrease in expected extinction risk.

Interpretation of the effect of environmental preference v on duration is slightly 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 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 preference on extinction risk.

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

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

This function $f(v_i)$ has a y-intercept of exp(0) or 1 because it does not have a 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 preference have greater durations than either extreme, and *vice versa* for concave up function.

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

The matrix Σ describing the covariance between the different coefficients

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

The estimates of the standard deviation of between-cohort coefficient estimates τ inidicate that some effects can vary greatly between-cohorts (Fig. 4). Coefficients with greater values of τ have greater between-cohort variation. The covariate effects with the greatest between origination cohort variation are β_r, 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 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 environmental affinity to be upward facing for some cohorts (Eq. 3), which corresponds to environmental generalists being shorted lived than specialists in that cohort.

The correlation terms of Ω (Fig. 5) describe the relationship between the 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 of particular interest for evaluating the Jablonski (1986) scenario (Fig. 5 first column/last row). Keep in mind that when β_0 is low, extinction risk is low; and conversely, when β_0 is high, then extinction risk is high.

Marginal posterior probabilities of the correlations between the level of baseline 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 particular note (Fig. 6).

There is approximately a 98% probability that β_0 and β_r are negatively

correlated (Fig. 6), meaning that as extinction risk increases, the effect/importance of geographic range on genus duration increases. This means that increases in baseline extinction rate are correlated with an increased importance of geographic range size. There is a 94% probability that β_0 and β_{v^2} are negatively correlated (Fig. 6), meaning that as extinction risk increases, the peakedness of $f(v_i)$ increases and the relationship tends towards concave 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).

While the overall group level estimates are of particular importance when 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.

In comparison to the overall mean extinction risk μ_0, cohort level estimates β_0 show some amount of variation through time as expected by estimates of τ_0 (Fig. 7). A similar, if slightly greater, amount of variation is also observable in cohort estimates of the effect of geographic range β_r (Fig. 8). Again, smaller values of β_0 correspond to lower expected extinction risk. Similarly, smaller 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 by using the cohort specific coefficients estimates. Following the same procedure used earlier (Fig. 4), but substituting cohort specific estimates of β_v and β_{v^2} for 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 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

the peakedness of $f(v_i)$ than there is variation between convave up and down functions (Fig. 9). 9 of the 33 cohorts have less than 50% posterior probability that generalists are potentially expected to be shorter lived than specialists, though two of those cases have approximately a 50% probability of being either concave up or down. This is congruent with the 0.86 posterior probability that μ_{v^2} is positive/$f(v_i)$ is concave down.

Additionally, for some cohorts there is a quite striking pattern where the effect of environmental preference v has a nearly-linear relationship (Fig. 9). These are primarily scenarios where one of the end member preferences is expected to have a greater duration than either intermediate or the opposite end member preference. Whatever curvature is present in these nearly-linear cases is due to the defintion of $f(v)$ as it is not defined for non-negative values of σ (Eq. 3). For most of the all stages between the Emsian through the Tournaisian, inclusive, intermediate preferences are of intermediate extinction risk when compared with epicontinental specialists (lowest risk) or open-ocean specialists (highest risk). This time period represents most of the Devonian.

4 Discussion

My results demonstrate that both the effects of geographic range and the peakedness/concavity of environmental preference are both negatively correlated with baseline extinction risk, meaning that as baseline extinction risk increases the effect sizes of both these traits are expected to increase (Fig. 6). This result supports neither of the two proposed macroevolutionary mechanisms for how biological traits should correlate with extinction risk. The observed correlation between the two effects as well as between the effects and baseline extinction risk instead implies that as baseline extinction risk increases, the

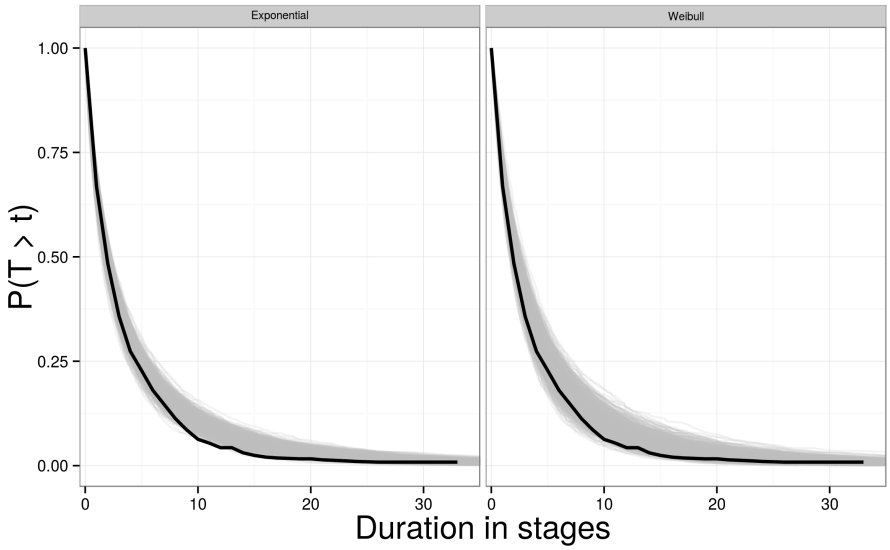

Figure 1: Comparison of empirical estimates of $S(t)$ versus estimates from 1000 posterior predictive data sets. $S(t)$ corresponds to $P(T > t)$ as it is the probability that a given genus observed at age t will continue to live. This is equivalent to the probability that t is less than the genus' ultimate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

strength of the total selection gradient on biological traits (except body size) increases. This manifests as greater differences in extinction risk for each unit difference in the biological covariates during periods of high extinction risk, while a relatively flater selection gradient during periods of low extinction risk.

There are two mass extinction events that are captured within the time frame considered here: the Ordovician-Silurian and the Frasnaian-Famennian. The cohorts bracketing these events are worth considering in more detail.

The proposed mechanism for the end Ordovician mass extinction is a decrease in sea level and the draining of epicontinental seas due to protracted glaciation (Johnson, 1974, Sheehan, 2001). My results are broadly consistent with this scenario with both epicontinental and open-ocean specialists having a much

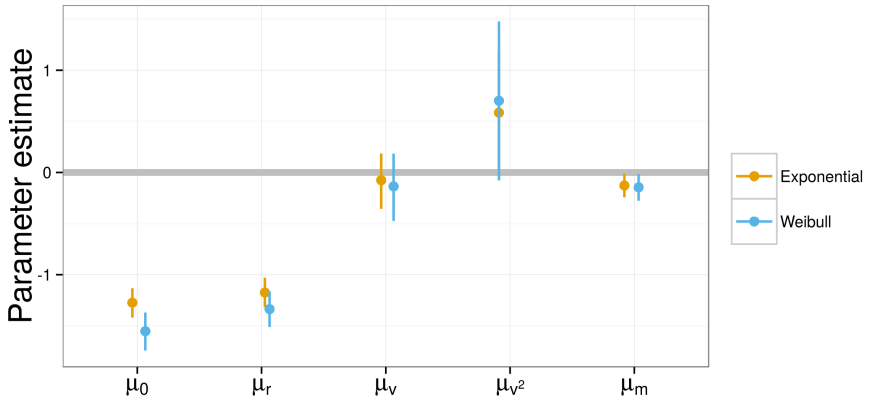

Figure 2: Estimates of the overall effects of the covariates on extinction risk. Included is also the estimate of μ_0 which corresponds to the intercept term or, because of standardization, the overall mean expected extinction risk. Estimates are presented for both the exponential (gold) and Weibull (blue) models. The point corresponds to the median of the posterior distribution, while the error bars correspond to the 80% credible intervals of the estimates.

lower expected duration than intermediate taxa (Fig. 9). All of the stages between the Darriwillian and the Llandovery, except the Hirnantian, have a greater than expected probability that $f(v)$ is concave down. The pattern for the Darriwilian, which marks the supposed start of Ordovician glacial activity, demonstrates that taxa tend to favor open-ocean environments are expected to have a greater duration than either intermediate of epicontinental specialists, in decreasing order.

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 intermediate preference (Fig. 9). This is consistent with Miller and Foote (2009). For the Givetian though the end of the Devonian and into the Tournasisian, I find that epicontinental favoring taxa are expected to have a greater duration than either intermediate or open-ocean specialists. Additionally, for nearly the

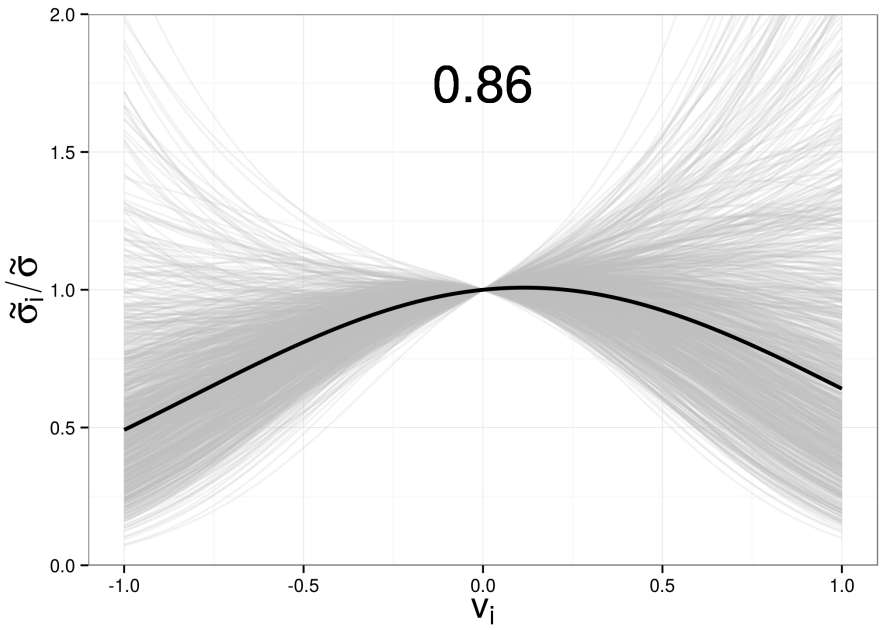

Figure 3: The overall expected relationship $f(v_i)$ between environmental affinity v_i and a multiplier of extinction risk (Eq. 3). Each grey line corresponds to a single draw from the posterior predictive distribution, while the black corresponds to the median of the posterior predictive distribution. 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.

entire Devonian except the Eifelian and through the Visean, the cohort-specific estimates of $f(v)$ are concave-up. This is the opposite pattern than what is expected (Fig. 3). This result, however, seems to 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 curvilinear pattern.

There is an approximate 86% posterior probability that taxa with intermediate environmental preferences are possibly expected to have a lesser extinction risk than either end members, the over all curvature of $f(v_i)$ is not very peaked, meaning that this relationship does not lead to very strong differences in

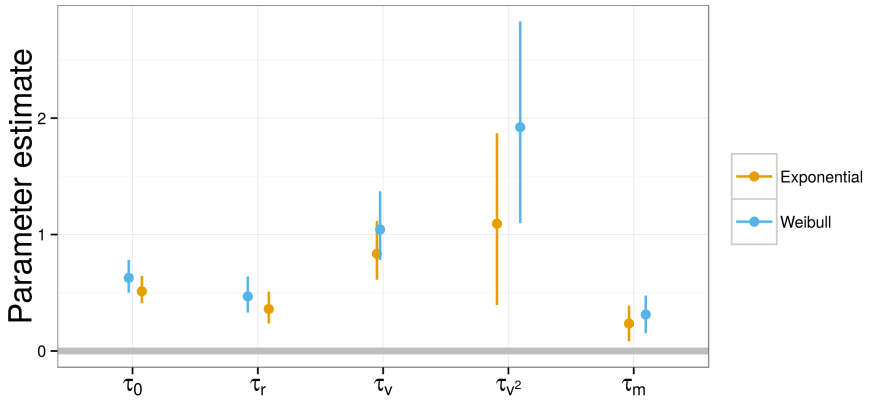

Figure 4: Estimates of the scale parameters describing the expected differences in the effect of the covariates, and of the intercept/baseline extinction risk, between cohorts. Higher values of τ correspond to greater expected differences between cohorts. Estimates are presented for both the exponential (gold) and Weibull (blue) models. The point corresponds to the median of the posterior distribution, while the error bars correspond to the 80% credible intervals of the estimates.

extinction risk (Fig. 3). This result gives weak support for the hypothesis that, in general, environmental generalists survive for longer than environmental specialists (Liow, 2004, 2007, Nürnberg and Aberhan, 2013, 2015, Simpson, 1944).

The variance in estimate of the overall $f(v_i)$ reflects the large between cohort variance in cohort specific estimates of $f(v_i)$ (Fig. 9). Given that there is only a 86% posterior probability that the expected overall estimate of $f(v_i)$ is concave down, it is not surprising that there are some stages where the theorized relationship is in fact reversed. Additionally, as discussed earlier, some of those same stages where $f(v_i)$ does not resemble the theorized nonlinear relation with the optimum in the middle, but are instead is highly skewed or effectively linear (Fig. 9).

These results do not necessarily refute "survival of the unspecialized" as a

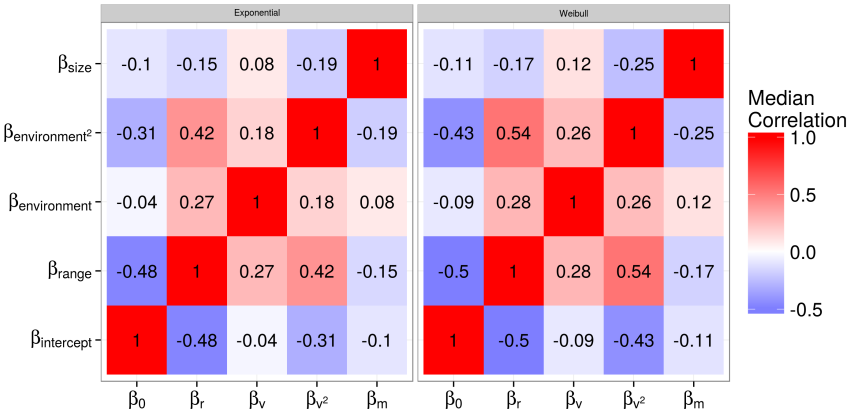

Figure 5: Heatmap for the median estimates of the terms of the correlation matrix Ω between cohort-level covariate effects. Both the exponential (left) and Weibull (right) models are presented. The off-diagonal terms are the correlation between the estimates of the cohort-level estimates of the effects of covariates, along with intercept/baseline extinction risk.

time-invariant generalization, but instead demonstrate how, while the expected group-level estimate of $f(v_i)$ might favor one hypothesis, there is still enough variability between cohorts so that in some realizations this pattern may not hold or can even be reversed. These results are also consistent with aspects of Miller and Foote (2009) who found that the effect of environmental preference on extinction risk was quite variable and without obvious patterning during times of background extinction.

This model can be improved through either increasing the number of analyzed taxon traits, expanding the hierarchical structure of the model to include other major taxonomic groups of interest, and the inclusion of explicit phylogenetic 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 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

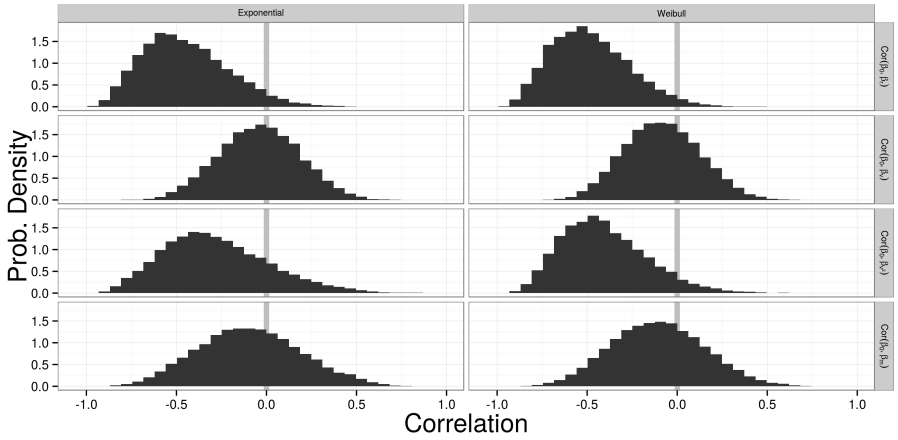

Figure 6: Marginal posterior distributions of the correlations between intercept terms/baseline extinction risk and the effects of each of the covariates. These are presented for both the exponential (left) and Weibull (right) models.

inclusion may be of particular interest.

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

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

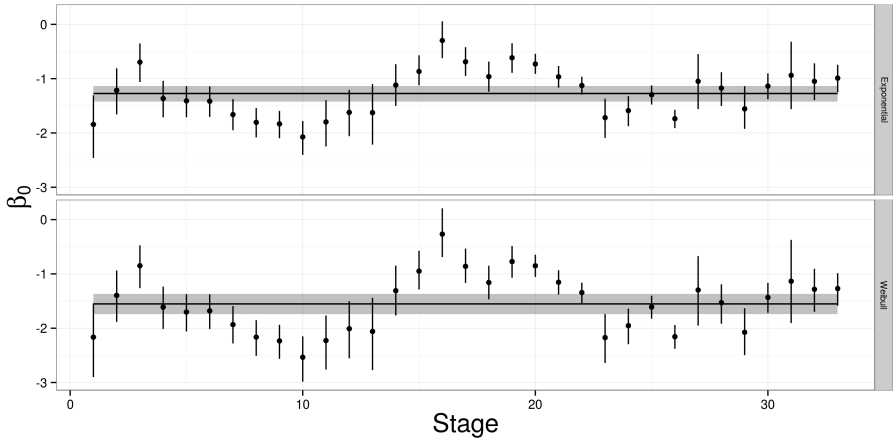

Figure 7: Comparison of cohort-specific estimates of β_0 presented along with the estimate for the overall baseline extinction risk. Points correspond to the median of the cohort-specific estimate, along with 80% credible intervals. The horizontal line is the median estimate of the overall baseline extinction risk along with 80% credible intervals. Results are presented for the exponential (top) and Weibull (bottom) models.

structure independent of origination cohort would allow for determining how much of the observed variability is due to shared evolutionary history versus actual differences associated with these taxonomic traits. For example, it has been shown that phylogeny contribute non-trivially to differences in mammal species durations SMITS IN PREP.

In summary, patterns of Paleozoic brachiopod survival were analyzed using a fully Bayesian hierarchical survival modelling approach. Using a varying-slopes, varying-intercepts approach I am able to model both the overall mean effect of biological covariates on extinction risk while also modeling the correlation between origination cohort-specific estimates of covariate effects. I find that as baseline extinction risk increases, the strength of the selection gradient on biological traits (except body size) increases. This manifests as greater differences in extinction risk for each unit difference in the biological covariates

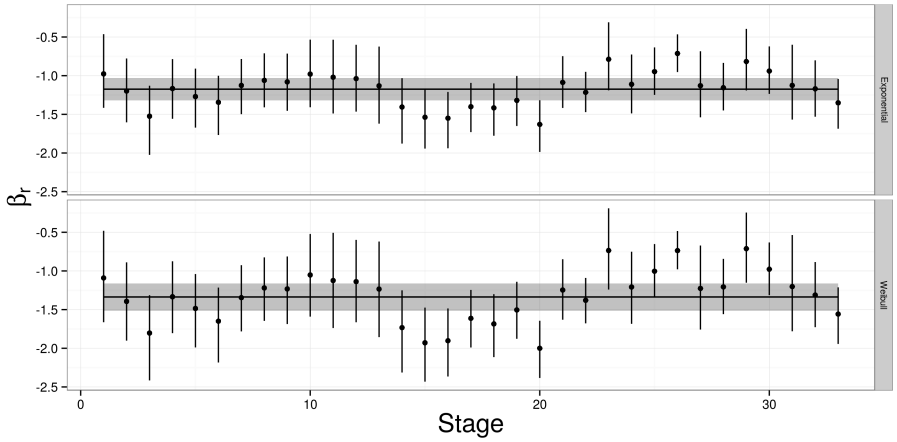

Figure 8: Comparison of cohort-specific estimates of the effect of geographic range on extinction risk β_r presented along with the estimate for the overall effect of geographic range. Points correspond to the median of the cohort-specific estimate, along with 80% credible intervals. The horizontal line 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.

during periods of high extinction risk, while a much flatter total selection gradient during periods of low extinction risk. I also find some support for "survival of the unspecialized" (Liow, 2004, 2007, Nürnberg and Aberhan, 2013, 2015, Simpson, 1944) as a general characterization of the effect of environmental preference on extinction risk (Fig. 3), though there is heterogeneity between origination cohorts (Fig. 9). Generally, this study demonstrates the advantages of a hierarchical Bayesian framework for taking into account the structured nature of the data. Future studies of structured data should adopt similar strategies in order to best model our knowledge instead of ignoring that structure which can lead to poor and/or incorrect inference.

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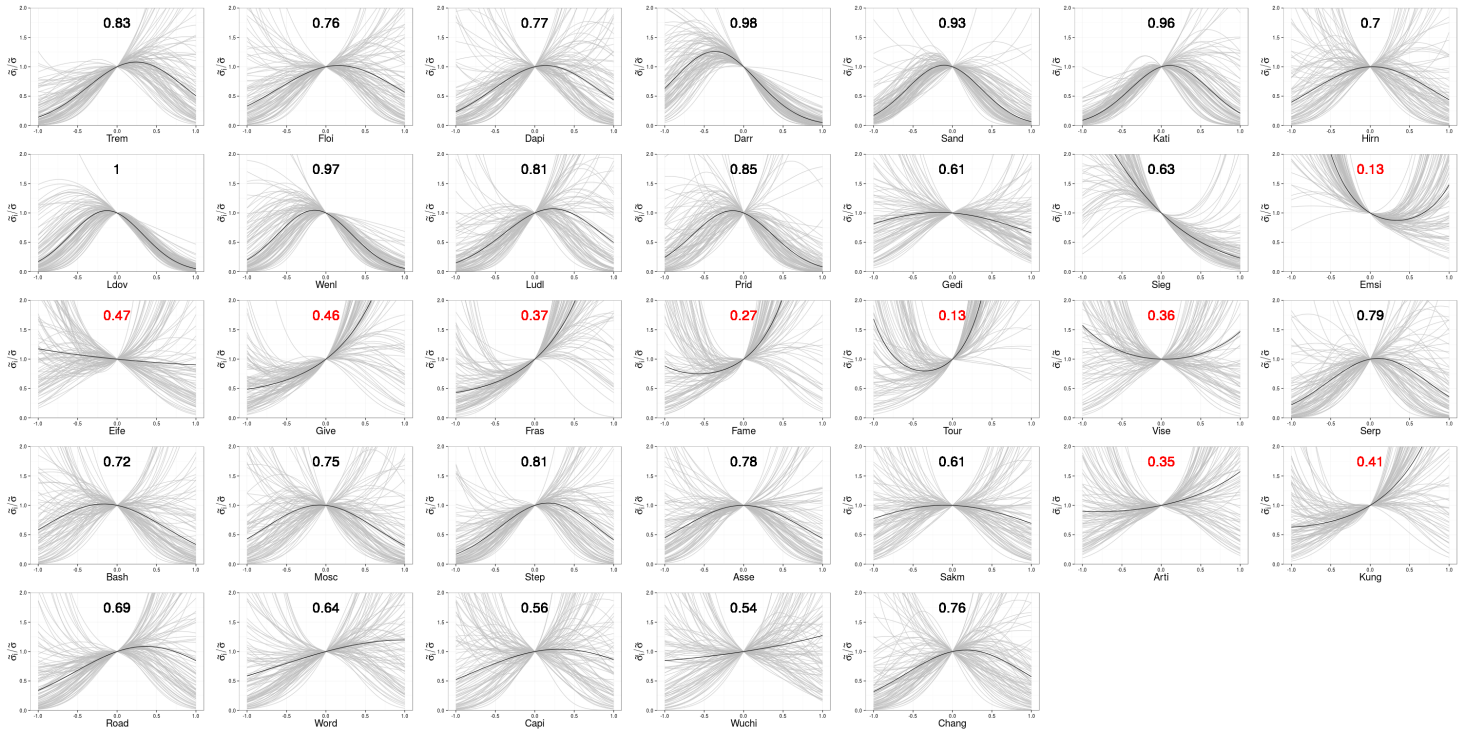

Figure 9: Comparison of the cohort-specific estimates of $f(v_i)$ (Eq. 3) for the 33 analyzed origination cohorts. The stage of origination is labeled on the x-axis of each panel. The oldest stage is in the upper left, while the youngest is in the lower left. The number in each panel corresponds to the posterior probability that $f(v_i)$ is concave down. Those that are highlighed in red have less than 51% posterior predictive probability that $f(v_i)$ is concave down.

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A Uncertainty in environmental preference

The calculation and inclusion of environmental affinity in the survival model is a statistical procedure that takes into account our uncertainty based on where fossils tend to occur. Because we cannot directly observe if a fossil taxon had occurrences restricted to only a single environment, instead we can only estimate its affinity with uncertainty. One advantage of using a Bayesian analytical approach is that both parameters and data are considered random samples from some underlying distribution, which means that is is possible to model the uncertainty in our covariates of interest (Gelman et al., 2013). My approach is conceptually similar to Simpson and Harnik (2009) but instead of obtaining a single point estimate, an entire posterior distribution is estimated.

The first step is to determine the probability θ at which genus i occurs in an epicontinental settings based on its own pattern of occurrences. Define e_i as the number of occurrences of genus i in an epicontiental sea and o_i as the number of occurrences of genus i not in an epicontinental sea (e.g. open ocean). Because the value of interest is the probability of occurring in an epicontinental environment, given the observed fossil record, I assume that probability follows a binomial distribution. We can then define our sampling statement as

$$e_i \sim \text{Binomial}(e_i + o_i, \theta_i). \tag{4}$$

I used a flat prior for θ_i defined as $\theta_i \sim \text{Beta}(1, 1)$. Because the beta distribution is the conjugate prior for the binomial distribution, the posterior is easy to compute in closed form. The posterior probability of θ is then

$$\theta_i \sim \text{Beta}(e_i + 1, o_i + 1) \tag{5}$$

It is extremely important, however, to take into account the overall environmental occurrence probability of all other genera present at the same time as genus i. This is incorporated as an additional probability Θ. Define E_i as the total number of other fossil occurrences (exceptfor genus i) in epicontinental seas during stages where i occurs and O_i as the number of other fossil occurrences not on epicontinental seas. We can then define the sampling statement as

$$E_i \sim \text{Binomial}(E_i + O_i, \Theta_i). \tag{6}$$

Again, I used a flat prior of Θ_i defined as $\Theta_i \sim \text{Beta}(1, 1)$. The posterior of Θ is then simply defined as

$$\Theta_i \sim \text{Beta}(E_i + 1, O_i + 1) \tag{7}$$

I then define the environmental affinity of genus i as $v_i = \theta_i - \Theta_i$. v_i is a value that can range between -1 and 1, where negative values indicate that genus i tends to occur more frequently in open ocean environments than background while positive values indicate that genus i tends to occur in epicontiental environments.

While this approach is noticeably more complicated than previous ones (Foote, 2006, Kiessling and Aberhan, 2007, Miller and Connolly, 2001, Simpson and Harnik, 2009) there are some important benefits to both using a continuous measure of affinity as well directly modeling our uncertainty. In order to show some of these benefits, I performed a simulation analysis of how modal/maximum *a posteriori* (MAP) estimates versus full posterior estimates.

In this simulation, I first defined the "background" epicontinental occurrence θ_b as 0.50 with a small amount of noise. This was represented as a beta distribution

$$\Theta_b = \text{Beta}(\alpha = 2500, \beta = 2500). \quad (8)$$

This choice of parameters for the distribution reflects the average number of background occurrences for either epicontinental or open ocean environments per genus.

Using this background occurrence ratio, I randomly generated the occurrence patterns of 1000 simulated taxa. This was done at multiple sample sizes (1, 2, 3, 4, 5, 10, 25, 50, 100) in order to demonstrate the effects of increasing sample size on the confidence of environmental affinity. For each simulated taxon I calculated the full posterior distribution while assuming a flat Beta prior (Beta$(1, 1)$). Using the full posterior I calculated the MAP probability of occurring in epicontinental environments. The environmental affinity was calculated for each of the simulated taxa using both the full posterior and the MAP estimate. In this toy example, environmental affinity can range between -0.5 and 0.5.

As should be expected, as sample size increases the distribution of MAP estimates converge on the true value (Fig. 10). For taxa with less than 10 occurrences, the MAP estimate is biased towards extreme values. Note that the mode of the beta distribution is not defined for situations where there were 0 draws of one of the environmental conditions. Instead, the vertical line is based entirely on the observed occurrences which are technically the modal estimates because they are the most frequently occurring/highest density.

In contrast, we can compare the true occurrence probability distribution versus the posterior estimate for a given sample (Fig. 11). When sample sizes are low, posterior estimates are flat and represent a compromise between the likelihood and the flat prior (Eq. 5). Because of this, estimates from small sizes are less

likely to be overly biased towards the extremes. This is further emphasized by inspection of the estimates of environmental affinity for the simulated taxa (Fig. 12). Posterior estimates from simulated taxa with small sample size have a much broader distribution that both allows for the extreme observation but still captures the "true" value (0).

By defining environmental preference as the difference in full posterior estimates of occurrence probability, it is possible to include taxa with low sample sizes that are normal discarded (Foote, 2006, Kiessling and Aberhan, 2007, Miller and Connolly, 2001, Simpson and Harnik, 2009). Additionally, 55+% of observed Paleozoic brachiopod genera have less than 10 occurrences which is the range of sample sizes where MAP (or ML) estimates would be potentially most biased. This is preferable to finding the difference between the MAP estimates (blue line; Fig. 12).

B Survival model

The simplest model of genus duration includes no covariate or structural information. Define y_i as the duration in stages of genus i, where $i = 1, \ldots, n$ and n is the number of observed genera. These two models are them simply defined as

$$\begin{aligned} y_i &\sim \text{Exponential}(\lambda) \\ y_i &\sim \text{Weibull}(\alpha, \sigma). \end{aligned} \tag{9}$$

$\lambda, \alpha, \text{and} \sigma$ are all defined for all positive reals. Note that λ is a "rate" or inverse-scale while σ is a scale parameter, meaning that $\frac{1}{\lambda} = \sigma$.

These simple models can then be expanded to include covariate information as predictors by reparameterizing λ or σ as a regression (Klein and Moeschberger,

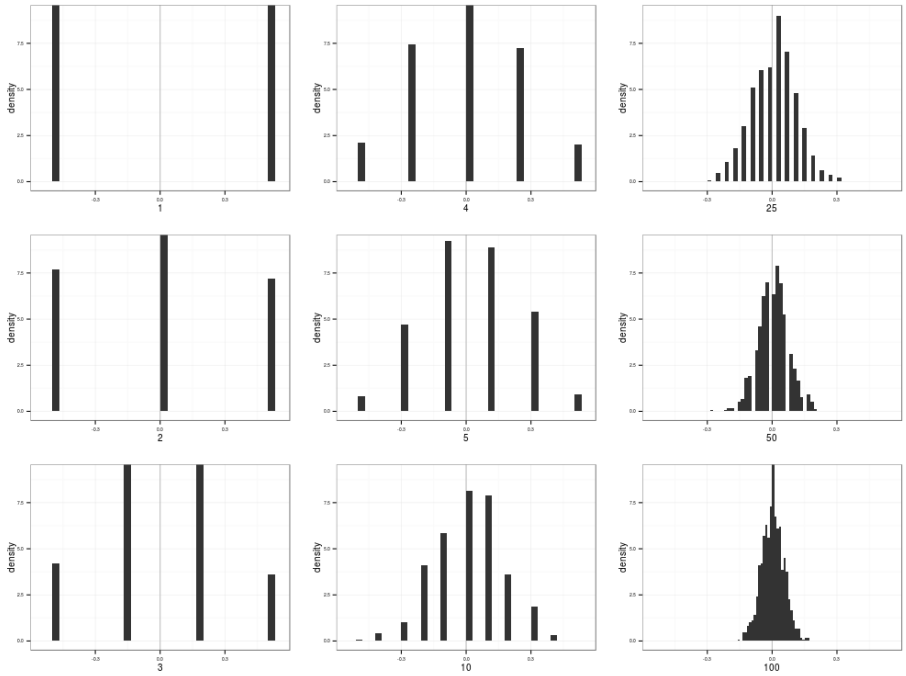

Figure 10: Histograms of the distributions of from the beta distribution defined in Eq. 8. As to be expected, as sample size increases the draws better resemble the underlying true distribution. Sample size is indicated as the label of the x-axis, increasing in column major order.

668 2003). Each of the covariates of interest is given its own regression coefficient (e.g. β_r) along with an intercept term β_0. There are some additional
670 complications to the parameterization of σ associated with the inclusion of α as well as for interpretability (Klein and Moeschberger, 2003). Both of these are
672 then written as

$$\begin{aligned} \lambda_i &= \exp(\beta_0 + \beta_r r_i + \beta_v v_i + \beta_{v^2} v_i^2 + \beta_m m_i) \\ \sigma_i &= \exp\left(\frac{-(\beta_0 + \beta_r r_i + \beta_v v_i + \beta_{v^2} v_i^2 + \beta_m m_i)}{\alpha}\right). \end{aligned} \tag{10}$$

The quadratic term for environmental affinity v is to allow for the possible
674 nonlinear relationship between environmental affinity and extinction risk.

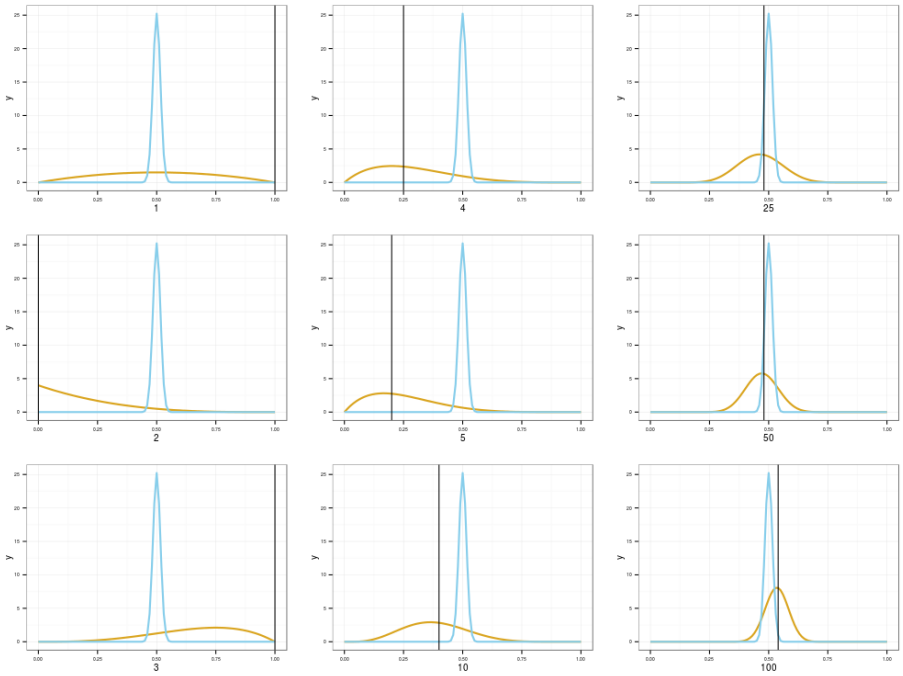

Figure 11: Comparisons of the underlying distribution (blue) to posterior estimates based on increasing sample size (gold). Each posterior estimate is represented for only a single realization of draws, each with sample size indicated as the x-axis label (increasing in column major order). Black vertical lines correspond to the MAP estimate of the simulated taxon's affinity. This stands in contrast to the posterior distribution of expected affinity in gold.

The models which incorporate both equations 9 and 10 can then be further expanded to allow all of the β coefficients, including β_0, to vary with origination cohort while also modeling their covariance and correlation. This is called a varying-intercepts, varying-slopes model (Gelman and Hill, 2007). It is much easier to represent and explain how this is parameterized using matrix notation. First, define $\mathbf{B}$ as $k \times J$ matrix of the k coefficients including the intercept term ($k = 5$) for each of the J cohorts. Second, define $\mathbf{X}$ as a $n \times k$ matrix where each column is one of the covariates of interest. Importantly, $\mathbf{X}$ includes a columns of all 1s which correspond to the constant term β_0. Third, define $j[i]$ as the

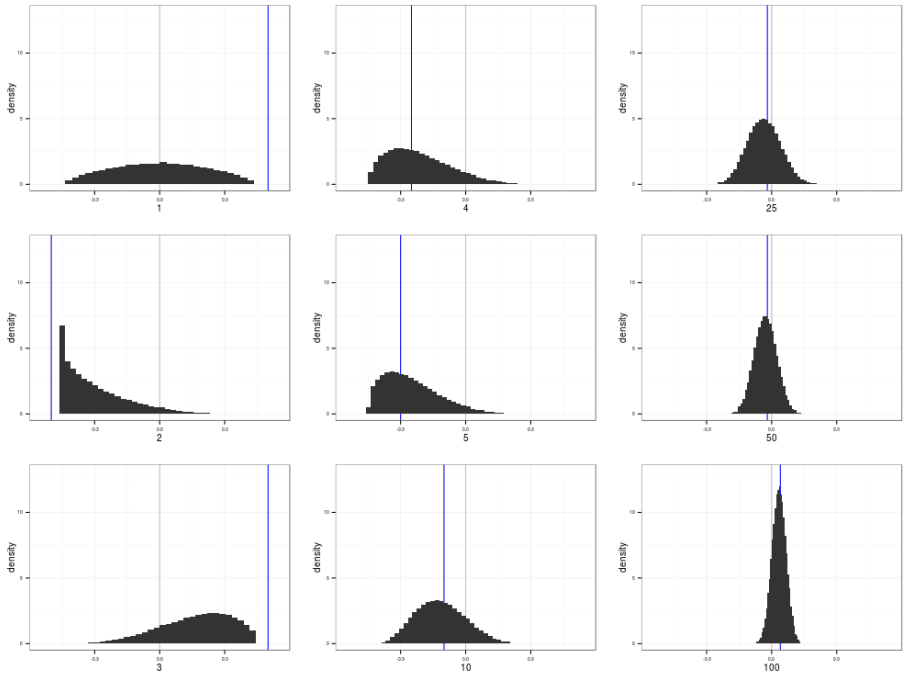

Figure 12: Histograms of the difference in the underlying occurrence distribution and the posterior distribution estimates from the previous graph (Fig. 11). The "true" value is included in all distributions of environmental affinities. Each affinity estimate is represented for only a single realization of draws, each with sample size indicated as the x-axis label (increasing in column major order). Blue vertical lines correspond to the difference in MAP estimates between the underlying distribution and the simulated taxon's draws. This stands in contrast to the distribution of the differences between the simulated taxon and background.

684 origination cohort of genus i, where $j = 1, \ldots, J$ and J is the total number of observed cohorts. We then rewrite λ and σ of equation 10 in matrix notation as

$$\begin{aligned} \lambda_i &= \exp(\mathbf{X}_i B_{j[i]}) \\ \sigma_i &= \exp\left(\frac{-(\mathbf{X}_i B_{j[i]})}{\alpha}\right). \end{aligned} \tag{11}$$

686 Because B is a matrix, I use a multivariate normal prior with unknown vector

of means μ and covariance matrix Σ. This is written as

$$B \sim \text{MVN}(\vec{\mu}, \Sigma) \tag{12}$$

where $\vec{\mu}$ is length k vector representing the overall mean of the distributions of β coefficients. Σ is a $k \times k$ covariance matrix of the β coefficients.

What remains is assigning priors the elements of $\vec{\mu}$ and the covariance matrix Σ. All elements of $\vec{\mu}$ except for μ_r were given weakly informative normal priors while μ_r was given an informative normal prior ($\mu_r \sim \mathcal{N}(-1, 1)$. The prior for Σ is a bit more complicated due to its multivariate nature. Following the Stan Development Team (2014b), I modeled the scale terms separate from the correlation structure of the coefficients. This is possible because of the relationship between a covariance and a correlation matrix, defined as

$$\Sigma_B = \text{Diag}(\vec{\tau})\Omega\text{Diag}(\vec{\tau}) \tag{13}$$

where $\vec{\tau}$ is a length k vector of variances and Diag(τ) is a diagonal matrix.

I used a LKJ prior distribution for correlation matrix Ω as recommended by Stan Development Team (2014b). The LKJ distribution is a single parameter multivariate distribution where values of the parameter η greater than 1 concentrate density at the unit correlation matrix, which corresponds to no correlation between the β coefficients. The scale parameters, $\vec{\tau}$, are given weakly informative half-Cauchy (C^+) priors following Gelman (2006).

C Censored observations

A key aspect of survival analysis is the inclusion of censored, or incompletely observed, data points (Ibrahim et al., 2001, Klein and Moeschberger, 2003). The two classes of censored observations encountered in this study were right and left censored observations. Right censored genera are those that did not go extinct during the window of observation, or genera that are still extant. Left censored observations are those taxa for which we know only an upper limit on their duration.

In the context of this study, I considered all genera that had a duration of only one geologic stage to be left censored as we do not have a finer degree of resolution.

The key function for modeling censored observations is the survival function, or $S(t)$. $S(t)$ corresponds to the probability that a genus having existed for t stages will not have gone extinct while $h(t)$ corresponds to the instantaneous extinction rate at taxon age t Klein and Moeschberger (2003). For an exponential model, $S(t)$ is defined as

$$S(t) = \exp(-\lambda t), \tag{14}$$

and for the Weibull distribution $S(t)$ is defined as

$$S(t) = \exp\left(-\left(\frac{t}{\sigma}\right)^{\alpha}\right). \tag{15}$$

$S(t)$ is equivalent to the complementary cumulative distribution function, $1 - F(t)$ (Klein and Moeschberger, 2003).

For right censored observations, instead of calculating the likelihood as normal

(Eq. 11) the likelihood of an observation is evaluated using $S(t)$. Conceptually, this approach calculates the likelihood of observing a taxon that existed for at least that long. For left censored data, instead the likelihood is calculated using $1 - S(t)$ which corresponds to the likelihood of observing a taxon that existed no longer than t.

The full likelihood statements incorporating fully observed, right censored, and left censored observations are then

$$\begin{aligned} \mathcal{L} &\propto \prod_{i \in C} \text{Exponential}(y_i|\lambda) \prod_{j \in R} S(y_j|\lambda) \prod_{k \in L} (1 - S(y_k|\lambda)) \\ \mathcal{L} &\propto \prod_{i \in C} \text{Weibull}(y_i|\alpha, \sigma) \prod_{j \in R} S(y_j|\alpha, \sigma) \prod_{k \in L} (1 - S(y_k|\alpha, \sigma)) \end{aligned} \tag{16}$$

where C is the set of all fully observed taxa, R the set of all right censored taxa, and L the set of all left-censored taxa.

D Widely applicable information criterion

WAIC can be considered a fully Bayesian alternative to the Akaike information criterion, where WAIC acts as an approximation of leave-one-out cross-validation which acts as a measure of out-of-sample predictive accuracy (Gelman et al., 2013). WAIC is calculated starting with the log pointwise posterior predictive density calculated as

$$\text{lppd} = \sum_{i=1}^{n} \log \left(\frac{1}{S} \sum_{s=1}^{S} p(y_i|\Theta^S) \right), \tag{17}$$

where n is sample size, S is the number posterior simulation draws, and Θ represents all of the estimated parameters of the model. This is similar to calculating the likelihood of each observation given the entire posterior. A

correction for the effective number of parameters is then added to lppd to adjust for overfitting. The effective number of parameters is calculated, following the recommendations of Gelman et al. (2013), as

$$p_{\text{WAIC}} = \sum_{i=1}^{n} V_{s=1}^{S}(\log p(y_i|\Theta^S)). \tag{18}$$

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

Given both equations 17 and 18, WAIC is then calculated

$$\text{WAIC} = \text{lppd} - p_{\text{WAIC}}. \tag{19}$$

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