

How predictable is extinction? Forecasting species survival at million-year timescales

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Abstract

A tenant of conservation paleobiology is that knowledge of past extinction patterns can help us to better predict future extinctions. Although the future is unobservable, we can test the strength of this proposition by asking how well models conditioned on past observations would have predicted subsequent extinction events at different points in the geological past. To answer this question we analyze the well-sampled fossil record of Cenozoic planktonic microfossil taxa (foramanifera, radiolarians, diatoms, and calcareous nanoplankton.) For each group we examine how extinction probability varies over time as a function of species age, time of observation, current geographic range, change in geographic range, climate state, and change in climate state. Although the best-performing model includes time-varying effects and historical covariates (change in range and change in climate state) the improvement in predictive power over models with constant effects and no historical covariates is very minor. This model has an approximately 78% median probability of correctly ranking the relative extinction risk any two randomly selected species. It performs nearly as well at out-of-sample prediction (70-80%), implying that determinants of extinction risk have varied only modestly through time. An important caveat is that human impacts may substantially disrupt range-risk dynamics so that the future will be less predictable than it has been in the past.

Keywords: conservation, paleobiology, extinction, forecasting

1 Introduction

Being able to predict which species are more likely than others to go extinct over a given time frame is crucial for planning decisions policies to ameliorate the current biodiversity crisis. Some species have been the focus of intense study to define short-term (e.g. decadal to centennial scale) abundance and geographic range trajectories.

We cannot know, however, we do not yet know which species are going to go extinct because this has not happened yet – it is unobservable. We approach this problem by analyzing the past in order to predict the future. The fossil record preserves past extinction events, allowing

us to develop a predictive model of species extinction based on this record and the properties
of the observed species, both extinct and extant [1, 2]. By assessing the predictive performance
of this model on unobserved data, we can quantify how precise our best estimates will be for
future extinctions – we ask the probability that, given two random species, we correctly rank
their relative risks of extinction.

Studying how species vary in their extinction risk over time means we can assess which
species are at greater risk under unobserved conditions. We know that a species’ risk of
extinction varies over time in both intensity (average rate) and selectivity (difference in risk
between taxa) [3–5]. Species, after all, can go extinct at any “moment” and the relative
risk of extinction exhibited by different taxonomic groups and how that risk varies over
time is an important dynamic which shapes the rate and structure of extinction. What has
not been evaluated is that as extinction intensity and selectivity change over time, how
accurate are our assessments based on past events likely to be when applied to the future?
By specifically including and modeling the temporal variation in extinction risk, we are able
to improve our overall predictions because we incorporate and explicitly model differences
between observations from across a range extinction intensities and selectivities.

By analyzing extinction and survival data from the fossil record, the hope is this can aide
in predicting the extinction risk of extant species – after all, the present must at some level
be a function of the past. Past paleobiological studies of extinction have frequently focused
on identifying and measuring the effect of various predictors on extinction risk [3, 5–10] or
on how to identify or measure these effects [11–16]. This focus means that while we have a
good understanding of which factors are strong and general determinants of extinction risk,
we have less knowledge of how accurate or strong our predictions about the differences in
extinction risk are.

A related question is if the changes to biotic or abiotic predictors, and not just their values,
are similarly important factors for predicting extinction. For example, we know that a species’
global geographic range changes over its duration [17–20]. We also know that a species’
geographic range size is a good predictor of differences extinction risk [3, 21–23]. This begs the
question: how does a species’ extinction risk change over its duration? While the phenomenon
of species’ geographic range change over time has been studied [17–20], the potential predictive
impact of this change has been under-evaluated (but see Kiessling and Kocsis [20]).

For this exercise we chose to analyze one of the best-sampled and studied fossil records – the
Cenozoic record of skeletonized marine planktonic microorganisms (Foraminifera, Radiolaria,
Diatoms, and Coccolithophores). These data are readily available through the Neptune
database, an online repository of species occurrences obtained through the Deep Sea Drilling
Program and the Ocean Drilling Project [24, 25]. This database provides abundant samples
in space and time, a high degree of temporal resolution for the entirety of the Cenozoic,
and has an internally consistent taxonomic identification strategy – as close to ideal data
for this analysis as possible. The Neptune database records multiple phyla-scale taxonomic
groups for over 60 million years, with incredible temporal resolution supported by the various
age-models of the deep-sea cores from which the occurrences are recorded. Analyzing patterns
of extinction and global occurrence at fine temporal scales means we can better elucidate
how well we can predict species extinction at human-relevant scales.

2 Materials and Methods

2.1 Data Specifications

We analyzed microfossil occurrence information which was downloaded from the Neptune Database <http://www.nsb-mfn-berlin.de/nannotax> [24, 25]. Occurrence information was downloaded for calcareous nannoplankton, diatoms, foraminifera, and radiolarians. This dataset of occurrences was then filtered to just those species which have their first occurrence at most 63 Mya. This choice means that our analysis avoids those taxa which survived the K/Pg boundary, those taxa which arose just after the K/Pg boundary, and means that our occurrence histories line up with the temperature time-series which was used as a predictor of extinction as discussed below.

All fossil occurrences were assigned to 1 My bins based on the estimated age of the fossil occurrence as listed in the Neptune Database. After binning, each taxon’s geographic range was calculated for each of the 1 My bins in which it occurred. Geographic range was calculated as the maximum great circle distance on an ellipsoid (i.e. the Earth) between any two occurrences of that species; this distance was measured in kilometers.

We also calculated the average global temperature of each 1 My bin as estimated from Magnesium/Calcium isotope ratios Cramer et al. [26]. These elemental ratios are considered more accurate estimates of past global temperature when compared to the frequently used Oxygen isotope-based estimates; this is because Mg/Ca based estimates are not effected by ice-volume and fresh-water input (e.g. meteoric water) which can alter Oxygen isotope ratios without reflecting changes to the climate itself. This property is of particular importance for this analysis as polar ice-caps develop midway through the Cenozoic. Our data source, Cramer et al. [26], provides temperature estimates for every 0.1 My from 0 to 63 Mya. The temperature estimate for each 1 My interval was calculated as the mean of all estimates within that interval.

See Section S1.1 for a further explanation on how observations were temporally binned and how our covariates were standardized and transformed prior to analysis.

2.2 Model Specifications

We used a discrete-time survival modelling framework in order to estimate how well we can predict extinction risk at one million year time scales. At its core, our model is a multilevel logistic regression with taxon age in millions of years as a varying intercept [27]. We considered four model variations of the predictors included in our model: covariate effects are constant over time and none of our historical covariates are included (Model C), covariate effects are allowed to vary over time but none of our historical covariates are included (Model V), covariate effects are constant over time and our historical covariates are included (Model CP), covariate effects are allowed to vary over time and historical covariates are included (Model VP). See Table 1 for further explanation of how these models differ from each other.

For a complete description of the statistical model used in this analysis, please see Section S1.2. For a full description of how our models were implemented, please see Section S1.3.

111 Importantly, we include species geologic age at time of observation as a non-nested varying
intercept term. This factor may or may not contribute to differences in species extinction
risk over time [7, 28–32], but its inclusion in our model is critical to its nature as a survival
114 model [27]. Again, see Section S1.2 for how this term was specified as part of our model.

Table 1: Models and their definitions

Code	Description	Covariates	R Formula Syntax ^a
C	Constant effects, no historical cov.	Geographic range, temperature	$\text{event}^b \sim \text{range}^c + \text{temp}^d + (1 \mid \text{age}^e/\text{phylum}^f)$
V	Varying effects, no historical cov.	Geographic range, temperature	$\text{event} \sim \text{range} + \text{temp} + (1 + \text{range} + \text{temp} \mid \text{phylum}) + (1 \mid \text{age}/\text{phylum})$
CP	Constant effects, historical cov.	Geographic range, change in geographic range, temperature, previous temperature	$\text{event} \sim \text{range} + \text{range_diff}^g + \text{temp} + \text{temp_lag}^h + (1 \mid \text{age}/\text{phylum})$
VP	Varying effects, historical cov.	Geographic range, change in geographic range, temperature, previous temperature	$\text{event} \sim \text{range} + \text{range_diff} + \text{temp} + \text{temp_lag} + (1 + \text{range} + \text{range_diff} + \text{temp} + \text{temp_lag} \mid \text{phylum}) + (1 \mid \text{age}/\text{phylum})$

^a See Equation S2 for full statistical model definition.

^b Species observation where 1 if time of last observation, otherwise 0.

^c Species geographic range in log km². Mean centered, scaled to sd = 1.

^d Global temperature in degrees C. Mean centered, scaled to sd = 1.

^e Species are at observation in millions of years.

^f Taxonomic group of species (i.e. Foraminifera, Diatoms, Radiolarians, Calcareous nannoplankton).

^g Change in geographic range since last observation.

^h Temperature at previous observation.

2.3 In-sample and out-of-sample forecasting

We are interested in our models' performance into two contexts: in-sample and out-of-sample
117 predictive performance i.e. forecasting.

In-sample forecasting means we are estimating how well our model predicts extinction
probability for observations that that model was fit to. This is a posterior predictive check in
120 that we are comparing the posterior predictive distribution to our observed data.

We are particularly interested in understanding how well our model forecasts extinction probability of data from the future that the model was not fit to (out-of-sample data). In-sample forecasting measures, however, are not necessarily good estimates of the model’s ability to predict data from the future [33]. To quantify our ability to forecast species’ extinction risk, we estimated average out-of-sample forecasting performance using 5-fold time-series cross-validation. For time-series data, the folds (data partitions) are approximately equal segments of time. Each fold represents a sequence of time points. With 63 time points, each of the five folds represents approximately 13 time points. Keep in mind, however, that each time point corresponds to many (100-1000) individual observations.

k-fold cross-validation for time series precedes as follows [34, 35]. First, the model is fit to the first fold (time segment), and the posterior estimates of that fit are then used to forecast the extinction probability of the second fold (i.e. the future). Then the model is fit to the combined first and second folds, and the posterior estimates of that fit are used to forecast the extinction probability of the third fold. This process continues with the model fit to the first three folds combined is then used to forecast extinction probabilities for the fourth fold. Finally, the model is fit to the first four folds combined and then is used to forecast the fifth fold. The results from these forecasts are then combined to yield our estimate of expected out-of-sample performance.

The relative adequacy of our four model variants were compared using the area under the receiver operating characteristic curve or AUC [36, 37]. This measure is commonly used in classification problems as it has the desirable characteristic of comparing the model’s true positive rate with its false positive rate, as opposed to accuracy which only considers true positives. AUC ranges between 0.5 and 1, with 0.5 indicating no difference in classification from random and 1 indicating perfect classification. AUC can be interpreted as the probability that our model correctly ranks the relative extinction risks of a randomly selected extinct-extant species pair [36, 37]. AUC values of approximately 0.8 or greater can be considered “good” [38], so we interpret values between 0.7 and 0.8 could then be considered “fair,” and values between 0.6 and 0.7 as “poor.”

See our code repository at <https://github.com/psmits/trident> for full code details. This entire analysis was coded in R and uses tidyverse and tidyverse adjacent tools such as `dplyr` [39], `purrr` [40], and `tidybayes` [41]. Additionally, all of our models were written using the `brms` [42, 43] R package, which implements Stan-based Bayesian models which are fit via Hamiltonian Monte Carlo [44].

3 Results

3.1 In-sample forecasting adequacy

The in-sample model comparisons are useful comparing the relative ability of our models to represent the data it was fit to. Comparison between the posterior distributions of in-sample AUC for each of the four models demonstrates that all of our models have approximately

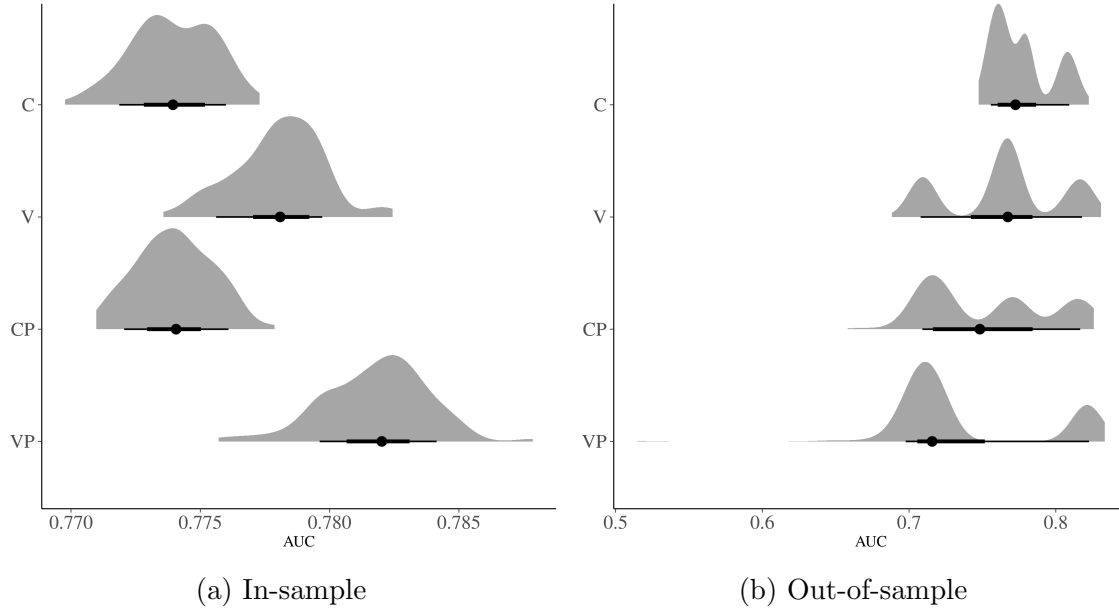


Figure 1: In-sample (1a) and out-of-sample (1b) AUC estimates for each of our four models. These estimates are calculated from the models posterior predictive distribution or from predictions made to new data, respectively. Models with a higher AUC values indicate better performance over models with lower AUC values. AUC is bounded between 0.5 and 1. See Table 1 for a description of each of the four models.

equal in-sample forecasting performance (Fig. 1a). The parameter rich model VP has the greatest median in-sample AUC when compared to the other three models, but there is substantial overlap in their posterior distributions. Additionally, while our parameter rich model VP is possibly the most adequately performing model, the difference or improvement to performance is minimal at best – all four models have approximately equal in-sample AUC posterior distributions. All the in-sample AUC estimates from our models are concentrated on an AUC value of 0.77. It is therefore hard to conclude that there is one “best” model which we can rely upon as they are all nearly functional equivalent.

There are one or more time periods where our posterior distribution of in-sample AUC has a median value less than or equal to 0.5 (Fig. 2). However, this pattern is absent for the posterior estimates of in-sample AUC for Foraminifera and Radiolaria as fit by the VP model. In contrast, there are fewer periods of low model performance for calcareous nannoplankton and Dinoflagellates as estimated from our VP model than in those estimates from the other three model variations.

3.2 Out-of-sample forecasting performance

Expected out-of-sample forecasting performance was estimated using five-fold cross-validation for time series [34, 35]. The resulting distribution when all folds are combined is very multimodal by their very nature of being fit to and estimated from different data sets and

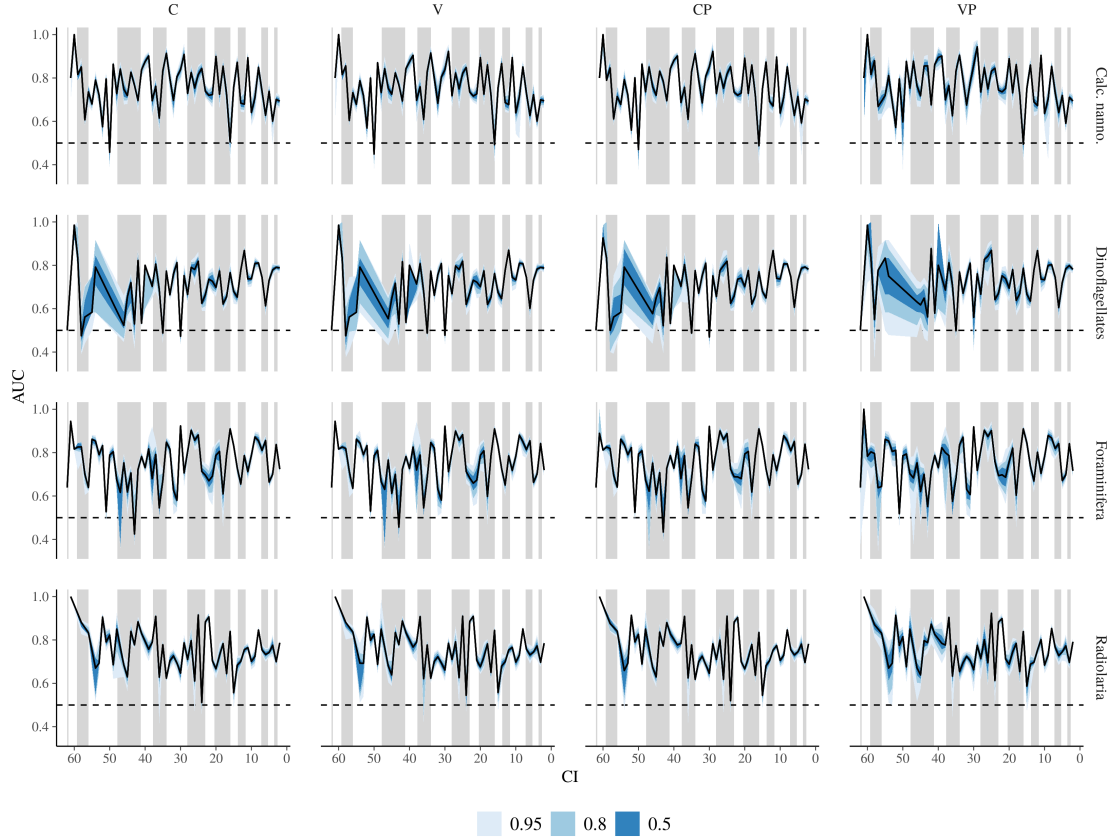


Figure 2: Comparison of in-sample forecasting performance measured by AUC for each of the four models, arranged over time and by taxonomic group. These estimates reflect each model’s fit to the various taxonomic groups over time. The black line corresponds to the median AUC value, while the envelopes correspond to multiple credible intervals as indicated in the legend. In all cases, higher AUC values indicate greater predictive performance versus lower AUC values. See Table 1 for a description of each of the four models.

amounts of data [33]. We find that this multimodality increases with model complexity (Fig. 1b), most likely because the complex models allow for predictor effects to vary with time which allows for a greater range in possible parameter values which in turn yield a greater range of posterior predictions.

Comparison between the in-sample forecasting performance estimates to the expected out-of-sample AUC estimates reveals a similar range in performance for all models (Fig. 1a, 1b). Interestingly, the differences in posterior predictive distributions of AUC between the four model variations has decreased. For example, the VP model no longer has the greatest median AUC of the four models (Fig. 1b). These differences mean that the rank order of median out-of-sample AUC is different from the rank order of median in-sample AUC. However, making interpretations based only incorrect – our estimates are the full posterior, not individual points. Because of this, the four models are effectively indistinguishable in their out-of-sample forecast performance (Fig. 1b).

We can also compare the posterior predictive distribution of expected out-of-sample AUC over time and taxonomic group for each of the four models (Fig. 3). In all cases, our four models are nearly identical in their out-of-sample forecasting performance over time and between each of the taxonomic groups.

In the analysis of the in-sample forecast performance of the four models, we noted that there were time intervals where our predictions were no better than random (Fig. 2). This occurrence is generally much rarer for the posterior distribution of AUC from the out-of-sample forecasts. The major exception to this pattern are our estimates for the Dinoflagellates, which has at least one time interval for all four models where the median AUC of the out-of-sample forecasts were no better random. In contrast, the only other group for which median posterior predictive estimate of out-of-sample AUC reaches 0.5 is calcareous nannoplankton, and then only with model V.

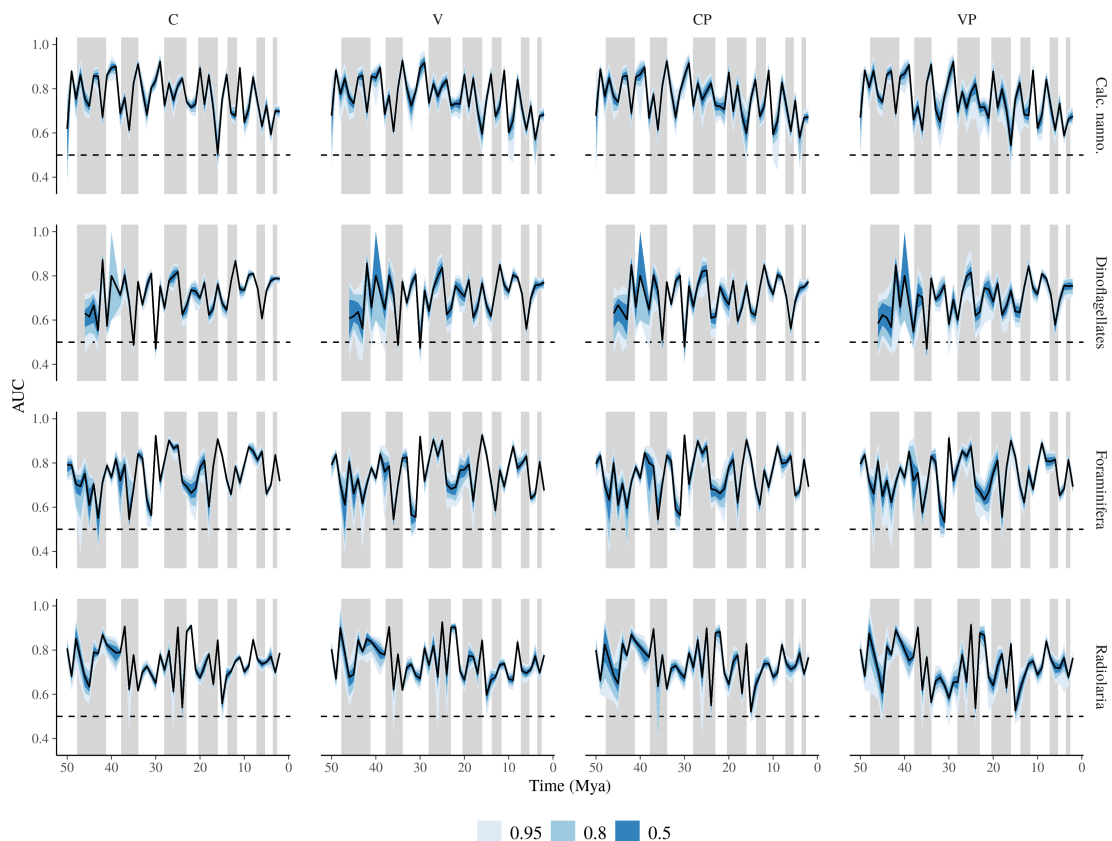


Figure 3: Comparison of out-of-sample AUC values over time as aggregated by taxonomic group for each of the four models. The AUC of the individual My intervals within each fold is plotted to highlight the heterogeneity in performance within and between folds. This presentation decomposes each of the 12-million year folds by each of the taxonomic groups into the predictions made for each of the million-year intervals. The black line corresponds to the median AUC estimate, with the envelopes corresponding to multiple credible intervals as indicated in the legend. See Table 1 for a description of each of the four models.

We compared the difference in our AUC estimates from the out-of-sample forecasts to the AUC estimates from our in-sample forecasts by subtracting the in-sample AUC estimates from the out-of-sample AUC estimates (Fig. 4). A difference in AUC close to 0 indicates complete congruence between the in-sample and out-of-sample forecasts. A positive difference indicates that our out-of-sample forecasts are actually higher performing than our in-sample forecasts, while negative difference indicates poorer out-of-sample performance than in-sample forecast. Divergences between our out-of-sample and in-sample forecasts are rare and tend to not form multimillion year patterns, something that is consistent with the broad visual congruence between the in-sample and out-of-sample forecast performance (Fig. 2, 3). The only major multimillion year pattern indicating significantly poorer out-of-sample forecast performance than in-sample forecast performance is for Radiolaria based on the VP model concentrated around 30 Mya (Fig. 4).

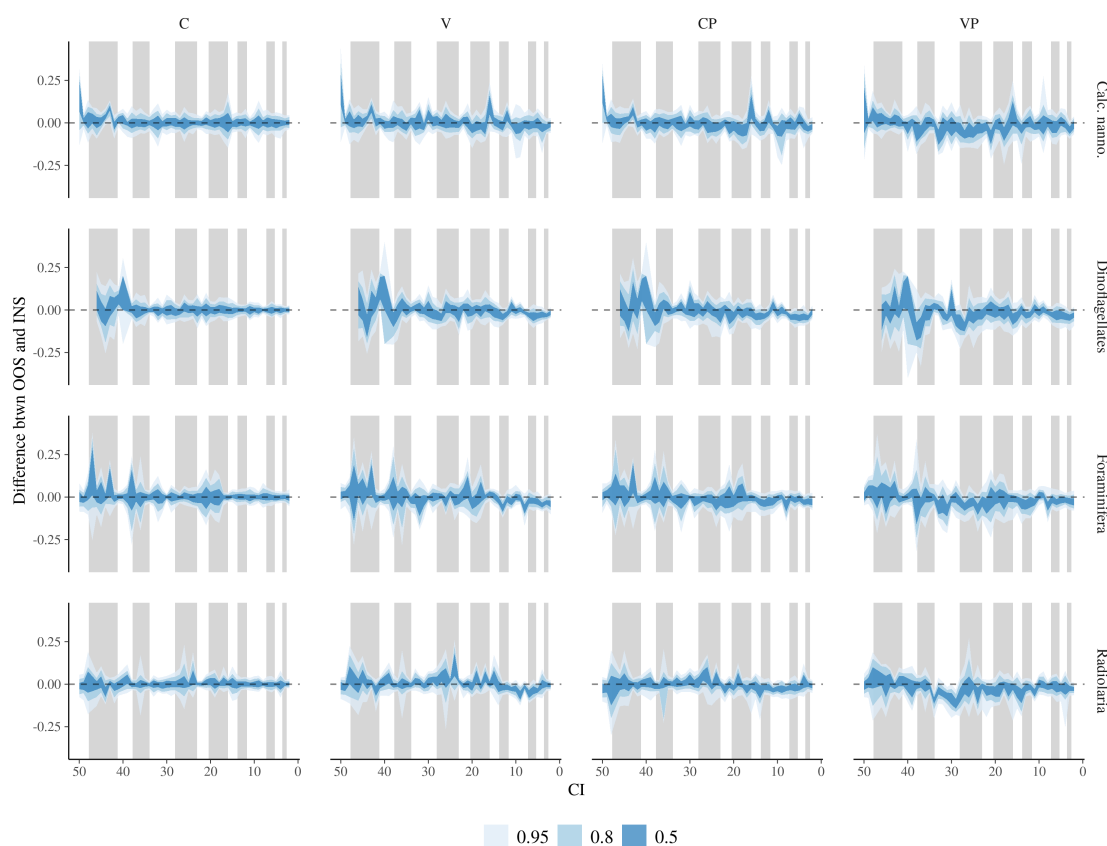


Figure 4: Comparison between our out-of-sample forecasts and in-sample forecasts for all models. This value is calculated as the values presented in Figure 3 minus those values presented in Figure 2. A differences close to 0 indicate complete congruence between in-sample and out-of-sample forecasts, while a positive difference indicates that our out-of-sample forecasts are actually higher performing than our in-sample forecasts, and a negative difference indicates poorer out-of-sample performance than in-sample forecast. See Table 1 for a description of each of the four models.

4 Discussion

The results of this paper set out our baseline ability to predict relative differences in extinction risk. We find that all of our model have an approximate 77% to 79% probability of correctly rank the extinction risk of two randomly selected in-sample observations. Similarly, these models are expected to correctly forecast the rank order in extinction risk of two randomly selected out-of-sample observations approximately 70% to 80% of the time. A slight decrease in performance when dealing with out-of-sample observations makes sense: each of the models fit during cross-validation is based on fewer data than the model fit on the full data (between 1/5th to 4/5ths of the original). Additionally, a potential decrease in precision when forecasting the future of extinction risk is almost to be expected as the future is not necessarily the same as the past. However, the similarity between the in-sample and out-of-sample results indicates that our model is fairly robust to how extinction intensity has changed over the Cenozoic.

One of the most striking results of this analysis is that the in-sample and out-of-sample forecasts made with our models demonstrate that while models where the historical covariates are predictors of species extinction have better in-sample performance (Fig. 1a, 2), all of them forecast the extinction risk of out-of-sample data with a similar degree of success (Fig. 1b, 3).

Other noteworthy aspects of the results of our in-sample forecasts are that although AUC estimates for our models differ significantly between models, all of these estimates are in a narrow range of possible AUC values (Fig. 1a). For our in-sample results, while the statistically best model does include the historical covariates and allows all covariate effects to vary over time, its practical difference in performance compared to the other models is virtually negligible (Fig. 1b). This means that even though model VP has a *statistically* greater AUC than the other three models, this result is not practically or *scientifically* significant.

The success of our models is partially driven by the size of our dataset and the hierarchical structure of our model. Our estimates are based on rather limited information about the taxa themselves, and our model only takes into account some aspects of species geographic range and their rough taxonomic grouping. Instead of relying on large amounts of ecological information to shape individual differences, our model leverages most of the Neptune dataset through a multilevel model to constrain and improve our parameter estimates by sharing information about those parameters across taxa and time.

The principal reason we were not able to include more biological information in our models is that we lack almost any life history or ecological information on most marine micro- and nanno-plankton. Forams are the exception to this problem – there is life history, ecological, and physiological information for a selection of foram species [5]. However, not this information does not exist all foram species. If we want to include this type of information in a predictive model of extinction risk, we would be able to analyze only a single taxonomic subset of the fossil occurrences present in the Neptune Database and then only a limited selection of those species. This means ignoring the majority of occurrence information present in the Neptune database.

In conclusion, our results provide a promising picture of our ability to predict the relative

extinction risk of two randomly selected species. Considering that conservation decisions are made based on a continuum of risk, from most to least, this means that our results are in the same language as how conservation resources are allocated.

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S1 Supplement to Materials and Methods

S1.1 Data Specifications

S1.1.1 Binning fossil occurrences

Because the estimated ages of each occurrence is a product of core-specific age-models and can be overly precise, the hope is that by binning the data this smooths over the between-core heterogeneity and thus homogenizes our disparate data sources. The occurrence histories of each species were then given binary codes used to model the presence or extinction of those species. For every occurrence of a species, except the last, that species is considered to have survived and was marked with a 0. The last occurrence of that species is considered the bin in which the taxon has gone extinct – and is assigned a 1. This protocol means that we are reading the fossil record “as written,” a practice that is potentially dangerous as it is an overconfident statement of preservation and may be shortening the actual duration of that species [1–10]. However, this practice is common with marine microfossil data due to their exceptional preservation rate [11–14]. In fact, with marine microfossils collected from cores a bigger problem may be over extending the duration of a species due to mixing and smearing within the cores CITATIONS.

S1.1.2 Covariate transforms and standardizations

Prior to analysis, geographic range was then log-plus-one transformed and standardized by mean-centering the data and then dividing by the standard deviation of the distribution of geographic ranges. This standardization means that a regression coefficient associated with this covariate describes the change in extinction probability per change in standard deviation of geographic range, that coefficients associated with similarly standardized covariates will be directly comparable in magnitude, and that the intercept term corresponds to the expected value of the outcome at when geographic range is its average value [15]. Change in geographic range between observations was measured from the standardized geographic range values and was not standardized separately.

Temperature was also transformed and standardized the in the same manner as geographic range. Difference in temperature between observations was measured from the standardized temperature values and was not standardized separately.

S1.2 Model Specifications

In survival analysis, the hazard function describes the instantaneous rate of extinction of a species given its age and relevant covariates. The hazard function is defined as the conditional probability of a species going extinct by the end of the t -th interval given that it survived up until t and the relevant covariate information X for all $k \geq 1$ My intervals [16]. For the discrete

time intervals $T = 1, \dots, k$, extinction is defined as $T = t$. The discrete time hazard function is defined as

$$\lambda(t|X) = P(T = t|T \geq t, X), \quad t = 1, \dots, k. \quad (\text{S1})$$

The hazard function (Eq. S1) is easily reparameterized as a logistic regression by defining that $\lambda(t|X) = h(\Theta)$ where $h(\cdot)$ is a logit inverse-link function and Θ is the probability of a taxon going extinction during interval t [16]. $h(\Theta)$ is then modeled as with any regression as it is defined for all real-values. In this case, we opted for a hierarchical/mixed-effects model with multiple non-nested varying intercepts and slopes [15].

Our covariates matrix X is a $N \times D$ matrix where N is the total number of observations and D is the total number of covariates. The first column of X is entirely 1's as it corresponds to the intercept term in the regression model. The next two columns of X are two aspects of geographic range as continuous covariates: geographic range r during interval t , and the difference d between the geographic range at $t - 1$ and t . Change in geographic range was calculated from the transformed and standardized geographic range values; this means that change in geographic range is in units of changes in standard deviations. The final two columns are two aspects of global temperature: mean temperature during interval t , and the lag of mean temperature (i.e. mean temperature during interval $t - 1$.) As with change to geographic range, the lag of temperature is based on the transformed and standardized temperature estimates.

The matrix of time and phylum varying regression coefficients describing the effects of the covariates on a species' risk of extinction is called B – a w by p matrix, where w is the number of time temporal intervals and p is the number of phyla. The elements of this matrix, the regression coefficients, are themselves modeled as being multivariate normally distributed with vector of means α describing the average intercept and regression coefficient estimates of each Coefficients for each phylum p . These phylum averages are themselves modeled as multivariate normally distributed with mean vector μ describing the overall average regression coefficients, including the intercept. μ has length D and is ordered intercept, range coefficient, change in range coefficient, temperature coefficient, temperature lag coefficient.

The effect of species age on the log-odds of species extinction is modeled as a non-nested random intercept A [16]. This term describes how the log-odds of extinction varies along a species duration, and how this effect can differ between the phyla. A is a l by p matrix, where l is the age at observation of a species and p is its phylum. A is modeled as following a multivariate normal distribution with phylum means being the vector δ and covariance matrix Σ_A . The covariation between the elements of vector δ are modeled as a multivariate normal distribution with a mean vector of all 0s and covariance matrix Σ_δ .

To complete the generative model, we need to assign final priors to the “top-level” parameters. In general, we favored weakly informative priors which help regularize our estimates. In the case of a regression coefficient, this means a Normal distribution with mean 0 and a standard deviation of 3. For our scale parameters (e.g. standard deviations), we used half-Cauchy distributed priors with heavy tails but the majority of probability density near 0.

Our top-level intercept was given a more diffuse prior than our regression coefficients, which

reflects our greater degree of uncertainty about its value. Our top-level regression coefficient for the effect of geographic range was given an informative prior reflecting the overwhelming amount of evidence that species with a larger than average geographic range have a lower risk of extinction than species with an average or less than average geographic range. In the context of this analysis, this means that we are again using a weakly informative prior but instead of centering the density around -1 (i.e. larger than average geographic range decreases extinction risk).

Instead of assigning a prior distribution for each of the covariance matrices in the model, we instead decomposed the covariance matrices (e.g. Σ_B) which allows us to assign independent priors for the scale and correlation aspects of covariance. The scale parameters were assigned half-Cauchy priors as described above in the context of all other scale parameters. The correlation matrices were assigned LKJ priors each with shape parameter set to 1. This choice of shape parameter produces a uniform distribution over possible correlation matrices. These priors are also slightly more interpretable than other common prior distributions for covariance matrices such as the inverse-Wishart distribution. This approach to assigning priors to a covariance matrix is recommended by the Stan Manual [17].

In total, our model can be expressed as:

$$\begin{aligned}
t_i &\sim \text{Bernoulli}(\Theta) \\
\Theta_i &= \text{logit}^{-1}(X_i B_{w[i],p[i]} + A_{l[i],p[i]}) \\
B_{w,p} &\sim \text{MVN}(\alpha_p, \Sigma_B) \\
\alpha_p &\sim \text{MVN}(\mu, \Sigma_\alpha) \\
A_{l,p} &\sim \text{MVN}(\delta_p, \Sigma_A) \\
\delta_p &\sim N(0, \sigma_\delta) \\
\mu_d &\sim \begin{cases} N(-2, 5) & \text{if } d = \text{intercept} \\ N(-1, 1) & \text{if } d = \text{geo. range} \\ N(0, 1) & \text{else} \end{cases} \\
\delta &\sim N(0, 1) \\
\Sigma_B &= \text{diag}(\tau_B) \Omega_B \text{diag}(\tau_B) \\
\Sigma_\alpha &= \text{diag}(\tau_\alpha) \Omega_\alpha \text{diag}(\tau_\alpha) \\
\Sigma_A &= \text{diag}(\tau_A) \Omega_A \text{diag}(\tau_A) \\
\tau_B &\sim C^+(1) \\
\tau_\alpha &\sim C^+(1) \\
\tau_A &\sim C^+(1) \\
\Omega_B &\sim \text{LKJ}(1) \\
\Omega_\alpha &\sim \text{LKJ}(1) \\
\Omega_A &\sim \text{LKJ}(1)
\end{aligned} \tag{S2}$$

with i indexing the observation and bracket subscripts referencing the class of the i -th observation where $w[i]$ is the time of the i -th observation, $p[i]$ is the phylum of the i -th observation, and $d[i]$ is the age of the i -th observation.

S1.3 Model Parameter Estimation

We implemented our model (Eq. S2 using the `rstanarm` package for the R programming language [17]. This package provides an interface to the Stan probabilistic programming language for writing hierarchical/mixed-effects models in native R. Posterior estimates were obtained through Hamiltonian Monte Carlo, using 2000 steps divided equally between warm-up and sampling. In order to prevent divergent transitions adapt delta was increased to 0.9999; all other HMC/NUTS sampling parameters were kept at the defaults for `rstanarm` 2.18.2 [18].

An implementation of our full model in `rstanarm`, given a `data.frame` of all necessary data in a `data.frame` called “data”, is coded as:

```
form <- event ~ range + range_diff + temp + temp_lag +
  (1 + range + range_diff + temp + temp_lag | mybin/phylum) +
  (1 | age/phylum),
stan_glmer(formula = form,
  data = data,
  family = 'binomial',
  prior = normal(c(-1, 0, 0, 0), rep(1, 4), autoscale = FALSE),
  prior_intercept = normal(-2, 5, autoscale = FALSE),
  prior_aux = cauchy(0, 1, autoscale = FALSE),
  chains = 4,
  thin = 4,
  adapt_delta = 0.999999)
```

Similarly, our full model can also be implemented using the `brms` Stan interface [19, 20] as:

```
priors <- c(set_prior('normal(-2, 5)', class= 'Intercept'),
  set_prior('normal(0, 1)', class = 'b'),
  set_prior('normal(-1, 1)', class = 'b', coef = 'range'),
  set_prior('cauchy(0, 1)', class = 'sd'),
  set_prior('lkj(1)', class = 'cor'))
form <- bf(event ~ range + range_diff + temp + temp_lag +
  (1 + range + range_diff + temp + temp_lag | mybin/phylum) +
  (1 | age/phylum))
brmfit <- brm(formula = form,
  data = data,
  family = bernoulli(),
  prior = priors,
  chains = 4,
  thin = 4,
  control = list(adapt_delta = 0.999999))
```

Posterior convergence was determined using the general and HMC-specific diagnostic criteria: scale reduction factor (\hat{R} ; target < 1.1), effective sample size (eff; target value eff/steps < 0.0001), number of samples that saturated the maximum trajectory length for avoiding

infinite loops (treedepth; target value 0), sample divergence, and the energy Bayesian Fraction of Mission Information (E-BFMI; target value > 0.2). For further explanation of these diagnostic criteria, see the Stan Manual [17].

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