SUPPORTING ONLINE MATERIAL:

COLLINS ET AL – PERIL: ESTIMATING EXTINCTION VULNERABILITY OF MARINE TAXA FROM FOSSIL AND RECENT DATA

PREPARATION OF PARAMETERS FOR CALCULATION OF PERIL:

*Geographic range:*

A dominant contributor to extinction risk is geographic range size [1:5]. A large range affords a species a greater chance of surviving a local or regional perturbation, providing the reach of that event is smaller than the range of the species. We use the convex hulls of species occurrences for both, which reflect overall range extent relative to potential perturbations, effectively viewing extinction risk in terms of spatial autocorrelation of environmental stresses. Modern bivalve convex hulls were derived from an extensive database of global occurrences [6]. Convex hulls for Pliocene Bivalvia were derived from the geographic extents of the sedimentary basins that species are recorded from (for California [7] and from the geographic extents of the NZMS260 map sheets that species are recorded from (for New Zealand; [8]).

For modern bivalves, an alternative for shelf-depth species is to intersect convex hulls with continental shelf polygons to omit uninhabitable deep water, effectively viewing extinction risk in terms of potential population sizes as determined by available habitat. We calculate the PERIL metric both ways and present both in Figure S1, but use full convex hulls in the version presented in text. Using larger hulls results in a greater buffering effect of range, and thus (slightly) fewer species in the high percentiles of risk. We prefer to use raw convex hulls to increase usability of this metric for non-bivalve taxa, and to prevent artefacts in the data that might be caused by incorrect or incomplete bivalve depth ranges in the literature.

Geographic ranges recorded for both modern and Pliocene bivalves are strongly skewed towards low values, owing to a preponderance of relatively small ranges, but genuinely or nearly cosmopolitan species also exist, producing a long-tailed distribution, which we log-transform. We also invert range size, so that large ranges give low numbers and small ranges give high numbers (indicating higher risk) and then range-standardise it, so that the largest ranges score zero and the smallest ranges score one.

*Realized Thermal niche:*

Taxa may occupy large overall geographic ranges while tracking a narrow set of temperatures (e.g. [9]). For marine taxa, the realized thermal niche of a species gives some indication of its resilience to large-scale climatic changes, as opposed to its likelihood of surviving a regional perturbation by extending beyond the spatial limits of the event. We calculate thermal niche for a species using temperature data from MARSPEC [10]. MARSPEC uses monthly climatological data downloaded from NASA’s Ocean Color website (<http://oceancolor.gsfc.nasa.gov/>) for the time period spanning Sept 2002 to August 2010. We used mean annual temperatures of the coldest ice-free month (variable ‘biogeo14’), and warmest ice-free month (variable ‘biogeo15’) to calculate realized thermal niche as the range of temperatures encountered by the convex hull of each species’ geographic range. As with geographic range, we invert thermal niche, as we expect that a small range is riskier than a large range, and range-scale it.

For the Pliocene faunas, temperature data were sourced from PRISM3 [11]. The range of temperatures encountered by each cell was calculated, and from this the range of temperatures encountered in each species’ convex hull was calculated.

*Extinction rate in family:*

Extinction rate of the clade that any given species belongs to summarizes the phylogenetic or historical propensity towards extinction of the members of that clade. In order to concentrate on background extinction and limit the contribution of mass extinctions to the metric, for this study we have calculated extinction rate ( ) for bivalves only over the Cenozoic Era (66 Ma-Present), for each family over all geologic stages, using Foote’s [12] boundary-crosser metric:

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where *nbt* = number of taxa that cross both the base and the top of the stage (range-through taxa); *nb* = number of taxa that cross the base of the stage (range-in taxa) and *t* = time in millions of years [8].

Calculating this way has the effect of weighting time intervals by the number of taxa within them, meaning that well-sampled intervals have more effect on the final score than poorly-sampled intervals. Families with non-sampled intervals (time periods in which no members of that family are recorded) in their stratigraphic duration can produce anomalous values, overestimating for that family. Only one small family, the Anatinellidae, is affected by this and we assigned to this family the average for Bivalvia. Small families with no gaps in their stratigraphic range do not have anomalously high scores, and are in fact distributed throughout the range of possible scores, suggesting that extinction estimates are not biased with respect to size of family.

Extinction rate is skewed towards low values with many families having quite low rates (note that genera confined to a single interval are omitted from the calculation following Foote [12]). High values of indicate high extinction rate in the family, which we hypothesize should correlate with higher risk of extinction in a species within that family, so we do not invert .

Past extinction rates cannot be calculated for individual species, and the fossil record is too incomplete to calculate extinction rates within genera across the entire Bivalvia. Accordingly, we use extinction rates of genera, aggregated into families. In bivalves, as in most fossil invertebrates, the stratigraphic ranges of genera are much better documented than that of species [13]; morphologically defined bivalve genera have been found to have macroevolutionary and macroecological properties highly correlated with genera defined on molecular grounds, so that paleontological and present-day units are likely to be consistent. Families represent a level of aggregation that is a compromise between phylogenetic resolution, taxonomic stability and sufficient numbers within units. Extinction rates of bivalve genera are significantly clustered within families [13] indicating that families can be treated as relatively cohesive units in terms of extinction risk.

Pairwise Spearman’s rank-order correlations between the contributing variables in PERIL are presented in Table S1. Comparisons of the use of different threshold levels are shown in Figure S2. Both figures show raw counts of species in cells, rather than proportions, for clarity.

Because of the range-scaling, PERIL is a relative, not absolute, measure of risk. Species are assessed as being at greater or lesser risk than other species in the dataset under consideration: a PERIL score of 0.5 in one analysis is not equivalent to a PERIL score of 0.5 in a separate analysis.

POST-PLIOCENE SURVIVORSHIP:

We tested PERIL scores using two different datasets: Pliocene California [11] and, because temporal resolution is more completely available there, Late Pliocene New Zealand ([www.fred.org.nz](http://www.fred.org.nz)). We calculate extinction rates from the K/Pg to the end-Pliocene and thus calculate PERIL as it would have been during the Pliocene. This way, we can calculate PERIL for the bivalves of the Pliocene as it would have been while they were alive, and then see if those with high PERIL scores are extinct by the Recent.

We used logistic regression to conduct a survivorship analysis for each fauna and compared the fit of each of the two contributing variables and the PERIL metric itself (see text of paper).

WEIGHTING:

As implemented here, PERIL is constructed with equally-weighted parameters. This assumes that all parameters contribute equally to risk, an assumption that may be violated to a greater or lesser extent depending on the fauna under study. It would be possible to weight PERIL based on, for example, the predictions from the model results of either of the two Pliocene logistic regressions. However, doing so assumes that the drivers of extinction (and therefore the relative importance of the contributory parameters) from the Pliocene are the same as those at play today. Weighting by past extinction is also sensitive to the choice of dataset – Figure 1 of the main paper shows why. Even though both datasets are the same age, the relative contribution of PERIL parameters differs between them.

To illustrate how these differences can affect the end result of using fossil datasets to provide a weighting scheme, we used glm.predict in R to find extinction probabilities for the modern dataset based on first the California Pliocene, and then the New Zealand Pliocene. When compared to the equal-weights PERIL, the results are different between the two weighted sets: California Pliocene-weights PERIL is highly correlated to equal-weights PERIL (cor = 0.89) and New Zealand Pliocene-weights PERIL is only moderately correlated to equal-weights PERIL (cor = 0.53) using a Pearson’s product-moment correlation test. Figure S4 shows the difference in graphical form.

Given that our focus in this paper is to assess extinction risk in the modern fauna, the drivers of which have no precise analogue in the fossil record, and given that we have shown that an equal-weights formulation of PERIL is capable of recovering extinction-risk signal in two different Pliocene datasets, we use equal-weights PERIL to examine the modern fauna, as the most parsimonious option.

SIZE SELECTIVITY:

To examine the putative relationship between size and PERIL score in Bivalvia, we used a Pearson’s product-moment correlation test across the entire modern Bivalvia dataset, and recovered a weakly negative correlation (-0.13, p=<2.2e-16). As an additional test, we thresholded PERIL scores at the 80th percentile and used a two-sample Kolmogorov-Smirnov test for size-selectivity in PERIL scores. Across all of Bivalvia, species above the 80th percentile for PERIL scores are significantly smaller than those below the threshold (p= < 2.2e-16) (Fig. S5).

Because of the phylogenetic clumping effect of the extinction rate parameter in the PERIL metric, we also ran the same test for each family individually (all analysed families having been independent for at least 50 Myr and most for >100 Myr), excluding families with fewer than two instances of either above or below the 80th percentile threshold. Most families do not have a significant difference in body size between those above and below the 80th percentile PERIL score threshold, but those that do are at significantly greater risk of extinction at *small* body sizes. (Fig. S5)

DISTRIBUTION OF PERIL SCORES ACROSS HIGHER CLADES:

Living species of marine bivalves with PERIL scores over the 80th percentile are not entirely randomly distributed phylogenetically (Fig. S1), but because of the use of family-level rates of extinction to calculate PERIL, this is unsurprising. A chi-squared test of the three-parameter PERIL metric across the orders within Bivalvia, does not find a significant relationship between PERIL and order.

To test for phylogenetic signal (Blomberg’s K) above the family level, we used the Combosch et al [14] family level phylogeny for Bivalvia. Seventy-one of the families included in that tree have PERIL data. Owing to the degree of paraphyly at the family level in the tree, we pruned at random all but one tip within each family, and repeated the analysis 100 times. In this way we avoided the spurious creation of close relatives that have their PERIL scores based on the same fossil data. PERIL does not exhibit significant phylogenetic signal in any of the replicates (*p* between 0.3 and 0.5). This approach has low power, but does not spuriously inflate phylogenetic signal in PERIL.

FIGURES AND TABLES:

Table S1: Spearman correlation values for the component variables of PERIL:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Extinction rate | Geographic range | Thermal niche |
| Extinction rate | 1 |  |  |
| Geographic range | -0.081 | 1 |  |
| Thermal niche | -0.015 | 0.665 | 1 |



Figure S1: The effect of using convex hulls or convex hulls clipped to shelf to calculate PERIL scores for marine Bivalvia. Each panel represents a clade, each ‘bar’ of points on the Y axis within each panel is a family (not labelled, for clarity), and each point is one species. Points coloured black are species over the 80th percentile PERIL score. The X axis is log body size. A: PERIL score with full convex hulls. B: PERIL score with convex hulls clipped to 200m shelf depth. Geographic range has a slightly greater buffering effect, unsurprisingly, when larger ranges are used (compare density of dark colors between top and bottom rows), but the effect is not large.



Figure S2: Effects of using different thresholds for PERIL scores, illustrated using raw counts of species over the given threshold in each cell. Breaks are quantiles. A. Using the 80th percentile threshold as in the main text. B. Using a threshold derived by finding the PERIL score of *Tridacna derasa*, the species of bivalve assessed as ‘Vulnerable’ by the IUCN with the lowest PERIL score. C. Using a 50th percentile threshold. There is little functional difference between B and C, although this would change if, as more species of bivalve are assessed by the IUCN, we correspondingly change the ‘Vulnerable’ threshold to use the lowest ‘Vulnerable’ IUCN score.



Figure S3: Subsets of the PERIL parameters for the Antarctic (solid) and Arctic (dashed) regions. A: Geographic range size. B: Extinction rate. C: Thermal niche. D: PERIL score (Geographic and temperature range parameters are reversed for risk calculation – a value of 1 is a small range, a value of 0 indicates a wide range). Antarctic taxa have much narrower thermal tolerances than Arctic taxa. Their wide geographic ranges are circumpolar but restricted to the Southern Ocean, whereas Arctic taxa have often even larger ranges that encompass temperate regions as well. The X axis of 0-1 is shared by all panels.



Figure S4: Two plots of modern Bivalvia by equal-weights PERIL score on the X axis and weighted PERIL score on the Y axis – on the left, weighted by New Zealand Pliocene data and on the right, by California Pliocene data. The distributions of points and the strength of correlation between the two different weighting schemes is different.



Figure S5: Boxplots illustrating Kolmogorov-Smirnov tests of log bivalve body size above and below the 80th percentile of PERIL scores. A: for all of Bivalvia. B: for the families in which there was a significant relationship between body size and high PERIL score. Species are plotted as grey points in facets of panel B, with a horizontal jitter for clarity. In all significant cases, smaller body sizes are associated with higher PERIL scores. Horizontal lines within boxplots indicate medians.

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