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Modelling determinants of extinction across two Mesozoic hyperthermal events

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The Late Triassic and early Toarcian extinction events are both associated with greenhouse warming events triggered by massive volcanism. These Mesozoic hyperthermals were responsible for the mass extinction of marine organisms and resulted in significant ecological upheaval. It has, however, been suggested that these events merely involved intensification of background extinction rates rather than significant shifts in the macroevolutionary regime and extinction selectivity. Here, we apply a multivariate modelling approach to a vast global database of marine organisms to test whether extinction selectivity varied through the Late Triassic and Early Jurassic. We show that these hyperthermals do represent shifts in the macroevolutionary regime and record different extinction selectivity compared to background intervals of the Late Triassic and Early Jurassic. The Late Triassic mass extinction represents a more profound change in selectivity than the early Toarcian extinction but both events show a common pattern of selecting against pelagic predators and benthic photosymbiotic and suspension-feeding organisms, suggesting that these groups of organisms may be particularly vulnerable during episodes of global warming. In particular, the Late Triassic extinction represents a macroevolutionary regime change that is characterised by (i) the change in extinction selectivity between Triassic background intervals and the extinction event itself; and (ii) the differences in extinction selectivity between the Late Triassic and Early Jurassic as a whole.

Key words: mass extinction, palaeoecology, modelling, Mesozoic, hyperthermal

1. Introduction

The Late Triassic to Early Jurassic interval contains two major extinction events: the Late Triassic mass extinction (LTE; c.201Ma) [1] and the early Toarcian extinction (EToE; c.187Ma) [2]. The LTE is recognised as the second largest marine biodiversity loss [3] and third biggest ecological crisis of the Phanerozoic [4], resulting in a global reef crisis [5], the most severe extinction of scleractinian corals [6, 7], significant extinctions amongst ammonoids [8], bivalves [9] and marine vertebrates [10], and the final demise of the conodonts [11]. By comparison, the EToE was smaller in magnitude, but records a similar pattern of selective losses, with an associated reef crisis [5], high levels of extinction amongst bivalves [12] and ammonoids [13], and the collapse of both benthic and pelagic marine ecosystems [7, 8]. Both of these events are associated with, and likely caused by, elevated atmospheric CO_2 levels and global warming [14-21]; i.e. they are hyperthermals. In each case, eruptions of Large Igneous Provinces (LIPs) probably caused the rise in CO_2 [18, 20-25], with proposed extinction drivers including rapid warming [14-17, 20, 26], ocean anoxia [16, 17, 26], and ocean acidification [27-29] as a direct result of the volcanic greenhouse gas emissions.

Several biological and ecological traits appear to have been selected against during the LTE, such as possessing a heavily calcified skeleton [27], inhabiting reef and/or inshore environments [30, 31], and residing at tropical latitudes [31, 32]. The greatest reduction in both taxonomic and functional richness occurred amongst sessile suspension-feeding guilds, particularly those dwelling in tropical reefs in the Panthalassa Ocean [31]. Despite this evidence for apparent selectivity during the LTE hyperthermal, it has been claimed that there was little change in “macroevolutionary regime” [30] compared to the rest of the Late Triassic and Early Jurassic, and that the LTE simply reflects intensification of the high rates of background extinction already experienced through the Late Triassic [30, 33, 34]. There has been less research on selectivity during the EToE hyperthermal, although there is some evidence for loss of reef taxa [5], selection against endemic taxa [12], the motile benthos [35], infaunal organisms [12, 17, 35, 36], as well as higher levels of extinction in the restricted basins of northwest Tethys, northeast Panthalassa [35], and the Boreal Ocean [2, 36] as well as in the southern hemisphere [37]. Whether this represents a macroevolutionary regime shift compared to Jurassic background extinction is unknown.

Here, we provide the first multivariate analysis of ecological selectivity during the Late Triassic and Early Jurassic, in order to determine whether there are any substantial differences between the LTE and EToE hyperthermal events and the periods of normal background extinction, and hence whether a shift in macroevolutionary regime occurred. A macroevolutionary regime shift is recognised when the suite of traits that promote extinction or survivorship are different, and particularly when the direction of selectivity changes so that traits that conferred survivorship during background times become an extinction risk [38]. We apply a generalised linear modelling (GLM) methodology to the largest and most comprehensive global database yet analysed in order to assess the relative importance of a number of intrinsic and extrinsic ecological variables as determinants of extinction in marine ecosystems. We aim to test the following hypotheses: (i) do certain ecological variables (e.g. latitudinal distribution, habitat preference, feeding mode and calcification) correlate with higher extinction risk during the LTE and EToE hyperthermal events; (ii) are similar trends recorded in both past hyperthermals despite differences in starting conditions and magnitude; and (iii) are similar trends recorded during background times, or do the LTE and EToE hyperthermals represent significantly different extinction selectivity?

2. Methods

We utilised a database of fossil occurrences of Middle Triassic to Middle Jurassic (Ladinian-Aalenian) marine animal genera collated from the Paleobiology Database (PaleoDB) [39, 40].

The total dataset comprises 55,428 occurrences of 2,621 genera, which is more than double the number that was available for previous analyses, e.g. [30, 32]. Each genus was then classified according to a number of extrinsic (i.e. abiotic) and intrinsic (i.e. biotic) ecological variables: (Table 1; see [31] for detailed download, vetting, and classification information). Proportional generic extinction rates were calculated and plotted at the stage level for guilds of fossil organisms defined by each ecological variable (Table 1). In order to account for biases brought about by uneven sampling across space and through time, we applied a subsampling protocol to standardize proportional extinction on the basis of the number of fossil occurrences. All variables were subsampled to $n = 250$ per stage, for 1000 iterations apart from feeding, which was subsampled to $n = 75$, due to the increased number of variable arguments and thus reduced sample sizes after splitting occurrences via feeding mode. Lightly calcified taxa, polar latitude, boreal ocean and reef taxa all fall short of the subsampling requirement for at least one of the time bins and are, therefore, not plotted in the univariate time series. However, when amalgamated with the other variables for the multivariate analyses, they provide sample sizes that are sufficient for the GLM analyses.

Multiple ecological variables are not independent of one another in terms of proportional extinction through time, therefore it is essential to test their effects on extinction within a multivariate framework. For example, pelagic taxa within the database are predominantly predatory and fast-moving as the majority of pelagic taxa are vertebrates or cephalopods. Therefore, it is impossible to determine which, if any, of these three variables is influencing extinction rates in a univariate analysis. We applied GLMs with a binomial distribution and a logit link function (i.e. multiple logistic regression models) to test the effects of multiple ecological variables on proportional generic extinction through the study interval [41]. The major extinction episodes of the LTE (Rhaetian/Hettangian) and EToE (Pliensbachian/Toarcian) were analysed separately and compared to the other stage boundaries which, together, are treated as representing the background intervals of the Triassic and Jurassic. However, because the binomial models were strongly underdispersed, we then used quasibinomial models and estimated the dispersion parameter from the data [42]. Underdispersal, where the variance is less than the nominal mean [43], can lead to over-conservatism and thus can result in type II errors. We applied the GLMs to two datasets: (i) including all the ecological variables, and (ii) a separate dataset compiled without the depositional setting variable, because reliable depositional setting data only exist for around 50% of the fossil occurrences in the entire data set. A number of model runs were carried out with different variable combinations for each of the four broad time intervals: Triassic background (Ladinian-Carnian, Carnian-Norian, Norian-Rhaetian); LTE (Rhaetian-Hettangian); Jurassic background (Hettangian-Sinemurian, Sinemurian-Pliensbachian, Toarcian-Aalenian); and EToE (Pliensbachian-Toarcian). Model selection was carried out by using the drop1() command in R, which drops one explanatory variable in turn and each time applies an analysis of deviance test (F-test) [41]. The data for the GLMs were not subsampled, but any ecological guilds with consistently low sample sizes (<10 occurrences per bin) were omitted from the analyses. All analyses were carried in R v.3.4.3 [44].

3. Results

(a) Univariate time series ~~analysis~~

The data show clear differences in extinction magnitude and selectivity between the hyperthermals and background intervals (Figure 1). For many, but not all variables (e.g. infaunal taxa at EToE, moderate calcifiers at LTE, mid-latitude taxa at LTE), extinction magnitude is greater during the hyperthermals than during their respective background times, as expected, and the pattern of relative selectivity remains the same (e.g. Figure 1A, B). During the LTE, however, feeding, calcification, latitude and ocean basin all record different patterns of selectivity compared to the Triassic background (Figures 1C-F). Photosymbiotic taxa suffered a substantially greater extinction during the LTE than during Triassic background periods, overtaking suspension- and deposit-feeders in relative extinction risk (Figure 1C). Likewise, heavily calcified taxa and those that live in the tropics and Panthalassa record the greatest extinction magnitudes during the LTE hyperthermal, which represents a marked shift in selectivity compared to the Triassic background (Fig. 1D-F). In contrast, the only similar shift in selectivity during the EToE, compared to the Jurassic background, occurs with latitude, with mid-latitude taxa showing greater extinction risk than tropical taxa during the hyperthermal (Figure 1E). With a few exceptions, remaining variables all increase during the EToE event, suggesting the event mainly represents an intensification of Jurassic background extinction rates.

Unexpectedly, there also appear to be clear differences in background extinction magnitude and selectivity between the Triassic and Jurassic. Background extinction appears much higher during the Triassic than the Jurassic, with extinction magnitude in some guilds being higher during the Triassic background intervals than during the EToE (Figure 1).

(b) Generalised linear modelling

Multivariate analyses demonstrate clear differences between background and mass extinction intervals (see Table 2 for GLM results). In general, the suite of ecological variables (see Table 1) analysed in this study explain far less of the recorded extinction during background times compared to the two hyperthermal events. During the Triassic background interval, depositional setting is the only significant predictor of extinction, and only in the single model that considers just the set of extrinsic factors. This is due to reef taxa having significantly lower extinction risk than taxa that live in other settings. During the Jurassic background interval, when all ecological variables are considered, motility, palaeo-ocean basin, and depositional setting are all significant predictors of extinction, with pelagic taxa and taxa residing in the Tethys Ocean having higher extinction and reef dwellers having lower extinction. The best fitting model identifies only palaeo-ocean (i.e. Tethys) and depositional setting (reefs) as being significant predictors of extinction. The only other model run that identifies a significant predictor of extinction is the one that considers just the extrinsic ecological variables. In that case, palaeo-oceanic basin is again identified as having a significant bearing on extinction, due to the higher extinction in Tethys. In contrast to the background times, during the LTE and EToE events, many more model runs identify significant ecological predictors of extinction. Furthermore, those variables that are identified as being significant are different to the ones identified during the background times.

During the LTE, feeding or latitude are the only variables identified as being significant predictors of extinction. Latitude alone significantly predicts extinction when (a) all ecological variables are considered and (b) when only extrinsic factors are considered, using the smaller dataset that includes depositional setting. In each case, taxa residing at tropical latitudes show significantly higher extinction than those inhabiting higher latitudes. In contrast, feeding is identified as a significant predictor of extinction in two other model runs, but only using the expanded dataset that excludes depositional setting. In both cases, where (a) all variables or (b) just the intrinsic ones are considered, excluding depositional setting, the best-fitting models identify predatory, photosymbiotic and suspension-feeding habits as being significant positive predictors of extinction.

For the EToE event, significant predictors of extinction are only identified in model runs that utilise the expanded dataset that excludes depositional setting. When all variables, apart from depositional setting, are considered, five factors (motility, feeding, latitude, palaeo-ocean basin and calcification) all appear to significantly predict extinction. Model selection reveals that the best-fitting model identifies just feeding and palaeo-ocean basin, with photosymbiotic taxa and taxa residing in the Boreal Ocean predicting significantly higher extinction than other categories within those variables. When considering just the extrinsic ecological variables, no variable predicts extinction. However, when we use the expanded data set with no depositional environment data, palaeo-ocean basin significantly predicts extinction with Boreal taxa having higher extinction and, after model selection, Panthalassa taxa show lower extinction than both Boreal and Tethys taxa. When considering only the intrinsic ecological variables, no variable predicts extinction until we use the expanded data set with no depositional environment variable, after which, feeding significantly predicts extinction, with photosymbiotic taxa showing higher extinction than other feeding guilds.

4. Discussion

There are marked changes in extinction selectivity between periods of normal background and the two hyperthermals (Figure 1; Table 2). Extinction magnitude is higher in most ecological guilds during the LTE and, although the EToE generally displays higher levels of extinction than Jurassic background intervals, for some guilds Triassic background extinction is higher than it is during the EToE (Figure 1). Not only do the LTE and EToE events represent an increase in extinction intensity above respective Triassic and Jurassic background rates but, more importantly, and contrary to previous claims [30], there are ~~stark~~ differences in extinction selectivity between times of both background and mass extinction, and between Triassic and Jurassic intervals in general. It is also evident that background extinction was higher in the Late Triassic, prior to the LTE hyperthermal, than it was during the Early Jurassic, in the aftermath of the mass extinction [30, 33] (Figure 1).

A tropical extinction peak characterises the LTE, whereas mid-latitude taxa display higher extinction during the EToE and during background times. Although the LTE data are consistent with expectations that an episode of global warming should result in extinction being concentrated in the tropics [32, 45], the EToE data suggest that high tropical extinction may not be ubiquitous to all hyperthermal events. Additionally, higher tropical extinction across the LTE is only significant in the models where the data are also partitioned by depositional setting, suggesting that some of the tropical extinction signal is rooted in a particular depositional setting, most probably tropical reefs. Although extinction is higher in the mid-latitudes through the EToE [31], latitude does not significantly predict extinction, suggesting that the higher rates of extinction in the mid-latitudes during the EToE may be governed by other factors such as ocean basin or that the warming was not as intense as during the LTE [2].

The peak in extinction in Panthalassa during the LTE is not replicated in the Tethys Ocean, despite the Tethys showing higher background extinction rates. However, modelling does not show palaeo-ocean as a significant predictor of extinction across the LTE, suggesting that this peak is a result of other factors, such as the high proportion of tropical data in Rhaetian-Hettangian Panthalassa. In contrast, Panthalassa displays significantly lower extinction than the Tethys and Boreal oceans during the EToE. The EToE appears to be characterised by raised extinction rates in the Tethyan and Boreal Oceans. This might be expected given the higher prevalence of restricted basins, particularly in north-western Tethys, when considering the repeated dysoxic conditions in the Early Jurassic, of which the EToE is the most severe [2, 26]. However, this pattern persists in light of evidence for prolonged anoxia and extinction in some Panthalassa basins [35]. It is also likely that the mid to high palaeolatitude of the Boreal and north-western Tethys basins of Europe are driving the mid-latitudinal peak in extinction intensity through the EToE.

Although difficult to show because of very small sample sizes, the reef crises at the LTE and EToE are evident in the data by the crashes in reef taxa abundances [31] and diversity [7, 31]. The reef crises are also highlighted by the high levels of extinction witnessed amongst photosymbiotic taxa and suspension feeders across the LTE, and photosymbiotic taxa across the EToE. In contrast to the extinction events, background extinction for reef taxa and photosymbiotic feeders was lower than those taxa residing in other depositional settings and feeding via different strategies. This highlights a major change in extinction selectivity during both the LTE and EToE and permits the rejection of the idea that the LTE is merely an intensification of background extinction seen during the Late Triassic [30].

Tiering does not appear to have an influence on extinction selectivity across the LTE, despite there being an increase in extinction magnitude across all guilds. However, the impact of the mass extinction on level-bottom communities was particularly short-lived with full recovery occurring by the upper Hettangian [46-48]. Therefore, the temporary disappearance of the deep infaunal and erect benthic tiers in the earliest Hettangian recorded by previous studies [46, 48], would not be detected here because of the coarser nature of the stage-level time bins. There is some evidence of increased extinction risk to pelagic taxa during intervals of background and mass extinction, possibly related to high turnover of ammonoids and vertebrates, which also drives the consistently high levels of extinction in predatory taxa [13, 49]. We see a similar pattern in terms of motility, with no apparent selectivity across the LTE or during periods of background extinction. There is some weak evidence for selectivity against non-motile taxa across the EToE, although this is not significant in the best-fitting model. The lack of any selectivity against non-motile and epifaunal taxa across the LTE suggests that the mass extinction did not result in an indirect intensification of the Mesozoic Marine Revolution (MMR) as previously suggested [31] and these previously detected high levels of extinction amongst non-motile epifauna are a result of elevated extinction amongst photosymbiotic/suspension feeding guilds in reef environments, which are predominantly non-motile and epifaunal. Our analyses do detect higher levels of background extinction amongst non-motile and epifaunal taxa during the Late Triassic compared to the Early Jurassic. Crucially, however, motility and tiering do not predict extinction in the Late Triassic background interval. Therefore, we cannot find solid evidence of selectivity against non-motile epifauna during a time period (Carnian-Norian) that has been identified as key to the MMR [50]. The cause of higher Triassic background extinction versus Jurassic background extinction is likely a result of the high faunal turnover associated with the Carnian Pluvial Event [51], rather than the MMR.

There is a peak in extinction amongst heavily calcified taxa during the LTE whereas during background periods and the EToE heavy calcifiers display lower extinction than moderate calcifiers. Although this may support the hypotheses that hypercapnia [52] and/or ocean acidification may have played a role in extinction during the LTE [5, 27], our modelling results show no evidence that calcification was a significant predictor of extinction during either the LTE or the EToE hyperthermal. The multivariate analyses show no evidence of selectivity against heavy calcifiers during the LTE and only very weak evidence at the EToE, although this result is non-significant in the best-fitting model. Our analyses support previous studies that found no strong link between calcification grade and extinction selectivity [30]. Therefore, it seems unlikely that hypercapnia or ocean acidification were the main or sole drivers of extinction during the LTE and EToE hyperthermals.

The LTE and, albeit to a lesser extent, the EToE are both characterised by ~~marked~~ shifts in extinction selectivity away from the macroevolutionary regimes of the Late Triassic and Early Jurassic background intervals. Background extinction rates in the Late Triassic were higher than those of the Early Jurassic [30, 33], but the LTE was not merely an intensification of those background rates as has been previously suggested [30]. Extinction selectivity changed dramatically across the LTE with the initiation of strong selection against tropical taxa with photosymbiotic, suspension or predatory feeding strategies. This pattern is consistent with a warming-driven tropical reef crisis. We find little evidence to support previous ideas that palaeo-ocean basin [31] or calcification [27] were important determinants of extinction at the

LTE. Despite differences in starting conditions, species involved, and magnitudes of global warming and environmental change, the LTE and EToE show some common patterns of selectivity. Both events record strong extinction selectivity against pelagic predatory guilds and against benthic photosymbiotic and suspension feeding organisms, suggesting that these groups of marine organisms may be particularly vulnerable during episodes of global warming. The effects of the LTE were most severe in the tropics whilst the EToE was felt more severely at higher latitudes, which may reflect differences in magnitude of environmental change or starting conditions, such as palaeogeography. However, the EToE shares some common selectivity patterns with periods of Jurassic background extinction, i.e. high extinction in the Tethys Ocean, suggesting that the EToE may have represented an intensification of Jurassic background extinction, albeit with a switch to selecting against reef inhabiting photosymbiotic taxa. The LTE shows a clear change in extinction selectivity and thus macroevolutionary regime which is characterised not only by a shift in extinction selectivity from Triassic background intervals across the LTE but also by the difference in extinction selectivity between the Late Triassic and Early Jurassic as a whole.

Data accessibility. The data set used in the statistical analyses and the statistical results are available in the Dryad Digital Repository: doi:10.5061/dryad.6t461hq).

Author's contributions. A.M.D., W.J.F. and R.J.T. conceived the study. A.M.D. and W.J.F. collected the data. S.A and J.S. wrote analytical code and advised on analytical methods. A.M.D. analysed the data. A.M.D. led the writing of the manuscript and W.J.F., S.A. and R.J.T. contributed to the writing and editing of the manuscript and preparation of figures.

Competing interests. We declare we have no competing interests.

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Table 1. Summary of intrinsic and extrinsic ecological determinants of extinction.

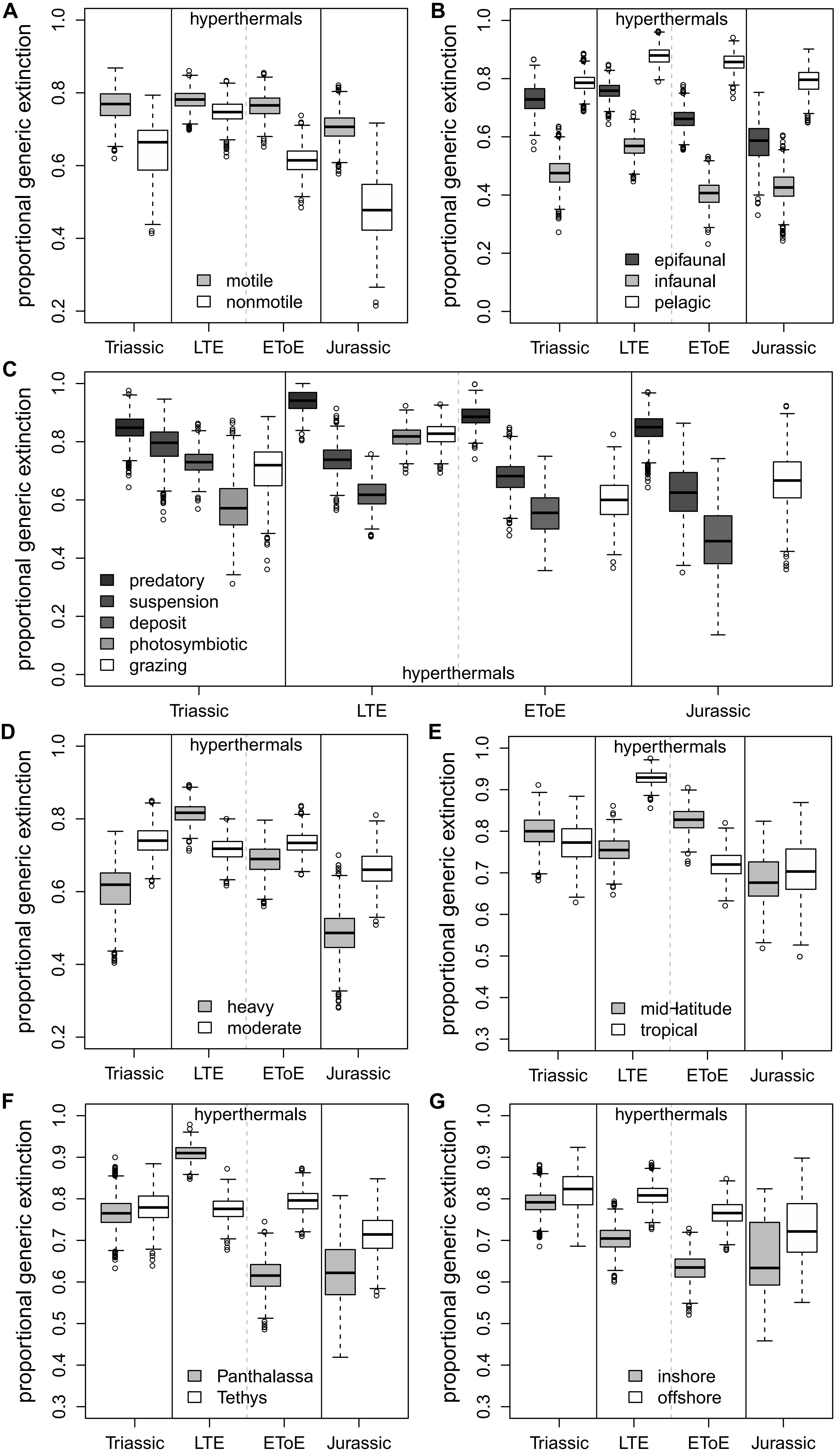
	Determinant	Levels	Ref.
Intrinsic	Motility	motile non-motile	[31, 53]
	Tiering	pelagic epifaunal infaunal	[31, 53]
	Feeding	suspension deposit/mining grazing predatory photosymbiotic	[31, 53]
	Calcification	heavy moderate light	[31, 52]
Extrinsic	Latitude	polar (>60˚) mid-latitude (30-60˚) tropical (<30˚)	[31, 39]
	Palaeo-ocean basin	Panthalassa Tethys Boreal	[31, 39]
	Environment	Onshore Offshore Reef	[31, 39]

Table 2. Summary of full and best fitting GLMs for predicting extinction through hyperthermal mass extinctions and periods of background extinction. LTE = Late Triassic mass extinction; EToE = early Toarcian extinction. “Full model” includes all variables (see electronic supplementary material for model definitions). “Best model” is the best fitting model following model selection procedure described in methods section. “Significant variables” identifies variables identified as significantly determining extinction; “significant arguments” identifies which arguments of a particular variables show significantly higher (+) or significantly lower (-) extinction than other arguments of that variables. “Explained deviance” = (null deviance-residual deviance)/null deviance; provides estimate of goodness-of-fit of model to extinction variable. Where no variables are listed, no variables significantly determine extinction.

	Model	**Full model**			**Best model**		
		significant variables	**significant arguments**	**explained deviance**	**significant variables**	**significant arguments**	**explained deviance**
LTE	all	latitude	tropical (+)	0.78	latitude	tropical (+)	0.32
	all no env	feeding	predatory (+) photosymbiotic (+) suspension (+)	0.60	feeding	predatory (+) photosymbiotic (+) suspension (+)	0.43
	extrinsic	latitude	tropical (+)	0.47	latitude	tropical (+)	0.32
	extrinsic no env	-	-	0.18	-	-	-
	intrinsic	-	-	0.40	-	-	-
	intrinsic no env	feeding	predatory (+) photosymbiotic (+)	0.48	feeding	predatory (+) photosymbiotic (+) suspension (+)	0.43
EToE	all	-	-	0.68	-	-	-
	all no env	motility feeding latitude basin calcification	non-motile (+) photosymbiotic (+) polar (-) Boreal (+) light (-)	0.71	feeding basin	photosymbiotic (+) Boreal (+)	0.5
	extrinsic	-	-	0.23	-	-	-
	extrinsic no env	basin	Boreal (+)	0.17	basin	Panthalassa (-)	0.14
	intrinsic	-	-	0.44	-	-	-
	intrinsic no env	feeding	photosymbiotic (+)	0.48	feeding	photosymbiotic (+)	0.33
Triassic background	all	-	-	0.34	-	-	-
	all no env	-	-	0.27	-	-	-
	extrinsic	environment	reef (-)	0.19	environment	reef (-)	0.19
	extrinsic no env	-	-	0.03	-	-	-
	intrinsic	-	-	0.31	-	-	-
	intrinsic no env	-	-	0.23	-	-	-
Jurassic background	all	motility basin environment	pelagic (+) Tethys (+) reef (-)	0.35	basin environment	Tethys (+) reef (-)	0.16
	all no env	-	-	0.28	-	-	-
	extrinsic	basin	Tethys (+)	0.16	basin	Tethys (+)	0.07
	extrinsic no env	-	-	0.03	-	-	-
	intrinsic	-	-	0.18	-	-	-
	intrinsic no env	-	-	0.25	-	-	-

Figure legends

Figure 1. Boxplots across all subsamples of proportional generic extinction per ecological variable through Late Triassic background periods (Triassic), the Late Triassic mass extinction (LTE), the early Toarcian extinction (EToE), and Early Jurassic background periods (Jurassic) by (A) motility; (B) tiering; (C) feeding; (D) calcification; (E) latitude; (F) ocean basin; (G) depositional setting. Proportional generic extinction is calculated from a subsample of n=250 across 1,000 iterations except for feeding which is calculated from a subsample of n=75 across 1,000 iterations. The solid black lines inside the boxes represent the medians, the top and bottom edges of the boxes correspond to the first and third quartiles, and whiskers represent the lowest and highest subsampled values within 1.5 times the interquartile range. Points outside the whiskers are outliers.


A
proportional generic extinction
hyperthermals
motile
nonmotile
Triassic
LTE
EToE
Jurassic
0.2
0.4
0.6
0.8
1.0
B
proportional generic extinction
hyperthermals
epifaunal
infaunal
pelagic
Triassic
LTE
EToE
Jurassic
0.0
0.2
0.4
0.6
0.8
1.0
C
proportional generic extinction
predatory
suspension
deposit
photosymbiotic
grazing
hyperthermals
Triassic
LTE
EToE
Jurassic
0.0
0.2
0.4
0.6
0.8
1.0
D
proportional generic extinction
hyperthermals
heavy
moderate
Triassic
LTE
EToE
Jurassic
0.2
0.4
0.6
0.8
1.0
E
proportional generic extinction
hyperthermals
mid-latitude
tropical
Triassic
LTE
EToE
Jurassic
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
F
proportional generic extinction
hyperthermals
Panthalassa
Tethys
Triassic
LTE
EToE
Jurassic
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
G
proportional generic extinction
hyperthermals
inshore
offshore
Triassic
LTE
EToE
Jurassic
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

Supplementary Material

Modelling determinants of extinction across two Mesozoic hyperthermal events

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Supplementary methods

Table S1: List of variables in each GLM. “no env” refers to models run without depositional environmental setting data which is only present for around 50% of the data set. Therefore, the removal of the depositional environmental setting doubles the sample size.

Model	Determinants
all	motility; tiering; feeding; calcification; latitude; palaeoocean basin; depositional setting
all no env	motility; tiering; feeding; calcification; latitude; palaeoocean basin
extrinsic	latitude; palaeoocean basin; depositional setting
extrinsic no env	latitude; palaeoocean basin
intrinsic	motility; tiering; feeding; calcification
intrinsic no env	motility; tiering; feeding; calcification

Supplementary results

GLM outputs

LTE

Model = all

```
> GLM_LTE_A1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fENVIRONMENT +
+ fCALCIFICATION,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_A1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fENVIRONMENT + fCALCIFICATION, family =
quasibinomial,
    data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.52039  -0.07450   0.00003   0.15316   0.55019

Coefficients: (1 not defined because of singularities)
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)               2.6340     1.5901   1.656   0.1320
fMOTILITYnonmotile       -0.6121     0.7194  -0.851   0.4170
fTIERINGinfaunal         -1.0261     0.6461  -1.588   0.1468
fTIERINGpelagic          -2.2947     1.8030  -1.273   0.2350
fFEEDINGphotosymbiotic    1.6102     2.0644   0.780   0.4554
fFEEDINGpredatory             NA         NA      NA       NA
fFEEDINGsuspension        0.7476     0.8971   0.833   0.4262
fLATITUDET                2.9924     1.1182   2.676   0.0254 *
fBASINTethys             -0.9580     0.9703  -0.987   0.3493
fENVIRONMENTOffshore      1.1036     0.7170   1.539   0.1581
fENVIRONMENTReef         16.1132  3723.9890   0.004   0.9966
fCALCIFICATIONmoderate   -1.7223     1.0296  -1.673   0.1287
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
(Dispersion parameter for quasibinomial family taken to be 0.1443989)

    Null deviance: 6.1229  on 19  degrees of freedom
Residual deviance: 1.3575  on  9  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 19
> # find best model
>
> drop1(GLM_LTE_A1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fENVIRONMENT + fCALCIFICATION
               Df Deviance F value   Pr(>F)
<none>              1.3576
fMOTILITY       1   1.4633  0.7010 0.424115
fTIERING        1   1.7343  2.4975 0.148485
fFEEDING        2   1.4873  0.4300 0.663196
fLATITUDE       1   3.1510 11.8898 0.007296 **
fBASIN          1   1.5097  1.0090 0.341381
fENVIRONMENT    2   1.7986  1.4619 0.281992
fCALCIFICATION  1   1.8601  3.3320 0.101236
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> # best model
>
> GLM_LTE_A1iii <- glm(extinction ~ fLATITUDE,
+ family = quasibinomial, data = LTE)
>
> summary(GLM_LTE_A1iii)

Call:
glm(formula = extinction ~ fLATITUDE, family = quasibinomial,
    data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.79806  -0.18099   0.08947   0.30075   0.81341
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)   
(Intercept)   0.9362     0.2806   3.336  0.00367 **
fLATITUDET    2.1372     0.8825   2.422  0.02623 * 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.207126)

    Null deviance: 6.1229  on 19  degrees of freedom
Residual deviance: 4.1803  on 18  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 6
```

Model = all no env

```
> GLM_LTE_B1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fCALCIFICATION,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_B1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING + 
    fLATITUDE + fBASIN + fCALCIFICATION, family = quasibinomial, 
    data = LTE)

Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-0.9482  -0.1619   0.1085   0.2678   0.7364  

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)  
(Intercept)             3.30683    1.90023   1.740   0.0965 .
fMOTILITYnonmotile     -0.16350    0.48100  -0.340   0.7373  
fTIERINGinfaunal        0.04299    0.51878   0.083   0.9347  
fTIERINGpelagic        -0.97680    1.26559  -0.772   0.4488  
fFEEDINGgrazing        -1.00009    1.39971  -0.715   0.4828  
fFEEDINGphotosymbiotic  2.28581    1.50753   1.516   0.1444  
fFEEDINGpredatory       3.24156    1.46390   2.214   0.0380 *
fFEEDINGsuspension      0.80595    0.79223   1.017   0.3206  
```

```
fLATITUDEP             -1.15779    1.14155  -1.014   0.3220
fLATITUDET              0.77683    0.48202   1.612   0.1220
fBASINPanthalassa      -2.38603    1.34792  -1.770   0.0912 .
fBASINTethys           -2.87926    1.46745  -1.962   0.0631 .
fCALCIFICATIONlight    -1.79362    1.26434  -1.419   0.1707
fCALCIFICATIONmoderate -1.03692    0.65945  -1.572   0.1308
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.2016485)

    Null deviance: 11.300  on 34  degrees of freedom
Residual deviance:  4.467  on 21  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 6

>
> # find best model
>
> drop1(GLM_LTE_B1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fCALCIFICATION
               Df Deviance F value  Pr(>F)
<none>              4.4670
fMOTILITY       1   4.4904  0.1099 0.74358
fTIERING        2   4.6018  0.3168 0.73189
fFEEDING        4   6.8103  2.7541 0.05507 .
fLATITUDE       2   5.2620  1.8687 0.17909
fBASIN          2   5.2717  1.8916 0.17566
fCALCIFICATION  2   5.1245  1.5455 0.23650
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>

> # best model
> GLM_LTE_B1iii <- glm(extinction ~ fFEEDING,
+ family = quasibinomial, data = LTE)
```

```
>
> summary(GLM_LTE_B1iii)

Call:
glm(formula = extinction ~ fFEEDING, family = quasibinomial,
    data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.94003  -0.24861   0.07654   0.30255   0.81753

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             -0.5878     0.6253  -0.940  0.35471
fFEEDINGgrazing         -1.0217     1.2975  -0.787  0.43724
fFEEDINGphotosymbiotic   3.6779     1.2119   3.035  0.00494 **
fFEEDINGpredatory        2.5197     0.7893   3.192  0.00330 **
fFEEDINGsuspension       1.5121     0.6580   2.298  0.02871 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1795301)

    Null deviance: 11.2997  on 34  degrees of freedom
Residual deviance:  6.4135  on 30  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Model = extrinsic

```
> GLM_LTE_A3ii <- glm(extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_A3ii)

Call:
glm(formula = extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
    family = quasibinomial, data = LTE)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7523  -0.1184   0.0339   0.3520   0.8552
```

```
Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)          7.396e-01  8.197e-01   0.902    0.381
fLATITUDET           1.933e+00  9.244e-01   2.090    0.054 .
fBASINTethys         7.801e-02  8.717e-01   0.089    0.930
fENVIRONMENTOffshore 2.407e-02  5.685e-01   0.042    0.967
fENVIRONMENTReef     1.884e+01  4.216e+03   0.004    0.996
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1914137)

    Null deviance: 6.1229  on 19  degrees of freedom
Residual deviance: 3.2701  on 15  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 19

> # find best model
>
> drop1(GLM_LTE_A3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN + fENVIRONMENT
             Df Deviance F value  Pr(>F)
<none>            3.2701
fLATITUDE     1   4.3804  5.0929 0.03937 *
fBASIN        1   3.2716  0.0070 0.93446
fENVIRONMENT  2   4.0752  1.8465 0.19191
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> # best model
>
> GLM_LTE_A3iii <- glm(extinction ~ fLATITUDE,
+ family = quasibinomial, data = LTE)
>
> summary(GLM_LTE_A3iii)
```

```
Call:
glm(formula = extinction ~ fLATITUDE, family = quasibinomial,
    data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.79806  -0.18099   0.08947   0.30075   0.81341

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.9362     0.2806   3.336  0.00367 **
fLATITUDET    2.1372     0.8825   2.422  0.02623 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.207126)

    Null deviance: 6.1229  on 19  degrees of freedom
Residual deviance: 4.1803  on 18  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 6
```

Model = extrinsic no env

```
> GLM_LTE_B3ii <- glm(extinction ~ fLATITUDE + fBASIN,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_B3ii)

Call:
glm(formula = extinction ~ fLATITUDE + fBASIN, family = quasibinomial,
    data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.41178  -0.28614   0.09095   0.42332   0.95988

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)         2.8905     1.4932   1.936   0.0624 .
fLATITUDEP         -0.8110     1.1499  -0.705   0.4861
fLATITUDET          0.8358     0.4875   1.714   0.0968 .
```

```
fBASINPanthalassa  -1.6740     1.4239  -1.176   0.2490
fBASINTethys       -2.3546     1.5076  -1.562   0.1288
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2688368)

    Null deviance: 11.2997  on 34  degrees of freedom
Residual deviance:  9.3068  on 30  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5

>
> # find best model
>
> drop1(GLM_LTE_B3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN
          Df Deviance F value Pr(>F)
<none>          9.3068
fLATITUDE  2  10.3885  1.7434 0.1922
fBASIN     2  10.2198  1.4715 0.2457
>
```

Model = intrinsic

```
> GLM_LTE_A4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_A4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = LTE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.71433  -0.26270   0.09925   0.32029   0.81238
```

```
Coefficients: (1 not defined because of singularities)
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)              2.7289     1.4630   1.865   0.0849 .
fMOTILITYnonmotile      -0.4503     0.8457  -0.532   0.6034
fTIERINGinfaunal        -0.4901     0.7625  -0.643   0.5315
fTIERINGpelagic          0.8460     1.5784   0.536   0.6010
fFEEDINGphotosymbiotic   1.5392     2.4689   0.623   0.5438
fFEEDINGpredatory            NA         NA      NA       NA
fFEEDINGsuspension       0.6659     0.9222   0.722   0.4831
fCALCIFICATIONmoderate  -1.9654     1.2570  -1.564   0.1419
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2485554)

    Null deviance: 6.1229  on 19  degrees of freedom
Residual deviance: 3.6698  on 13  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 6

>
> # find best model
>
> drop1(GLM_LTE_A4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              3.6698
fMOTILITY       1   3.7409  0.2521 0.6240
fTIERING        1   3.7737  0.3683 0.5544
fFEEDING        2   3.8385  0.2988 0.7467
fCALCIFICATION  1   4.5139  2.9904 0.1074
>
```

Model = intrinsic no env

```
> GLM_LTE_B4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = LTE)
```

```
> summary(GLM_LTE_B4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = LTE)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.8854  -0.2175   0.1099   0.2983   0.8137

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             0.05624    0.87501   0.064   0.9493
fMOTILITYnonmotile     -0.12162    0.47360  -0.257   0.7994
fTIERINGinfaunal       -0.28702    0.49595  -0.579   0.5680
fTIERINGpelagic        -0.76296    1.31530  -0.580   0.5671
fFEEDINGgrazing        -1.16221    1.41697  -0.820   0.4198
fFEEDINGphotosymbiotic  3.15546    1.43793   2.194   0.0377 *
fFEEDINGpredatory       3.37268    1.53674   2.195   0.0377 *
fFEEDINGsuspension      1.38256    0.75596   1.829   0.0794 .
fCALCIFICATIONlight    -1.68717    1.26360  -1.335   0.1938
fCALCIFICATIONmoderate -0.50346    0.57528  -0.875   0.3898
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2078436)

    Null deviance: 11.2997  on 34  degrees of freedom
Residual deviance:  5.8432  on 25  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5

>
> # find best model
>
> drop1(GLM_LTE_B4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
```

```
               Df Deviance F value Pr(>F)  
<none>              5.8432                 
fMOTILITY       1   5.8569  0.0588 0.8104  
fTIERING        2   5.9886  0.3111 0.7354  
fFEEDING        4   9.0390  3.4183 0.0232 *
fCALCIFICATION  2   6.2321  0.8320 0.4469  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> 
> # best model
> 
> GLM_LTE_B4iii <- glm(extinction ~ fFEEDING,
+ family = quasibinomial, data = LTE)
> summary(GLM_LTE_B4iii)

Call:
glm(formula = extinction ~ fFEEDING, family = quasibinomial, 
    data = LTE)

Deviance Residuals: 
     Min        1Q    Median        3Q       Max  
-0.94003  -0.24861   0.07654   0.30255   0.81753  

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)   
(Intercept)             -0.5878     0.6253  -0.940  0.35471   
fFEEDINGgrazing         -1.0217     1.2975  -0.787  0.43724   
fFEEDINGphotosymbiotic   3.6779     1.2119   3.035  0.00494 **
fFEEDINGpredatory        2.5197     0.7893   3.192  0.00330 **
fFEEDINGsuspension       1.5121     0.6580   2.298  0.02871 * 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1795301)

    Null deviance: 11.2997  on 34  degrees of freedom
Residual deviance:  6.4135  on 30  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

EToE

Model = all

```
> GLM_OAE_A1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fENVIRONMENT +
+ fCALCIFICATION,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_A1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fENVIRONMENT + fCALCIFICATION, family =
quasibinomial,
    data = OAE)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.4337  -0.1391   0.0000   0.2102   0.4509

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)              0.7777     1.1233   0.692   0.5031
fMOTILITYnonmotile       0.7891     0.5491   1.437   0.1785
fTIERINGinfaunal        -0.1401     0.4658  -0.301   0.7693
fTIERINGpelagic          1.1627     1.0537   1.103   0.2934
fFEEDINGgrazing          1.1905     0.7983   1.491   0.1640
fFEEDINGphotosymbiotic  -1.7160     1.2277  -1.398   0.1897
fFEEDINGpredatory        0.7080     0.9654   0.733   0.4787
fFEEDINGsuspension      -0.3624     0.7043  -0.515   0.6170
fLATITUDET              -1.0360     0.5591  -1.853   0.0909 .
fBASINTethys             0.8423     0.5712   1.475   0.1683
fENVIRONMENTOffshore    -1.3328     0.6372  -2.092   0.0605 .
fENVIRONMENTReef         3.3873     1.8921   1.790   0.1009
fCALCIFICATIONmoderate   0.1033     0.6401   0.161   0.8747
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1186548)

    Null deviance: 4.1787  on 23  degrees of freedom
Residual deviance: 1.3477  on 11  degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 5

>
> # find best model
>
> drop1(GLM_OAE_A1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fENVIRONMENT + fCALCIFICATION
               Df Deviance F value  Pr(>F)
<none>              1.3477
fMOTILITY       1   1.5974  2.0381 0.18117
fTIERING        2   1.4956  0.6036 0.56398
fFEEDING        4   2.0222  1.3763 0.30423
fLATITUDE       1   1.7801  3.5289 0.08705 .
fBASIN          1   1.6114  2.1526 0.17033
fENVIRONMENT    2   2.2438  3.6571 0.06058 .
fCALCIFICATION  1   1.3508  0.0252 0.87681
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> GLM_OAE_A1iii <- glm(extinction ~ fENVIRONMENT,
+ family = quasibinomial, data = post)
>
> summary(GLM_OAE_A1iii)

Call:
glm(formula = extinction ~ fENVIRONMENT, family = quasibinomial,
    data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.20688  -0.35287  -0.00746   0.35180   1.15096

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)           0.069080   0.205914   0.335    0.739
fENVIRONMENTOffshore -0.006514   0.308166  -0.021    0.983
```

```
fENVIRONMENTReef     -1.860839   1.175805  -1.583    0.119

(Dispersion parameter for quasibinomial family taken to be 0.3282142)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 22.425  on 55  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Model = all no env

```
> GLM_OAE_B1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fCALCIFICATION,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fCALCIFICATION, family = quasibinomial,
    data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.72266  -0.16491   0.01584   0.13465   0.39736

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)              1.5538     0.8060   1.928 0.065311 .
fMOTILITYnonmotile       0.6758     0.2645   2.554 0.017111 *
fTIERINGinfaunal        -0.3910     0.2695  -1.451 0.159156
fTIERINGpelagic          1.3641     0.7013   1.945 0.063097 .
fFEEDINGgrazing          0.9163     0.6374   1.438 0.162935
fFEEDINGphotosymbiotic   1.7089     0.7801   2.191 0.038023 *
fFEEDINGpredatory        0.2133     0.7339   0.291 0.773756
fFEEDINGsuspension      -0.1212     0.4878  -0.248 0.805786
fLATITUDEP              -1.2973     0.5271  -2.461 0.021108 *
fLATITUDET              -0.2105     0.2368  -0.889 0.382505
fBASINPanthalassa       -2.0205     0.5022  -4.023 0.000467 ***
fBASINTethys            -1.8369     0.5214  -3.523 0.001667 **
fCALCIFICATIONlight     -1.5820     0.7751  -2.041 0.051937 .
fCALCIFICATIONmoderate   0.2521     0.3502   0.720 0.478244
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.08575427)

    Null deviance: 8.2940  on 38  degrees of freedom
Residual deviance: 2.3843  on 25  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_OAE_B1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fCALCIFICATION
               Df Deviance F value   Pr(>F)
<none>              2.3843
fMOTILITY       1   2.9536  5.9686 0.021967 *
fTIERING        2   2.8716  2.5548 0.097824 .
fFEEDING        4   3.8265  3.7802 0.015446 *
fLATITUDE       2   2.9693  3.0667 0.064403 .
fBASIN          2   4.0320  8.6382 0.001406 **
fCALCIFICATION  2   3.0072  3.2653 0.054965 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> # motility, feeding, basin and calcification
>
> GLM_OAE_B1iii <- glm(extinction ~ fMOTILITY + fFEEDING +
+ fBASIN + fCALCIFICATION,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B1iii)

Call:
glm(formula = extinction ~ fMOTILITY + fFEEDING + fBASIN + fCALCIFICATION,
    family = quasibinomial, data = OAE)
```

```
Deviance Residuals: 
     Min        1Q    Median        3Q       Max  
-1.05867  -0.06024   0.06304   0.17024   0.47845  

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)   
(Intercept)              0.7819     0.7250   1.078  0.28975   
fMOTILITYnonmotile       0.5395     0.2818   1.914  0.06551 . 
fFEEDINGgrazing          1.0024     0.6641   1.509  0.14200   
fFEEDINGphotosymbiotic   1.9016     0.8129   2.339  0.02641 * 
fFEEDINGpredatory        1.3548     0.5620   2.411  0.02249 * 
fFEEDINGsuspension      -0.1287     0.5147  -0.250  0.80428   
fBASINPanthalassa       -1.4785     0.4084  -3.620  0.00111 **
fBASINTethys            -1.2531     0.4027  -3.112  0.00415 **
fCALCIFICATIONlight     -1.1713     0.7957  -1.472  0.15178   
fCALCIFICATIONmoderate   0.2469     0.3424   0.721  0.47666   
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1015277)

    Null deviance: 8.294  on 38  degrees of freedom
Residual deviance: 3.348  on 29  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4


> 
> drop1(GLM_OAE_B1iii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fFEEDING + fBASIN + fCALCIFICATION
               Df Deviance F value    Pr(>F)    
<none>              3.3480                      
fMOTILITY       1   3.7264  3.2771 0.0806257 .  
fFEEDING        4   6.9142  7.7223 0.0002299 ***
fBASIN          2   4.8737  6.6073 0.0043207 ** 
fCALCIFICATION  2   3.7888  1.9088 0.1664198    
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> # best model
> GLM_OAE_B1iv <- glm(extinction ~ fFEEDING + fBASIN,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B1iv)

Call:
glm(formula = extinction ~ fFEEDING + fBASIN, family = quasibinomial,
    data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.06388  -0.16613   0.02477   0.21597   0.51343

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)              0.9920     0.6327   1.568  0.12674
fFEEDINGgrazing          1.0024     0.7081   1.416  0.16656
fFEEDINGphotosymbiotic   2.1544     0.7617   2.828  0.00801 **
fFEEDINGpredatory        1.0702     0.5717   1.872  0.07039 .
fFEEDINGsuspension       0.0665     0.5207   0.128  0.89918
fBASINPanthalassa       -1.3316     0.4153  -3.206  0.00305 **
fBASINTethys            -1.2164     0.4081  -2.981  0.00546 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1154421)

    Null deviance: 8.2940  on 38  degrees of freedom
Residual deviance: 4.1213  on 32  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Model = extrinsic

```
> GLM_OAE_A3ii <- glm(extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_A3ii)

Call:
```

```
glm(formula = extinction ~ fLATITUDE + fBASIN + fENVIRONMENT, 
    family = quasibinomial, data = OAE)

Deviance Residuals: 
     Min        1Q    Median        3Q       Max  
-0.82785  -0.19980   0.02194   0.30345   0.68123  

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)            0.4679     0.5296   0.884    0.388
fLATITUDET            -0.3157     0.4468  -0.707    0.488
fBASINTethys           0.8458     0.5224   1.619    0.122
fENVIRONMENTOffshore  -0.4707     0.4937  -0.953    0.352
fENVIRONMENTReef       2.0464     1.9653   1.041    0.311

(Dispersion parameter for quasibinomial family taken to be 0.1625729)

    Null deviance: 4.1787  on 23  degrees of freedom
Residual deviance: 3.2273  on 19  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
> 
> # find best model
> 
> drop1(GLM_OAE_A3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN + fENVIRONMENT
             Df Deviance F value Pr(>F)
<none>            3.2273               
fLATITUDE     1   3.3089  0.4802 0.4967
fBASIN        1   3.6534  2.5082 0.1298
fENVIRONMENT  2   3.7659  1.5854 0.2308
> 
```

Model = extrinsic no env

```
> GLM_OAE_B3ii <- glm(extinction ~ fLATITUDE + fBASIN,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B3ii)
```

```
Call:
glm(formula = extinction ~ fLATITUDE + fBASIN, family = quasibinomial,
    data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.85850  -0.31552  -0.02386   0.29006   0.88380

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        1.76124    0.67687   2.602   0.0136 *
fLATITUDEP        -0.83310    0.70090  -1.189   0.2428
fLATITUDET         0.08532    0.30341   0.281   0.7803
fBASINPanthalassa -1.73653    0.69143  -2.512   0.0169 *
fBASINTethys      -1.53097    0.70095  -2.184   0.0359 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1816417)

    Null deviance: 8.2940  on 38  degrees of freedom
Residual deviance: 6.8489  on 34  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_OAE_B3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN
          Df Deviance F value  Pr(>F)
<none>         6.8489
fLATITUDE  2   7.1629  0.7795 0.46668
fBASIN     2   8.2454  3.4663 0.04265 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
>
> # best model
>
> GLM_OAE_B3iii <- glm(extinction ~ fBASIN,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B3iii)

Call:
glm(formula = extinction ~ fBASIN, family = quasibinomial, data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.18153  -0.25543  -0.03494   0.30631   0.86954

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)         1.2160     0.4466   2.723  0.00991 **
fBASINPanthalassa  -1.2064     0.5035  -2.396  0.02190 *
fBASINTethys       -0.9534     0.4832  -1.973  0.05621 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.175851)

    Null deviance: 8.2940  on 38  degrees of freedom
Residual deviance: 7.1629  on 36  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Model = intrinsic

```
> GLM_OAE_A4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_A4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = OAE)

Deviance Residuals:
```

```
     Min        1Q    Median        3Q       Max  
-0.50167  -0.26405  -0.00598   0.31718   0.51395  

Coefficients:
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)             0.865721   0.835866   1.036    0.317
fMOTILITYnonmotile      0.586772   0.546392   1.074    0.300
fTIERINGinfaunal       -0.408294   0.492615  -0.829    0.420
fTIERINGpelagic         0.792790   1.106530   0.716    0.485
fFEEDINGgrazing         0.718156   0.810390   0.886    0.390
fFEEDINGphotosymbiotic  0.001459   1.107503   0.001    0.999
fFEEDINGpredatory       0.570980   1.078225   0.530    0.604
fFEEDINGsuspension     -0.281368   0.685727  -0.410    0.687
fCALCIFICATIONmoderate -0.338089   0.645988  -0.523    0.608

(Dispersion parameter for quasibinomial family taken to be 0.1482437)

    Null deviance: 4.1787  on 23  degrees of freedom
Residual deviance: 2.3502  on 15  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

> 
> # find best model
> 
> drop1(GLM_OAE_A4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              2.3502               
fMOTILITY       1   2.5215  1.0938 0.3122
fTIERING        2   2.5248  0.5572 0.5842
fFEEDING        4   2.6545  0.4857 0.7462
fCALCIFICATION  1   2.3916  0.2642 0.6148
> 
```

Model = intrinsic no env

```
> GLM_OAE_B4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
```

```
+ fCALCIFICATION,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.09670  -0.21032   0.05265   0.18855   0.54955

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)            -0.60947    0.64645  -0.943   0.3536
fMOTILITYnonmotile      0.32053    0.30686   1.045   0.3049
fTIERINGinfaunal       -0.45118    0.31438  -1.435   0.1619
fTIERINGpelagic         1.28321    0.84016   1.527   0.1375
fFEEDINGgrazing         0.77966    0.77486   1.006   0.3226
fFEEDINGphotosymbiotic  2.17951    0.91122   2.392   0.0235 *
fFEEDINGpredatory       0.18390    0.90933   0.202   0.8411
fFEEDINGsuspension      0.09612    0.56283   0.171   0.8656
fCALCIFICATIONlight    -1.14531    0.93795  -1.221   0.2319
fCALCIFICATIONmoderate  0.60790    0.40898   1.486   0.1480
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.1320506)

    Null deviance: 8.2940  on 38  degrees of freedom
Residual deviance: 4.3038  on 29  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_OAE_B4ii, test = "F")
Single term deletions
```

```
Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value  Pr(>F)
<none>              4.3038
fMOTILITY       1   4.4486  0.9758 0.33142
fTIERING        2   4.8737  1.9200 0.16479
fFEEDING        4   5.9884  2.8378 0.04223 *
fCALCIFICATION  2   5.1747  2.9342 0.06910 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> # best model
>
> GLM_OAE_B4iv <- glm(extinction ~ fFEEDING,
+ family = quasibinomial, data = OAE)
> summary(GLM_OAE_B4iv)

Call:
glm(formula = extinction ~ fFEEDING, family = quasibinomial,
    data = OAE)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.16779  -0.21337   0.07018   0.28404   0.70741

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             -0.2243     0.5481  -0.409   0.6849
fFEEDINGgrazing          1.0024     0.8026   1.249   0.2202
fFEEDINGphotosymbiotic   2.1149     0.8568   2.468   0.0188 *
fFEEDINGpredatory        1.1659     0.6367   1.831   0.0758 .
fFEEDINGsuspension       0.2016     0.5693   0.354   0.7254
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.1483219)

    Null deviance: 8.294  on 38  degrees of freedom
Residual deviance: 5.546  on 34  degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 4
```

Triassic background

Model = all

```
> GLM_pre_A1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fENVIRONMENT +
+ fCALCIFICATION,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_A1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fENVIRONMENT + fCALCIFICATION, family =
quasibinomial,
    data = pre)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.0239  -0.2825   0.0781   0.3665   0.7342

Coefficients: (1 not defined because of singularities)
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)             2.307822   1.126560   2.049   0.0479 *
fMOTILITYnonmotile     -0.001491   0.475700  -0.003   0.9975
fTIERINGinfaunal       -0.205156   0.553408  -0.371   0.7130
fTIERINGpelagic         0.611297   0.891845   0.685   0.4975
fFEEDINGphotosymbiotic -1.734707   1.161870  -1.493   0.1441
fFEEDINGpredatory             NA         NA      NA       NA
fFEEDINGsuspension     -0.609533   0.809037  -0.753   0.4561
fLATITUDET             -0.369263   0.552370  -0.669   0.5081
fBASINTethys           -0.029463   0.632788  -0.047   0.9631
fENVIRONMENTOffshore    0.146258   0.821322   0.178   0.8597
fENVIRONMENTReef       -0.438626   0.491499  -0.892   0.3781
fCALCIFICATIONlight    -0.778322   0.724403  -1.074   0.2898
fCALCIFICATIONmoderate -0.821088   0.571830  -1.436   0.1597
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2401432)

    Null deviance: 13.8327  on 47  degrees of freedom
Residual deviance:  9.1254  on 36  degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 4
>
> # find best model
>
> drop1(GLM_pre_A1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fENVIRONMENT + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              9.1254
fMOTILITY       1   9.1254  0.0000 0.9976
fTIERING        1   9.1584  0.1302 0.7204
fFEEDING        2   9.7804  1.2920 0.2872
fLATITUDE       1   9.2353  0.4334 0.5145
fBASIN          1   9.1260  0.0021 0.9641
fENVIRONMENT    2   9.3238  0.3912 0.6791
fCALCIFICATION  2   9.6563  1.0471 0.3614
>
```

Model = all no env

```
> GLM_pre_B1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fCALCIFICATION,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_B1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fCALCIFICATION, family = quasibinomial,
    data = pre)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.30649  -0.24242   0.03913   0.31504   1.06498

Coefficients:
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)             0.493783   0.609139   0.811    0.420
fMOTILITYnonmotile      0.132692   0.255165   0.520    0.604
```

```
fTIERINGinfaunal       -0.249179   0.288659  -0.863    0.390
fTIERINGpelagic         0.422510   0.386715   1.093    0.278
fFEEDINGgrazing        -0.221395   0.879548  -0.252    0.802
fFEEDINGother          -0.773554   1.111817  -0.696    0.488
fFEEDINGphotosymbiotic -0.867489   0.713520  -1.216    0.227
fFEEDINGpredatory       0.415223   0.689365   0.602    0.549
fFEEDINGsuspension     -0.501679   0.610900  -0.821    0.414
fLATITUDEP             -0.002709   0.397414  -0.007    0.995
fLATITUDET             -0.245379   0.223035  -1.100    0.274
fBASINPanthalassa       0.438921   0.406209   1.081    0.283
fBASINTethys            0.129194   0.440649   0.293    0.770
fCALCIFICATIONlight    -0.275846   0.441214  -0.625    0.533
fCALCIFICATIONmoderate -0.048012   0.292650  -0.164    0.870

(Dispersion parameter for quasibinomial family taken to be 0.1870975)

    Null deviance: 24.442  on 100  degrees of freedom
Residual deviance: 17.897  on  86  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

> # find best model
>
> drop1(GLM_pre_B1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              17.897
fMOTILITY       1   17.948  0.2431 0.6232
fTIERING        2   18.279  0.9181 0.4032
fFEEDING        5   19.132  1.1867 0.3224
fLATITUDE       2   18.141  0.5861 0.5587
fBASIN          2   18.465  1.3633 0.2613
fCALCIFICATION  2   17.979  0.1956 0.8227
>
```

Model = extrinsic

```
> GLM_pre_A3ii <- glm(extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_A3ii)

Call:
glm(formula = extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
    family = quasibinomial, data = pre)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.21401  -0.28266   0.08969   0.32510   0.83503

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)            0.9568     0.5688   1.682   0.0998 .
fLATITUDET             0.1052     0.5020   0.210   0.8350
fBASINTethys          -0.1877     0.5423  -0.346   0.7309
fENVIRONMENTOffshore   1.0662     0.6413   1.663   0.1036
fENVIRONMENTReef      -0.7343     0.3295  -2.229   0.0311 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.2421453)

    Null deviance: 13.833  on 47  degrees of freedom
Residual deviance: 11.197  on 43  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_pre_A3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN + fENVIRONMENT
             Df Deviance F value  Pr(>F)
<none>            11.197
fLATITUDE     1   11.207  0.0405 0.84141
```

```
fBASIN        1   11.226  0.1132 0.73814
fENVIRONMENT  2   13.831  5.0590 0.01064 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> # best model
>
> GLM_pre_A3iii <- glm(extinction ~ fENVIRONMENT,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_A3iii)

Call:
glm(formula = extinction ~ fENVIRONMENT, family = quasibinomial,
    data = pre)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2179  -0.2782   0.1173   0.3223   0.8322

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)            0.8824     0.2038   4.330 8.24e-05 ***
fENVIRONMENTOffshore   1.0400     0.6238   1.667    0.102
fENVIRONMENTReef      -0.7314     0.3222  -2.270    0.028 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.232193)

    Null deviance: 13.833  on 47  degrees of freedom
Residual deviance: 11.228  on 45  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Model = extrinsic no env

```
> GLM_pre_B3ii <- glm(extinction ~ fLATITUDE + fBASIN,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_B3ii)

Call:
```

```
glm(formula = extinction ~ fLATITUDE + fBASIN, family = quasibinomial,
    data = pre)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.29562  -0.30561   0.02562   0.39844   1.02334

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        0.35325    0.39494   0.894    0.373
fLATITUDEP        -0.07958    0.38308  -0.208    0.836
fLATITUDET        -0.24219    0.22525  -1.075    0.285
fBASINPanthalassa  0.26273    0.39198   0.670    0.504
fBASINTethys       0.02883    0.42502   0.068    0.946

(Dispersion parameter for quasibinomial family taken to be 0.2223776)

    Null deviance: 24.442  on 100  degrees of freedom
Residual deviance: 23.767  on  96  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 3

>
> # find best model
>
> drop1(GLM_pre_B3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN
          Df Deviance F value Pr(>F)
<none>         23.767
fLATITUDE  2   24.025  0.5220 0.5950
fBASIN     2   24.093  0.6592 0.5196
>
```

Model = intrinsic

```
> GLM_pre_A4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = pre)
```

```
> summary(GLM_pre_A4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING + 
    fCALCIFICATION, family = quasibinomial, data = pre)

Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-0.9961  -0.2672   0.1008   0.3637   0.6452  

Coefficients: (1 not defined because of singularities)
                       Estimate Std. Error t value Pr(>|t|)  
(Intercept)             1.85156    0.84290   2.197   0.0339 *
fMOTILITYnonmotile     -0.06775    0.45827  -0.148   0.8832  
fTIERINGinfaunal       -0.02356    0.47980  -0.049   0.9611  
fTIERINGpelagic         0.78405    0.78742   0.996   0.3254  
fFEEDINGphotosymbiotic -1.88930    0.97094  -1.946   0.0587 .
fFEEDINGpredatory            NA         NA      NA       NA  
fFEEDINGsuspension     -0.71681    0.74704  -0.960   0.3431  
fCALCIFICATIONlight    -0.88807    0.69239  -1.283   0.2070  
fCALCIFICATIONmoderate -0.76356    0.55221  -1.383   0.1744  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2293279)

    Null deviance: 13.8327  on 47  degrees of freedom
Residual deviance:  9.5384  on 40  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

> 
> # find best model
> 
> drop1(GLM_pre_A4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
```

```
<none>              9.5384
fMOTILITY       1   9.5434  0.0210 0.8854
fTIERING        1   9.5389  0.0023 0.9618
fFEEDING        2  10.6146  2.2568 0.1179
fCALCIFICATION  2  10.0601  1.0941 0.3447
>
```

Model = intrinsic no env

```
> GLM_pre_B4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = pre)
> summary(GLM_pre_B4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = pre)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.43602  -0.23872   0.07058   0.28717   1.09648

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             0.55518    0.58195   0.954    0.343
fMOTILITYnonmotile      0.11194    0.25563   0.438    0.663
fTIERINGinfaunal       -0.26538    0.27564  -0.963    0.338
fTIERINGpelagic         0.44883    0.38590   1.163    0.248
fFEEDINGgrazing        -0.38720    0.80757  -0.479    0.633
fFEEDINGother          -0.92316    1.07130  -0.862    0.391
fFEEDINGphotosymbiotic -0.77628    0.66080  -1.175    0.243
fFEEDINGpredatory       0.44291    0.63581   0.697    0.488
fFEEDINGsuspension     -0.41397    0.54340  -0.762    0.448
fCALCIFICATIONlight    -0.42882    0.42755  -1.003    0.319
fCALCIFICATIONmoderate -0.05979    0.28712  -0.208    0.836

(Dispersion parameter for quasibinomial family taken to be 0.1891681)

    Null deviance: 24.442  on 100  degrees of freedom
Residual deviance: 18.780  on  90  degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_pre_B4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              18.780
fMOTILITY       1   18.816  0.1738 0.6777
fTIERING        2   19.212  1.0348 0.3595
fFEEDING        5   19.953  1.1242 0.3533
fCALCIFICATION  2   19.003  0.5347 0.5877
>
```

Jurassic background

Model = all

```
> GLM_post_A1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fENVIRONMENT +
+ fCALCIFICATION,
+ family = quasibinomial, data = post)
> summary(GLM_post_A1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fENVIRONMENT + fCALCIFICATION, family =
quasibinomial,
    data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.51234  -0.21406   0.08584   0.31578   0.87603

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             0.04533    1.14542   0.040   0.9686
fMOTILITYnonmotile      0.44139    0.48417   0.912   0.3668
fTIERINGinfaunal        0.09458    0.44038   0.215   0.8309
fTIERINGpelagic         1.93865    0.90292   2.147   0.0372 *
fFEEDINGgrazing        -0.13636    0.94827  -0.144   0.8863
fFEEDINGphotosymbiotic -1.08787    1.29808  -0.838   0.4064
fFEEDINGpredatory      -0.07292    0.99946  -0.073   0.9422
fFEEDINGsuspension     -0.81351    0.88483  -0.919   0.3628
fLATITUDET             -0.61547    0.42484  -1.449   0.1544
fBASINTethys            1.08666    0.50557   2.149   0.0370 *
fENVIRONMENTOffshore   -1.20987    0.45935  -2.634   0.0115 *
fENVIRONMENTReef       -1.66180    1.39474  -1.191   0.2397
fCALCIFICATIONmoderate  0.15080    0.53518   0.282   0.7794
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2844998)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 15.391  on 45  degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 4
> # find best model
>
> drop1(GLM_post_A1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fENVIRONMENT + fCALCIFICATION
               Df Deviance F value  Pr(>F)
<none>              15.391
fMOTILITY       1   15.629  0.6965 0.40836
fTIERING        2   16.803  2.0641 0.13878
fFEEDING        4   15.811  0.3069 0.87182
fLATITUDE       1   15.991  1.7543 0.19203
fBASIN          1   16.748  3.9680 0.05246 .
fENVIRONMENT    2   18.316  4.2762 0.01994 *
fCALCIFICATION  1   15.414  0.0661 0.79830
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> # best model
> GLM_post_A1iii <- glm(extinction ~ fBASIN + fENVIRONMENT,
+ family = quasibinomial, data = post)
>
> summary(GLM_post_A1iii)

Call:
glm(formula = extinction ~ fBASIN + fENVIRONMENT, family = quasibinomial,
    data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39697  -0.23517   0.01493   0.36667   1.15096

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           -0.7316     0.3532  -2.072  0.04309 *
fBASINTethys           1.2343     0.4345   2.841  0.00633 **
fENVIRONMENTOffshore  -0.4401     0.3350  -1.314  0.19450
```

```
fENVIRONMENTReef      -2.2945     1.1370  -2.018  0.04856 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.3009023)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 19.858  on 54  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Model = all no env

```
> GLM_post_B1ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fLATITUDE + fBASIN + fCALCIFICATION,
+ family = quasibinomial, data = post)
> summary(GLM_post_B1ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fLATITUDE + fBASIN + fCALCIFICATION, family = quasibinomial,
    data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.17245  -0.30500   0.02441   0.33190   0.97939

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)           -0.652952   0.840734  -0.777   0.4392
fMOTILITYnonmotile     0.022546   0.265609   0.085   0.9325
fTIERINGinfaunal       0.013179   0.276256   0.048   0.9620
fTIERINGpelagic        0.953836   0.574465   1.660   0.1000 .
fFEEDINGgrazing        1.153372   0.628432   1.835   0.0694 .
fFEEDINGother          1.335053   1.178406   1.133   0.2600
fFEEDINGphotosymbiotic  0.625865   0.691337   0.905   0.3675
fFEEDINGpredatory      1.241876   0.690106   1.800   0.0749 .
fFEEDINGsuspension     0.264316   0.497767   0.531   0.5966
fLATITUDEP             0.180565   0.518066   0.349   0.7282
fLATITUDET            -0.004722   0.228922  -0.021   0.9836
fBASINPanthalassa     -0.462281   0.516853  -0.894   0.3732
```

```
fBASINTethys           -0.002421   0.539806  -0.004   0.9964
fCALCIFICATIONlight    -0.577693   0.674157  -0.857   0.3935
fCALCIFICATIONmoderate  0.005010   0.354818   0.014   0.9888
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.251139)

    Null deviance: 42.295  on 114  degrees of freedom
Residual deviance: 30.418  on 100  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_post_B1ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fLATITUDE + fBASIN +
    fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              30.418
fMOTILITY       1   30.420  0.0059 0.9387
fTIERING        2   31.094  1.1106 0.3334
fFEEDING        5   32.449  1.3355 0.2555
fLATITUDE       2   30.449  0.0512 0.9501
fBASIN          2   31.475  1.7371 0.1813
fCALCIFICATION  2   30.660  0.3979 0.6728
>
```

Model = extrinsic

```
> GLM_post_A3ii <- glm(extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
+ family = quasibinomial, data = post)
> summary(GLM_post_A3ii)

Call:
glm(formula = extinction ~ fLATITUDE + fBASIN + fENVIRONMENT,
    family = quasibinomial, data = post)
```

```
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.42597  -0.23507   0.02656   0.37338   1.14446

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           -0.6267     0.4674  -1.341   0.1857
fLATITUDET            -0.1288     0.3728  -0.345   0.7312
fBASINTethys           1.1943     0.4527   2.638   0.0109 *
fENVIRONMENTOffshore  -0.4896     0.3676  -1.332   0.1886
fENVIRONMENTReef      -2.2306     1.1610  -1.921   0.0601 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.3059362)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 19.822  on 53  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_post_A3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN + fENVIRONMENT
             Df Deviance F value  Pr(>F)
<none>            19.822
fLATITUDE     1   19.858  0.0975 0.75609
fBASIN        1   22.058  5.9786 0.01784 *
fENVIRONMENT  2   21.794  2.6368 0.08096 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> # best model
> GLM_post_A3iii <- glm(extinction ~ fBASIN,
```

```
+ family = quasibinomial, data = post)
>
> summary(GLM_post_A3iii)

Call:
glm(formula = extinction ~ fBASIN, family = quasibinomial, data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.25583  -0.36205   0.04317   0.45311   1.10095

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   -0.7316     0.3614  -2.024   0.0477 *
fBASINTethys   0.9141     0.3971   2.302   0.0251 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.3151467)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 21.850  on 56  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 3
```

Model = extrinsic no env

```
> GLM_post_B3ii <- glm(extinction ~ fLATITUDE + fBASIN,
+ family = quasibinomial, data = post)
> summary(GLM_post_B3ii)

Call:
glm(formula = extinction ~ fLATITUDE + fBASIN, family = quasibinomial,
    data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.18921  -0.41443   0.07206   0.36821   1.23843

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)       -0.15073    0.50156  -0.301    0.764
fLATITUDEP         0.09206    0.51178   0.180    0.858
fLATITUDET         0.04691    0.22530   0.208    0.835
fBASINPanthalassa -0.35305    0.50998  -0.692    0.490
fBASINTethys       0.13156    0.51975   0.253    0.801

(Dispersion parameter for quasibinomial family taken to be 0.3064222)

    Null deviance: 42.295  on 114  degrees of freedom
Residual deviance: 40.896  on 110  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 3

>
> # find best model
>
> drop1(GLM_post_B3ii, test = "F")
Single term deletions

Model:
extinction ~ fLATITUDE + fBASIN
          Df Deviance F value Pr(>F)
<none>         40.896
fLATITUDE  2   40.917  0.0279 0.9725
fBASIN     2   42.294  1.8799 0.1575
>
```

Model = intrinsic

```
> GLM_post_A4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
+ fCALCIFICATION,
+ family = quasibinomial, data = post)
> summary(GLM_post_A4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.23841  -0.35885   0.07215   0.42268   1.11761
```

```
Coefficients:
                       Estimate Std. Error t value Pr(>|t|)  
(Intercept)             0.48986    0.93482   0.524   0.6026  
fMOTILITYnonmotile      0.02496    0.46913   0.053   0.9578  
fTIERINGinfaunal       -0.16568    0.44754  -0.370   0.7128  
fTIERINGpelagic         1.77230    0.92260   1.921   0.0606 .
fFEEDINGgrazing        -0.15181    0.97205  -0.156   0.8765  
fFEEDINGphotosymbiotic -1.00033    1.12559  -0.889   0.3785  
fFEEDINGpredatory      -0.20319    1.05564  -0.192   0.8482  
fFEEDINGsuspension     -0.37252    0.87741  -0.425   0.6730  
fCALCIFICATIONmoderate -0.28667    0.51093  -0.561   0.5773  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 0.3181259)

    Null deviance: 23.615  on 57  degrees of freedom
Residual deviance: 19.476  on 49  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

> 
> # find best model
> 
> drop1(GLM_post_A4ii, test = "F")
Single term deletions

Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              19.476               
fMOTILITY       1   19.477  0.0023 0.9622
fTIERING        2   20.768  1.6259 0.2072
fFEEDING        4   19.804  0.2067 0.9335
fCALCIFICATION  1   19.576  0.2526 0.6175
> 
```

Model = intrinsic no env

```
> GLM_post_B4ii <- glm(extinction ~ fMOTILITY + fTIERING + fFEEDING +
```

```
+ fCALCIFICATION,
+ family = quasibinomial, data = post)
> summary(GLM_post_B4ii)

Call:
glm(formula = extinction ~ fMOTILITY + fTIERING + fFEEDING +
    fCALCIFICATION, family = quasibinomial, data = post)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.07893  -0.38812   0.07983   0.34490   1.05144

Coefficients:
                        Estimate Std. Error t value Pr(>|t|)
(Intercept)            -0.617533   0.530221  -1.165   0.2468
fMOTILITYnonmotile     -0.029025   0.255465  -0.114   0.9098
fTIERINGinfaunal       -0.042630   0.264686  -0.161   0.8724
fTIERINGpelagic         0.810725   0.557628   1.454   0.1490
fFEEDINGgrazing         1.123169   0.615087   1.826   0.0707 .
fFEEDINGother           1.358299   1.150768   1.180   0.2406
fFEEDINGphotosymbiotic  0.410438   0.637146   0.644   0.5209
fFEEDINGpredatory       1.157417   0.682559   1.696   0.0929 .
fFEEDINGsuspension      0.123304   0.467416   0.264   0.7925
fCALCIFICATIONlight    -0.452490   0.659257  -0.686   0.4940
fCALCIFICATIONmoderate -0.004989   0.332452  -0.015   0.9881
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.2494198)

    Null deviance: 42.295  on 114  degrees of freedom
Residual deviance: 31.582  on 104  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

>
> # find best model
>
> drop1(GLM_post_B4ii, test = "F")
Single term deletions
```

```
Model:
extinction ~ fMOTILITY + fTIERING + fFEEDING + fCALCIFICATION
               Df Deviance F value Pr(>F)
<none>              31.582
fMOTILITY       1   31.585  0.0106 0.9182
fTIERING        2   32.103  0.8577 0.4271
fFEEDING        5   33.904  1.5293 0.1871
fCALCIFICATION  2   31.732  0.2482 0.7806
>
```