Supplementary Text S1

INLA does not implement multinomial or ordinal response models, so we used the R package brms (Bürkner 2017) to implement a phylogenetic multi-response model in the stan programming language (Carpenter et al. 2017). To determine which of the response structures available in stan best suited our data, we ran two sampling chains of 10,000-20,000 iterations with half the iterations as burnin or warmup. We then added the leave-one-out cross-validation (loo) to each model using the add_criterion routine specifying "loo", an unbiased measure of predictive accuracy for Bayesian models (Vehtari et al. 2017), then compared all models using the loo_compare command. Four response structures were compared: cumulative, continuation ratio, stopping ratio, and adjacent category. The best fit among the response models was then used in a series of models of varying complexity of predictors by specifying up to 25,000 iterations in two chains. Unlike INLA, stan requires missing data to be imputed for analysis, so we formulated two sets of models: (1) discarding rows with missing predictor values; (2) with imputed predictor values. We used multivariate imputation by chained equations implemented in the R package mice (Buuren and Groothuis-Oudshoorn 2010) to impute missing predictor values. As with INLA models, a single phylogeny was used to determine if there were any covariates with coefficients of posterior excluding 0 in the model. As there were none, we did not proceed to full implementation across 100 phylogenies.

For ordinal responses, Bayesian comparisons revealed the adjacent category response structure had better predictive power, but more complex predictor combinations could only be compared with the cumulative link, which identified the simpler model including only area and mean elevation as better with both missing and imputed data. None of the analyses estimated coefficients non-overlapping with 0, indicating insufficient power to detect the influence of the covariates on multinomial responses.

References

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Carpenter B, Gelman A, Hoffman MD, Lee D, Goodrich B, Betancourt M, Brubaker M, Guo J, Li P, Riddell A. 2017 Stan: a probabilistic programming language. *J. Stat. Softw*. **76(1)**, 1-32.

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Table S3. Sample-wide coefficients for covariates of survival probability. HPI, high probability interval. Coefficients with HPIs that do not cross zero are highlighted in bold.

Covariate	Mean	2.5% HPI	97.5% HPI
Intercept	-4.43	-10.61	-0.78
Mass	2.07	-0.81	5.16
Mass²	-3.04	-6.07	-1.14
Island area	0.29	-1.28	1.74
Mean island elevation	-2.56	-4.60	-0.93
Active volcano	-5.66	-49.89	16.28
Hurricane frequency	-3.24	-7.66	-0.12
First human arrival	0.06	-0.59	0.69
Forest cover	0.15	-0.59	0.93
Forest loss	4.66	-35.93	48.45
Human Footprint Index	0.00	-0.08	0.09
Mass: First human arrival	-0.75	-1.47	-0.16