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Assessing patterns of extinction risk among mammal species in Nigeria: A comparative analysis of human impact

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Abstract

This study aimed to evaluate how biological traits influence extinction risk among mammal species in Nigeria, and how these traits interact with specific anthropogenic threats such as agriculture, urbanization and climate change. Focusing on mammal species in Nigeria, we used phylogenetic logistic regression to test the influence of five biological traits: body mass, brain mass, generation time, current geographic range and historical range contraction, on extinction risk across 9 IUCN threat categories. Standardized models were used to compare trait sensitivity across threats. Brain mass emerged as the most consistent and influential predictor of extinction risk, particularly under threats such as agriculture, biological resource use and urban development. Species with larger brains, often primates and carnivores, were highly vulnerable. Geographic range size was a strong negative predictor of risk across most models, with range-restricted species more susceptible to habitat loss and fragmentation. Generation time was positively associated with risk under direct human pressures but inversely linked under climate threats. Body mass showed weak and inconsistent effects, which suggests its influence may be secondary to cognitive or spatial traits. The number of species affected was highest under human threats, compared to climate change or pollution. Extinction risk in Nigerian mammals is shaped by intrinsic traits that interact predictably with human pressures. Species with large brains, small ranges and slow reproduction are at greatest risk. Trait-based models can improve conservation planning by identifying vulnerable species before population declines become critical, especially in regions facing intensive land-use change.

Keywords

Extinction risk, brain size, Nigerian mammals, human impact

Introduction

The rate at which global biodiversity is declining presents significant environmental, economic and social challenges, which continue to result in extinction risk levels rising at unprecedented scale due to human activities in this present age (Estrada et al. 2017). This decline is typically observed in regions that are known for their high levels of species richness and vulnerability to anthropogenic impacts (Pereira et al. 2012). According to the current International Union for Conservation of Nature's Red List database, over 46,300 species are threatened with extinction globally (IUCN 2024). This includes examples such as the Javan rhinoceros, African elephant, western gorilla and chimpanzee. Not only are species with limited geographical range, large body mass, large brain mass and low reproductive rates confronted with increased extinction risk, they are also faced with threats due to human activities, habitat degradation, climate change and invasive species (Maxwell et al. 2016).

Mammals which play important roles within ecosystems such as predators, prey, and seed dispersers are increasingly threatened with approximately 26% of its species at risk of extinction (IUCN 2024). In Nigeria, mammal species are facing significant extinction risk due to human activities such as agriculture, urbanization, poaching and deforestation, which have continuously degraded their habitats (Anwadike 2020). Being part of the Africa's Guinean-forest biodiversity hotspot, the Nigerian lowland forest region is particularly vulnerable to these threats (Ukpoju et al. 2023).

This study offers the possibility to identify specific traits linked to extinction risks among mammal species in Nigeria. Species with smaller geographical ranges, such as the chimpanzee, are usually vulnerable due to habitat fragmentation from deforestation and agricultural development (Sesink et al. 2015). Large-bodied mammals such as elephants are at high risk because they require extensive habitats and are frequently in conflict with human activities (Montero-Botey et al. 2024). Larger brained mammals, such as Olive baboons and Leopards (primates and carnivores), are often associated with enhanced cognitive abilities and behavioral complexity, traits that can improve survival in natural environments but may also increase sensitivity to anthropogenic changes (Abelson 2019, Chichorro et al. 2019).

Despite Nigeria region's richness in biodiversity, studies on extinction risk, especially on mammalian populations are limited, thereby creating a knowledge gap in conservation science and intervention in the region (Gbadegesin and Gbadamosi 2024, Imarhiagbe et al. 2019, Ukpoju et al. 2023). The project addresses this gap by focusing what biological traits increase the vulnerability of Nigerian mammal species to extinction, and how do these interact with specific human caused threats?

Aim

The study aims to examine extinction risk patterns among Nigerian mammals to identify traits that correlate with higher susceptibility to extinction, in order to provide data-driven insights that can inform conservation policies particularly in regions where resources for biodiversity protection are limited and need to be prioritized effectively.

To achieve this objective, the study design follows the approach as stated below; firstly, it involves compiling a comprehensive data of Nigeria's mammal species. Following this, the study will analyze what factors predict if a species is threatened overall, then we will see if the same predictors can predict if a species is being threatened by one of these individual factors. Correspondingly, we will analyze specific biological traits such as body mass, brain mass, geographic range and reproductive rates to determine their correlation with extinction risk levels.

Material and methods

Study design and data compilation

We compiled data from several trusted sources, including the IUCN Red List, phylogenetic trees and trait databases (Faurby et al. 2018, Upham et al. 2019, IUCN 2024). We focused on biological traits that are known to influence extinction risks specifically, body mass, brain mass, reproductive rate (using generation time) and geographic range (Chichorro et al. 2019, Healy et al. 2019).

The first dataset we downloaded and compiled was a comprehensive dataset of mammalian species in Nigeria from the IUCN Red List database. The downloaded raw spatial data in the form of a polygon shapefile (SHP) was processed in RStudio software (Lander 2014). We performed the extraction and transformation of the SHP file using the sf and tidyverse packages (Wickham 2014) in R studio. The transformed data was loaded to a CSV file for final cleaning in Microsoft Excel where 314 observations of mammalian species in Nigeria were obtained.

We carried out dataset matching for the 314 IUCN Red List mammalian species name. "SCI_NAME" is the name given by IUCN to the column with the species name. The primary data in the column SCI_NAME was matched with the Phylogeny mammalian taxonomy and the PHYLACINE mammalian taxonomy (Faurby et al. 2018, Moura et al. 2024). The extraction of the Phylogeny taxonomy, which contains phylogenetic trees that include mammalian species was obtained from the online tool in the paper – 'Inferring the mammal tree', that contains credible sets of 10,000 trees at https://vertlife.org/phylosubsets (Upham et al. 2019). We extracted the PHYLACINE taxonomy from the resources on mammal tree from PHYLACINE 1.2: The Phylogenetic Atlas of Mammal Macroecology (Faurby et al. 2018). Species names from the IUCN, Phylogeny, and PHYLACINE datasets were imported into consecutive columns in an Excel spreadsheet, standardized, matched using VLOOKUP, and any mismatches or outdated names were verified against the IUCN Red List and relevant taxonomic references to ensure consistency before compiling the final dataset.

To better understand extinction risk, we incorporated additional datasets into the IUCN species data. These include:

A. Biological Traits (Body mass, Brain mass and Reproductive rate):

Source:

We obtained the trait data from two major databases: PHYLACINE 1.2 and COMBINE. (Faurby et al. 2018, Soria et al. 2021).

How it was obtained:

Body mass was downloaded from PHYLACINE 1.2 database. We extracted the obtained compressed folder under the 'Traits' subdirectory, the file 'Trait_data.csv' was available for use. We renamed the trait column for consistency in my dataset (from 'Mass.g' to 'Body_Mass_g') and merged with Microsoft Excel using the species' scientific names as identifiers.

For Brain mass and Reproductive rate, we obtained these by extracting the zip file from the Combine Database where the file 'imputation_phylo_825.csv' was used because it has the summary of all imputations. Generation time was used as a proxy for Reproductive rate as it encapsulates the pace of life and species with longer generation times generally exhibit slower reproductive strategies, a pattern observed across various taxa (Healy et al. 2019). The dataset was filtered using the R package dplyr (Wickham et al. 2023) to read and clean the data for the required variables and observations.

B. Geographic Range (in km2)

Source:

The range was obtained from the IUCN Red List (Faurby and Svenning 2015).

How it was obtained:

To extract and analyze geographic range from the IUCN Red List spatial data, we applied the following steps using key R packages:

The required R Packages: sf, dplyr and ggplot2 were loaded into R studio (Pebesma 2018, Wickham 2009, Wickham et al. 2023).

The mammalian polygon shapefile upon been loaded into R, was converted into an R spatial object for processing.

The subsets based on species were prepared while the categories were also defined. Categories such as Extant (resident), Extant & Reintroduced (resident) and Possibly

Extant (resident) are designated as extant items. While the categories; Extinct, Possibly Extinct and Presence Uncertain are designated as extinct items.

The appropriate Coordinate Reference System (CRS), i.e. CRS = 32633 was assigned for spatial analysis.

The required spatial data obtained for the 314 observations includes three variables, which are Total geographic area (Extant and Extinct), Current Area (Extant) and Extinct Area.

C. We additionally integrated into this dataset, the full hierarchical structure of the threat types (IUCN 2025) as listed in the IUCN Threats Classification Scheme (Version 3.3). This dataset was constructed classifying the mammals as threatened or not-threatened based on their assessed conservation status according to the classification scheme.

We accessed threat data manually from individual IUCN 2025 Red List species web profiles and recorded in structured format. We assigned each species a value of “Yes” or “No” for each of the 12 threat classes, which were treated as separate binary variables. A “Yes” was recorded in the dataset if the threat was listed for the species on its web profile at any severity or scope, while “No” indicated the threat was not reported. For species listed under multiple threats, all applicable classes were coded as “Yes”. We cross-checked all 314 observations with the IUCN Threats Classification Scheme to ensure consistency and accuracy.

Data and statistical analysis

The dplyr and tidyverse packages (Wickham et al. 2023) were utilized for data loading, cleaning and transformation, ensuring only relevant traits were extracted and merged (Wickham 2014). We normalized all these continuous trait variables using the R scale() function on only the CurrentArea_TotalArea variable, while we used the R scale(log10()) function on Body_Mass, Brain_Mass, Current_Area and Generation_time. We use the log10() function in R to normalize trait variables by first reducing skewness and stabilizing variance through log-transformation and then scale() function to standardize them to have a mean of zero and standard deviation of one, ensuring comparability across predictors in regression models. The variable CurrentArea_TotalArea was not log-transformed because it is a bounded ratio ranging from 0 to 1. Applying a log transformation to such values can distort the distribution (Warton and Hui 2011).

The ink to my openly available dataset that underpins my work is: https://doi.org/10.5281/zenodo.17259884.

We constructed a series of phylogenetic logistic regression models to examine the relationship between biological traits and extinction risk among Nigerian mammals (Ives and Garland 2010). We used a set of five key trait variables in the modeling process, all of which were previously log-transformed and scaled. These variables are:

1. Scaled_CurrentArea_TotalArea

2. Scaled_Log_Brain_Mass_g
3. Scaled_Log_Current_Area_KM2
4. Scaled_Log_Generation_time_d
5. Scaled_Log_Mass_g

We tested all possible combinations of the 5 trait predictors across models and applied multicollinearity diagnostics to refine the final models. To do this, we calculated Variance Inflation Factor (VIF) scores in car; a R package (Fox and Weisberg 2019), for all trait combinations and excluded those with VIF > 2 to minimize multicollinearity. This step ensured the statistical independence of predictors.

Using these 5 traits, we constructed comprehensive phylogenetic logistic regression models (Ives and Garland 2010) that included combinations of the traits against extinction risk across 12 IUCN threat categories derived from the Threats Classification Scheme (Version 3.3). These threat categories initially included:

1. Residential & commercial development (n = 57 species)
2. Agriculture & aquaculture (n = 106)
3. Energy production & mining (n = 38)
4. Transportation & service corridors (n = 28)
5. Biological resource use (n = 169)
6. Human intrusions & disturbance (n = 33)
7. Natural system modifications (n = 23) — **excluded**
8. Invasive and other problematic species, genes & diseases (n = 16) — **excluded**
9. Pollution (n = 28)
10. Geological events (n = 0) — **excluded**
11. Climate change & severe weather (n = 36)
12. Other options (n = 3) — **excluded**

Above, “n” refers to the number of mammal species in the dataset that we classified as being threatened in each specific IUCN threat category.

We excluded categories 7, 8, 10 and 12 with fewer than 25 observations because models with very small sample sizes (e.g., fewer than five observations per predictor variable) lack sufficient statistical power, increase the risk of overfitting, and produce unreliable or unstable estimates in logistic regression analysis.

In total, we ran nine separate phylogenetic logistic regression models; one total-threats model and eight threat-specific models based on the filtered IUCN threat categories listed above. To account for shared evolutionary history among species, we used a phylogenetic logistic regression framework. We conducted this using the phylolm and ape packages in R (Ives and Garland 2010, Ho and Ané 2014, Paradis et al. 2004).

Visualization of model outputs

To visually represent the effect sizes of biological traits across different threat models, we utilized the ggplot2 package in R (Wickham 2009), a widely used tool for data visualization in scientific research. Other R packages used alongside ggplot2 include, dplyr, readr and scales (Wickham 2009, Wickham et al. 2023). We loaded the visualization dataset into R and we added significance labels based on p-values by computing vertical position for the asterisk annotations. To avoid overlapping with the bars, we computed vertical offsets for significance indicators (asterisks) based on each trait's effect size and standard error. We annotated significance levels using conventional asterisk notation (***p < 0.001, **p < 0.01, *p < 0.05), reflecting standard p-value thresholds.

We ordered threat models for interpretability and applied a high-contrast colour palette, with the Total Threats Model highlighted in black for emphasis. We generated the final plot by creating bar plots with error bars to display the direction, magnitude and precision of trait effects across each phylogenetic logistic regression model. We formatted plot titles, axis labels and legends for clarity and consistency. We applied this computation to generate both the raw effect size plot (Fig. 1) and the standardized effect size plot (Fig. 2).

Results

Trait effects across threat models

Among all the models we evaluated, the Total Threat Model (Fig. 1, black bars) provided the broadest insight into extinction risk across Nigeria's mammalian fauna. This model identified the small current geographic range as the most robust predictor. Larger brain mass also emerged as a strong predictor. Although generation time showed a negative relationship with extinction risk in this model, the association was not statistically significant. These results are visualized in Fig. 1, which summarizes trait effects across all threat models.

Four threat-specific models stood out: Agriculture & Aquaculture, Biological Resource Use (hunting), Residential & Commercial Development and Climate Change & Severe Weather. In the agriculture model, extinction risk was significantly higher among species with longer generation times, larger brains and smaller range sizes. Similarly, the best model for hunting, which is the Biological Resource Use model, shows that brain mass and range size were significant, reflecting patterns of targeted extraction in species with higher cognitive or social traits.

In the Residential & Commercial Development model, brain mass was again a highly significant predictor. Although other traits like body mass and range size were also negatively associated with risk, they did not reach statistical significance. Other models such as Energy Production & Mining, Transportation and Climate Change & Severe Weather also revealed meaningful trait associations, particularly with generation time and range size. For instance, species with longer generation times were at significantly higher risk from infrastructure development and mining activities, while brain mass was a key vulnerability factor under climate-related threats.

Key findings

Brain Mass was the most consistent and influential predictor across models (Fig. 2), with the highest standardized effect sizes in Climate Change & Severe Weather, Residential & Commercial Development and Biological Resource Use. Its strong and repeated significance suggests that larger-brained species may be more vulnerable.

Current Area (km^2) exhibited consistently negative effects and was highly significant in Agriculture & Aquaculture, Biological Resource Use, Human Intrusions and the Total Threats Model. These results highlight that species with limited geographic ranges are particularly susceptible to a variety of threats.

Generation Time showed strong positive associations in Energy Production & Mining, Agriculture & Aquaculture and Transportation & Service Corridors, implying that species with longer life cycles and slower reproduction are more at risk under rapid anthropogenic change.

Body Mass had weaker, generally non-significant effects. The only marginally significant relationship appeared in Agriculture & Aquaculture, suggesting body mass is not a consistent risk predictor in this context.

Current Area Relative to Total Range had variable effects. It was significantly negative in Human Intrusions & Disturbance and positively associated in the Total Threats Model, indicating that its influence may depend on the spatial nature of specific threats.

The effects of trait predictors across the threat models are collectively visualized in Fig. 1 and Fig. 2, providing both standardized and raw perspectives. Fig. 1 displays the raw model outputs as a bar plot of standardized effect sizes for each trait across nine IUCN threat categories, with error bars indicating standard errors and red asterisks marking significance levels. Color-coded bars distinguish individual models, while the Total Threat Model is highlighted in black to provide a cumulative reference. Fig. 2 complements this by presenting fully standardized coefficients, allowing direct comparison of trait influence across different threat contexts on a common scale.

Discussion

Brain size emerged as the most consistent and statistically significant predictor in our result across multiple threat categories. This result was particularly evident under threats such as Residential & Commercial Development, Agriculture & Aquaculture, Biological Resource Use and Climate Change & Severe Weather (Fig. 1). In all cases, larger brain mass was positively associated with increased extinction risk. This supports earlier findings that large-brained species, especially primates, tend to be more behaviorally specialized and are extremely affected by human-induced pressures (Chichorro et al. 2019, Gonzalez-Voyer et al. 2016). Larger brains are often associated with traits such as longer developmental periods, delayed reproduction and higher energy demands (Gonzalez-Voyer et al. 2016). These traits, although beneficial in stable environments, may impair resilience in the face of rapid anthropogenic change. Furthermore, such species are often the targets of wildlife trade and hunting (Maxwell et al. 2016), exacerbating their vulnerability.

Species with smaller current geographic ranges were significantly more at risk under Agriculture & Aquaculture, Biological Resource Use, Human Intrusions and in the Total Threats Model. This aligns with well-established evidence that range-restricted species are particularly susceptible to extinction (Sesink et al. 2015, Slatyer et al. 2013). In Nigeria, habitat loss from agriculture and logging has disproportionately impacted forest-dwelling species, many of which already occupy limited ranges in the Guinean forest zone (Luiselli et al. 2019, Maxwell et al. 2016). Our findings reinforce the critical role of spatial extent in mediating species persistence, particularly under land-use pressure (Halley et al. 2014).

A longer generation time predicted higher extinction risk under threats such as Agriculture & Aquaculture and Energy Production & Mining (Fig. 1). This aligns with life-history theory, which suggests that slow-reproducing species recover more slowly from population declines (Gaillard et al. 2000, Robbins and Sawyer 2007). However, under Climate Change & Severe Weather, the relationship was reversed, with shorter generation times associated with greater risk. This suggests that reproductive strategy interacts differently with threat type, possibly due to fast-living species being more sensitive to environmental variability (Chichorro et al. 2022).

Body mass displayed weak or non-significant effects in most models in our findings (Fig. 1), reaching marginal significance only in the Agriculture & Aquaculture. While larger body size is often linked to increased extinction risk due to higher energetic demands and larger home range requirements (Cardillo et al. 2005, Chichorro et al. 2019, Montero-Botey et al. 2024), our findings suggest that in Nigeria, this relationship is less robust than for brain size or range extent. This weak association between body size and extinction risk in Nigerian mammals may reflect context-specific factors such as indiscriminate human pressures on both small and large species from hunting and habitat loss (Fa and Brown 2009), historical loss of large-bodied species (Faith 2014) and stronger influences of traits like brain size or range extent (Sol et al. 2002, Sesink et al. 2015).

The extent of range contraction, quantified as the ratio of the current to the historical geographic range, showed mixed results across the threat models. It was significantly associated with increased vulnerability only under Human Intrusions & Disturbance and in the Total Threats Model (Fig. 1). This ratio reflects the cumulative loss of habitat and range contraction due to anthropogenic pressures. Compared to the absolute current range size, which was a consistently strong negative predictor across multiple threat models, this metric appears less predictive of extinction risk. This may be due to the variability in estimating historical ranges, or the fact that range contraction does not always equate to current vulnerability (Luiselli et al. 2019, Montero-Botey et al. 2024).

Conservation implications

- Large-brained species such as primates and carnivores should be prioritized due to their elevated risk under multiple threats. Many of these species are already targets of hunting and trade (Fa et al. 2002, Luiselli et al. 2019).
- Species with small geographic ranges require focused habitat protection, especially in unprotected or highly fragmented areas.
- Long generation species, often large mammals, face increased risk under slow landscape recovery conditions and may benefit from population management and long-term monitoring.

Limitation

While this study provides valuable insights into the trait-based determination of extinction risk among Nigerian mammals, several limitations need to be mentioned. Foremostly, the IUCN threat data used to classify species exposure to different threats may have limited resolution or attribution accuracy, especially for indirect threats such as pollution and climate change (IUCN 2024). These threats often act gradually or through complex pathways, making it difficult to establish direct cause-effect relationships (Maxwell et al. 2016). As a result, trait-risk associations under these categories may be less precise. Second, although trait data were obtained from robust global databases, a subset of species required manual correction or estimation due to missing values or taxonomic mismatches. For instance, some traits were inferred using genus-level means or close relatives, which may introduce uncertainty into model estimates (Penone et al. 2014). Finally, while the phylogenetic logistic regression framework helps correct for shared evolutionary history, results are inherently shaped by the completeness and accuracy of the phylogenetic tree and underlying species taxonomy (Rabosky 2016).

Conclusions

This study provides evidence that extinction risk among Nigerian mammal species is not random but biologically patterned. This suggests that certain biological traits, particularly brain size, geographic range and generation time, consistently make species more vulnerable. Species with larger brains, notably primates and carnivores, were consistently more vulnerable across multiple threat categories such as agriculture, biological resource use, urban development and exceptionally, climate change. This vulnerability likely stems from their behavioral specialization, low reproductive output, and increased interaction with human-altered environments (Chichorro et al. 2019, Gonzalez-Voyer et al. 2016). Similarly, we found species with restricted geographic ranges to be significantly at risk due to their limited adaptability and heightened sensitivity to localized disturbances, a pattern well-documented in biodiversity hotspots like Nigeria’s Guinean forest region (Luiselli et al. 2019, Maxwell et al. 2016).

While longer generation time increased risk under direct anthropogenic pressures, its relationship with extinction risk varied under climate-related threats, where short-lived species appeared more susceptible, possibly due to their physiological sensitivity to rapid environmental change (Gonzalez-Voyer et al. 2016). In contrast, body mass, often highlighted in global extinction studies, showed weak and inconsistent effects in this study. This may suggest that in the Nigerian context, both large and small mammals may be equally impacted by these pressures, or that other traits, such as cognitive ability and spatial range, offer greater predictive strength. Although climate change showed a particularly strong trait-based effect on brain size, pollution exhibited little to no significant trait associations, possibly reflecting more diffuse, indirect mechanisms or limitations in threat attribution (Rhind 2009). These findings reinforce the need for localized trait-based analyses, as extinction dynamics can diverge meaningfully from broader global patterns.

Our findings support the integration of trait-based and phylogenetically informed models into conservation planning, which is even more critical in underrepresented regions like Nigeria, where data-driven strategies are urgently needed. Prioritizing species with high trait-based vulnerability, such as those with large brains, small ranges and slow reproduction, could improve the efficiency of conservation efforts (Kumschick and Richardson 2013). In addition, the study underscores the value of tailoring responses to specific threats, as different drivers filter species along different biological axes. This research enhances our understanding of extinction dynamics in a key region of African biodiversity hotspots and based on intrinsic species biological traits; it provides a scalable framework for guiding conservation interventions.

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Hosting institution

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Conflicts of interest

The authors have declared that no competing interests exist.

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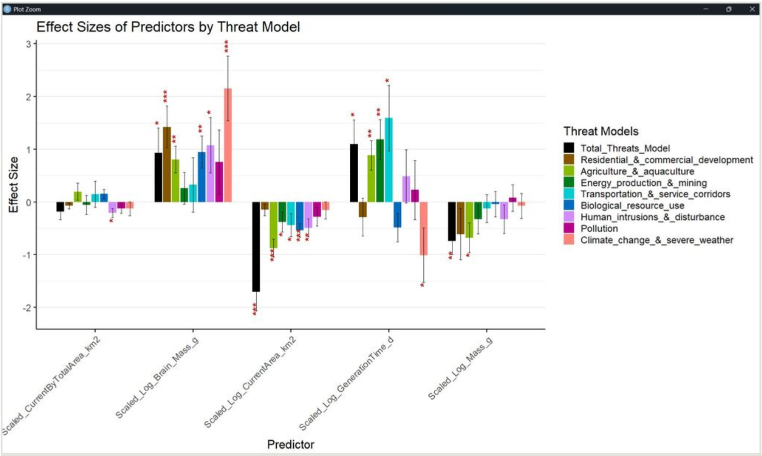

Figure 1.

Effect sizes of biological trait predictors across IUCN threat models. Bars represent regression coefficients (± SE) from phylogenetic logistic regression models. Asterisks indicate significance: ***p < 0.001, **p < 0.01, *p < 0.05. Colours represent different threat models; the black bar indicates the Total Threat Model.

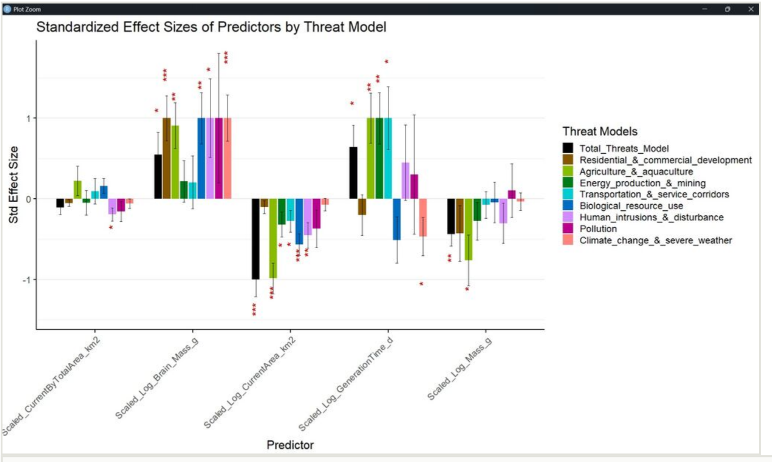

Figure 2.

Standardized effect sizes (Std_SE) of trait predictors across threat models. All predictors are standardized (mean = 0, SD = 1) to allow direct comparison of effect sizes across traits. Bars indicate standardized regression coefficients derived from phylogenetic logistic regression. Predictors include current-area by total-area, brain mass, current area, generation time and body mass. Asterisks indicate significance (***p < 0.001, **p < 0.01, *p < 0.05). Colours represent different threat models; the black bar indicates the Total Threat Model.