



DEPARTMENT OF BIOLOGICAL AND  
ENVIRONMENTAL SCIENCES

# 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.

## Abstract (SE)

Denna studie syftade till att utvärdera hur biologiska egenskaper påverkar utrotningsrisken bland däggdjursarter i Nigeria, och hur dessa egenskaper interagerar med specifika antropogena hot såsom jordbruk, urbanisering och klimatförändringar. Med fokus på däggdjursarter i Nigeria använde vi fylogenetisk logistisk regression för att testa inflytandet av fem biologiska egenskaper: kropps massa, hjärn massa, generationstid, nuvarande geografiska utbredning och historisk utbredning, på utrotningsrisk över 9 IUCN-hotkategorier. Standardiserade modeller användes för att jämföra egenskapernas känslighet mellan hot. Hjärn massa framstod som den mest konsekventa och inflytelserika prediktorn för utrotningsrisk, särskilt under hot som jordbruk, biologisk resursanvändning och stadsutveckling. Arter med större hjärnor, ofta primater och köttätare, var mycket sårbara. Geografisk utbredningsområdesstorlek var en stark negativ prediktor för risk i de flesta modeller, där arter med begränsat utbredningsområde var mer mottagliga för förlust av livsmiljöer och fragmentering. Generationstid var positivt associerad med risk under direkt mänsklig påverkan men omvänt kopplad under klimathot. Kroppsmassa uppvisade svaga och inkonsekventa effekter, vilket tyder på att dess inflytande kan vara sekundärt till kognitiva eller rumsliga egenskaper. Antalet drabbade arter var högst under mänskliga hot, jämfört med klimatförändringar eller föroreningar. Utrotningsrisken hos nigerianska däggdjur formas av inneboende egenskaper som interagerar förutsägbart med mänsklig påverkan. Arter med stora hjärnor, små utbredningsområden och långsam reproduktion löper störst risk. Egenskapsbaserade modeller kan förbättra bevarandeplaneringen genom att identifiera sårbara arter innan populationsminskningarna blir kritiska, särskilt i regioner som står inför intensiva förändringar i markanvändningen.

Nyckelord: Utrotningsrisk, hjärnstorlek, Nigerianska däggdjur, mänsklig påverkan.

# 1. 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 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 their species at risk of extinction (IUCN, 2024). The loss of key mammalian species can lead to ripple effects within the ecosystem, with significant ecological consequences. 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). Located in the heart of Africa, Nigeria harbours many species - including mammals - that may contribute to the alarming global extinction risk highlighted by the IUCN. This area is understudied yet a critically important region for biodiversity.

This study offers the possibility to identify specific traits linked to extinction risks among mammal species in Nigeria. Several biological traits contribute to the extinction risk of mammalian species, reflecting evidence already seen in global patterns. 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, which includes habitat encroachment and land conversion to agriculture (Montero-Botey, 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). In addition, slow-reproducing species such as Western gorillas face serious challenges in recovering from population declines (Robbins & Sawyer, 2007).

These findings suggest that human-driven environmental factors, such as agriculture and overexploitation, maybe the major drivers of extinction risk, especially for mammals with small ranges, large body mass, large brain mass, or slow reproduction. In the same way, these patterns may suggest that globally, mammals with limited geographic ranges, large body mass, large brain mass, or slow reproduction rates may be more susceptible to extinction across diverse ecosystems. Despite Nigeria region's richness in biodiversity, studies on extinction risk are limited, thereby creating a knowledge gap in conservation science and intervention in the region. There are recent studies that show emerging concerns (Gbadegesin *et al.*, 2024; Imarhiagbe *et al.*, 2019; Ukpoju *et al.*, 2023). However, little has been done that is specific to its mammalian populations. The project addresses this gap by focusing on what biological traits increase the vulnerability of Nigerian mammal species to extinction, and how do these interact with specific human-caused threats?

## 1.1 Aim

The study aims to examine extinction risk patterns among Nigerian mammals to identify traits that correlate with higher susceptibility to extinction. By highlighting these patterns, the project aims 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. This data will serve as the basis for investigating extinction risks which are specific to Nigerian mammals. 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. This will allow for a comparative analysis of the types of threats caused by the different impacts as listed on the IUCN Threats Status and Classification Scheme across different species within Nigeria. 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.

These traits are used based on previous studies that indicate a link between these characteristics, and the vulnerability of mammalian species to anthropogenic pressures (Chichorro *et al.*, 2019). Data for these analyses will be obtained from reputable databases as well as the literature on Nigerian biodiversity and mammal populations. This is to ensure comprehensive and reliable input. Statistical analyses will be conducted using R software (Lander, 2014), in which phylogenetic logistic regression will be applied to assess which closely related forms are more similar than random.

This study seeks to deepen the understanding of extinction risks among Nigerian mammals by analyzing species-specific traits that increase vulnerability to human impacts. The project's findings will address the pressing need for data-driven conservation efforts in Nigeria, a region with high biodiversity and substantial conservation challenges. By identifying specific traits that heighten extinction risks, new insights will be added to existing knowledge on mammal conservation in biodiversity hotspots and offer practical insights for targeted conservation strategies.

## 2. Material and method

### 2.1 Study Area and Context

We conducted the study within Nigeria, a key region of the Guinean forest biodiversity hotspot in Africa (Luiselli *et al.*, 2019). We investigated patterns of extinction risk among Nigerian mammal species by analyzing biological traits, geographical ranges, anthropogenic threats, and the interactions between traits and threats. We focus on data analysis of Nigerian mammal species with the main target group being the mammalian species found within Nigeria as listed in the International Union for Conservation of Nature's (IUCN) Red List Version 2024-2 (IUCN, 2025b). Human activities were considered as external variables that influence mammalian extinction risks. Understanding extinction risks in this region is crucial due to its ecological significance and the insufficiency of conservation-focused studies.

### 2.2 Study Design and Data Compilation

To begin our analysis of extinction risk in Nigerian mammals, we first built a clear and consistent dataset that combined species, traits, and threat information. 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). Our goal was to make sure the data were well-organized, matched across sources, and ready for analysis. 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. These traits are widely used in conservation science because they reflect how species respond to human pressures and environmental change (Chichorro *et al.*, 2019; Healy *et al.*, 2019). We also included information about the types of threats each species faces, based on the IUCN Threats Status (IUCN, 2025a) and the IUCN Threats Classification Scheme (IUCN, 2025b). This gave us a complete picture that allowed us to explore how different traits relate to extinction risk under different human impacts. We conducted all R analyses in RStudio version 2024.12.1+563 using relevant packages, and Microsoft Excel 365 was used for additional data cleaning and integration.

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 exported to a CSV file for final cleaning in Microsoft Excel where 314 observations of mammalian species in Nigeria were obtained.

To ensure data consistency and comparability across different research studies for correct extinction risk assessments, we carried out dataset matching for the 314 IUCN Red List mammalian species name (SCI\_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). This dataset consisting of 5831 mammalian species was used from the compressed folder (named PHYLACINE\_1.2.1) downloaded from PHYLACINE database. Without integrating these datasets into one, the primary data from IUCN Red List was revalidated with the others (Upham Phylogeny and PHYLACINE) to resolve inconsistencies in taxonomic rank formats. As a result, this updated

the species' names to achieve harmony while reflecting recent taxonomic revisions (Moura *et al.*, 2024). We took the following steps in matching the datasets species name:

1. The datasets from IUCN, Phylogeny and PHYLACINE were loaded into Excel workbook, each into different spreadsheets.
2. The column names (e.g. Species Name) were standardized to ensure consistency.
3. We used VLOOKUP to check if the IUCN species name exists in the Phylogeny and the PHYLACINE datasets. If the species' name is found, it returns the corresponding value. If not found, it returns #N/A.
4. For the mis-matched entries, such as the species names that were not found, we checked for alternative names using our authoritative source from IUCN to re-validate the names checking for synonyms or name changes to resolve the mismatch.
5. In cases where we encountered outdated names, they were cross-checked using the IUCN Red List and relevant taxonomic references to avoid duplication and ensure taxonomic consistency.
6. In creating the final species name dataset sheet, the IUCN species name column, which is the primary variable came first, and then the next variables were the Phylogeny and the PHYLACINE 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. PHYLACINE provided data on body mass from the source file 'Trait\_data.csv' (Faurby *et al.*, 2018), while we obtained brain mass and generation time from the COMBINE dataset from the source file 'imputation\_phylo\_825.csv' (Soria *et al.*, 2021).

**How it was obtained:**

Body mass was downloaded from PHYLACINE 1.2 database. We extracted the obtained compressed folder to a computer desktop and 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. Taxonomic mismatches were resolved manually by using the average size of related Genus, inferring from close relatives and deferring to the Combine database in few cases. Body mass metrics in the PHYLACINE database used consistent measurement protocols, minimizing variability across species and sources.

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. The trait columns in the cleaned data were renamed for consistency in Brain mass (from 'brain\_mass\_g' to 'Brain\_Mass\_g') and in Generation time (from 'generation\_length\_d' to 'Generation\_time\_d'). We merged the data further with Microsoft Excel application using species' scientific names as identifiers. Taxonomic mismatches were resolved manually by inferring from close relatives in a few cases.

## B. Geographic Range (in km<sup>2</sup>)

### Source:

The range was obtained from the IUCN Red List (Faurby & Svenning, 2016).

### 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.

Data was filtered for the species data points; to ensure that the logic works correctly and catch errors before looping over all data.

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. Geographic range sizes were calculated, and the area units were converted from square meters (m<sup>2</sup>) to square kilometers (km<sup>2</sup>).

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. This data was saved in R as a CSV file for further use. From this, we selected the current range size variable as a trait.

In addition to the current range size variable utilized as a trait, we calculated a measure of historical range contraction for each species. This metric was computed in Microsoft Excel by dividing each species' current geographic range (from the column, *Current\_Area\_KM2*) by its estimated Total geographic area. The resulting ratio provides a proxy for the extent of habitat loss over time, with lower values indicating greater contraction. The area ratio column is referred to as *CurrentArea\_TotalArea* in the dataset. This variable was included as a predictor in the models to assess whether species that have experienced significant range reduction are more likely to be at risk of extinction under current threat conditions (Montero-Botey *et al.*, 2024). We integrated the calculated range sizes into the primary dataset.

Range data could not be computed for 17 species due to missing geographic information in the IUCN polygon shapefile (IUCN, 2024). These species were predominantly aquatic mammals, except for one arboreal species, *Casinyceteris campomaanensis*. For consistency in data formatting and downstream analyses, a value of '0' was assigned to the range variable for each of these species in the final dataset.

We reviewed the units for all traits to ensure consistency: body and brain mass were in grams, generation time in days, current area and historical range contraction in kilometers.

C. We additionally integrated into this dataset, the full hierarchical structure of the individual threat types (IUCN, 2025b) 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 (2025b) Red List species profiles and recorded in structured format. For each species, we visited corresponding web profiles, and all threats listed (or not) under the IUCN Red List ‘Threats in detail’ subsection were thoroughly reviewed. Upon verification of each species’ threats, the responses were manually coded into the dataset, which has been structured to have 12 new variables, each column representing the IUCN threats class classification. 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.” No prioritization of primary threats was performed.

To represent an overall extinction risk status, we created a separate binary variable for the Total Threats Model using the IUCN Red List status (IUCN, 2025a). Species listed as Vulnerable (VU), Endangered (EN), or Critically Endangered (CR) were classified as threatened (“1”), while those listed as Near Threatened (NT) or Least Concern (LC) were classified as not-threatened (“0”). Species listed as Data Deficient (DD) were excluded from the analysis due to uncertainty in their extinction risk status. The categories Not Evaluated (NE), Extinct in the Wild (EW), and Extinct (EX) were not present in our dataset during the filtering process.

We cross-checked all 314 observations with the IUCN Threats Classification Scheme and the Red List conservation status to ensure consistency and accuracy.

We integrated all results into the dataset of primary variables, which include species names; SCI\_NAME from IUCN, Phylogeny taxonomy and PHYLACINE taxonomy, ensuring completeness and accuracy. The final list of 314 species represents all terrestrial mammal species with valid and complete trait and threat data available across the IUCN, PHYLACINE, and phylogenetic sources. However, geographic range data could not be computed for 17 of these species—primarily aquatic or semi-aquatic mammals, with the exception of the arboreal bat *Casinycotis campomaanensis*, due to missing polygon data in the IUCN shapefile.

### **2.3 Trait Selection and Justification**

The biological traits we selected for analysis; body mass, brain mass, reproductive rate, and geographic range, were based on their established links to extinction risk (Chichorro *et al.*, 2019; Gonzalez-Voyer *et al.*, 2016). We consider body mass because larger mammals often require extensive habitats and are disproportionately impacted by human activities. Brain mass is selected because it is often associated with cognitive abilities which can influence a species' ability to cope with environmental changes, human impacts, and resource scarcity—factors that affect extinction risk. We analyzed reproductive rates due to their influence on population recovery following declines. Geographic range was included to evaluate the extent of habitat specialization, as species with limited ranges are more vulnerable to habitat loss. We extracted these traits from databases and corroborated with published studies to maintain data reliability (Montero-Botey, 2024, Upham *et al.*, 2019).

### **2.4 Data and Statistical Analysis**

We conducted data analysis using phylogenetic logistic regression, a statistical method that helps identify which biological traits are linked to a species being threatened or not, while also accounting for how closely related the species are to one another. This approach is important because closely related species often share similar traits, and may face similar extinction risks (Ives & Garland, 2010). Before running the analysis, we carefully extracted, filtered, and cleaned the data using

Microsoft Excel application and R software (Lander, 2014) to make sure everything was accurate and ready for modeling. We used specific R packages at different stages of the 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).

All continuous trait data, such as body mass, brain mass, generation time, and geographical ranges, were first transformed to normalize their distribution and reduce the impact of extreme values. This transformation helps meet statistical assumption of normality, making the data more suitable for analysis. 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 & Hui, 2011). Therefore, we applied only *scale()* to standardize the variable for comparability across predictors while preserving the interpretability of proportional range contraction.

## 2.5 Phylogenetic Modelling and Threat-Specific Analysis

We constructed a series of phylogenetic logistic regression models to examine the relationship between biological traits and extinction risk among Nigerian mammals (Ives & Garland, 2010). We developed a total threats model, derived from an overall binary measure of whether a species is classified as threatened or not, based on its IUCN Red List conservation status (IUCN, 2025a), and we also built individual threat-specific models to assess how trait-risk relationships varied across specific human-induced and environmental pressures, according to the IUCN Threats Classification Scheme (IUCN, 2025b).

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

These trait variables represent core biological characteristics related to space use, physiology, and reproductive dynamics, which are known to influence extinction vulnerability (Chichorro *et al.*, 2019). 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, thereby enhancing the interpretability and reliability of model estimates. The strict cutoff helps ensure more robust and reliable coefficient estimates, particularly in models where ecological and trait variables may be inherently correlated.

Using these 5 traits, we constructed specific phylogenetic logistic regression models (Ives & Garland, 2010) that included combinations of the traits against extinction risk across particular 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 (Ives & Garland, 2010).

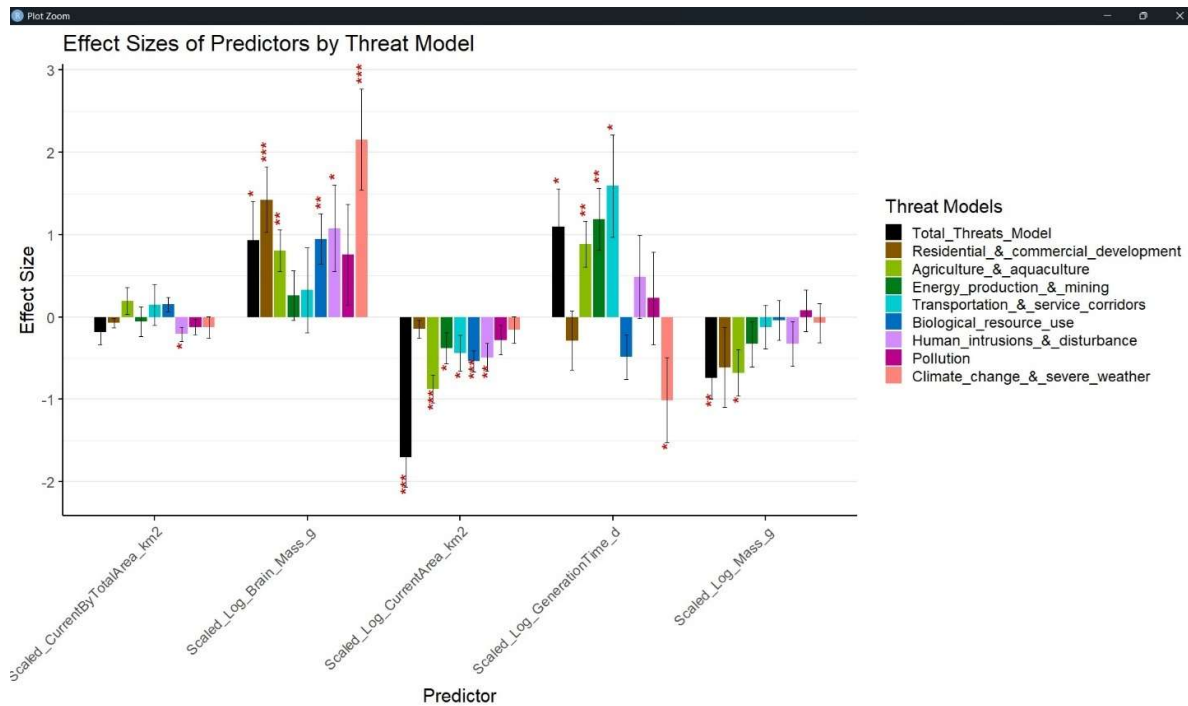
In total, we ran nine separate phylogenetic logistic regression models; one total-threats model (an overall measure of all the threat exposures to any of the IUCN threat categories) and eight threat-specific models based on the filtered IUCN threat categories listed above. To account for shared evolutionary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

For each of these models, we applied the *phylolm()* function from the *phylolm* package in R, incorporating a binary response variable (0 or No = not threatened, 1 or Yes = threatened), allowing for a clear distinction between species at risk and those that are not (Anthony, 2010). This helps us reduce biases that could arise from closely related species having similar extinction risks. We adjusted for phylogenetic correlation by using the species-level phylogenetic tree, which was pruned to match the species present in our data. We obtained the phylogenetic tree used for this analysis from the PHYLACINE 1.2 database (Faurby *et al.*, 2018), and provided in Newick format as ‘Complete\_phylogeny.nex’, which includes a comprehensive, time-calibrated phylogeny for mammals. The tree was pruned in R using the *drop.tip()* function from the *ape* package (Paradis *et al.*, 2004), retaining only the 314 mammal species present in our dataset.

For each of the 9 models, we applied 5 biological trait variables as predictors, resulting in a total of 45 predictor-effect estimates. All 5 biological predictors were included simultaneously in each model. Using R, we first constructed a ‘Total Threats Model’, representing an overall binary measure (e.g., threatened vs. non-threatened) of whether a species is classified as threatened under the IUCN Red List conservation status (IUCN, 2025a). We implemented this in R by creating a composite response variable (*ThreatStatus\_bin*) that assigned a value of “1” if the species was listed as Vulnerable, Endangered, or Critically Endangered, and a value of “0” if listed as Near Threatened or Least Concern. We then fitted a phylogenetic logistic regression using the *phylolm()* function with the “*logistic\_MPLE*” method (Anthony, 2010). In addition, we fitted this model using the full set of biological predictors and the pruned phylogenetic tree (Ho & Ané 2014). Subsequently, we ran separate models for each of the eight IUCN threat-specific classes by looping through the corresponding threat columns of our dataset derived from the IUCN threats classification scheme (IUCN, 2025b). For each class, we generated a binary response variable

indicating whether a species was affected ("Yes") or not ("No") by that specific threat (Anthony, 2010). We then applied the same model function, predictor set, and phylogenetic tree across all models to ensure consistency and comparability of trait-threat relationships.

From the models, we extracted the raw effect sizes, their associated standard errors (SE), and the significance for each predictor variable, which were used for visual representation in Figure 1. To allow meaningful comparison across predictors and models, we standardized both the effect sizes and their associated standard errors. This procedure was done by first scaling all predictors to have a mean of 0 and a standard deviation of 1 (Gelman, 2008). We also normalized the effect sizes such that we scaled the strongest predictor within each model to either +1 or -1. This normalization yielded standardized effect sizes (Std\_Effect\_size) and standard errors (Std\_SE), placing all variables on a common scale and enhancing interpretability across the different threat contexts (Nakagawa & Cuthill, 2007). Data extracted manually from the 9 models based on 5 predictors each, resulted in 45 observations with variables having columns titled: 'Model', 'Predictor', 'Effect\_size', 'SE', 'Sig', 'Std\_Effect\_size', 'Std\_SE'. This became our visualization dataset.

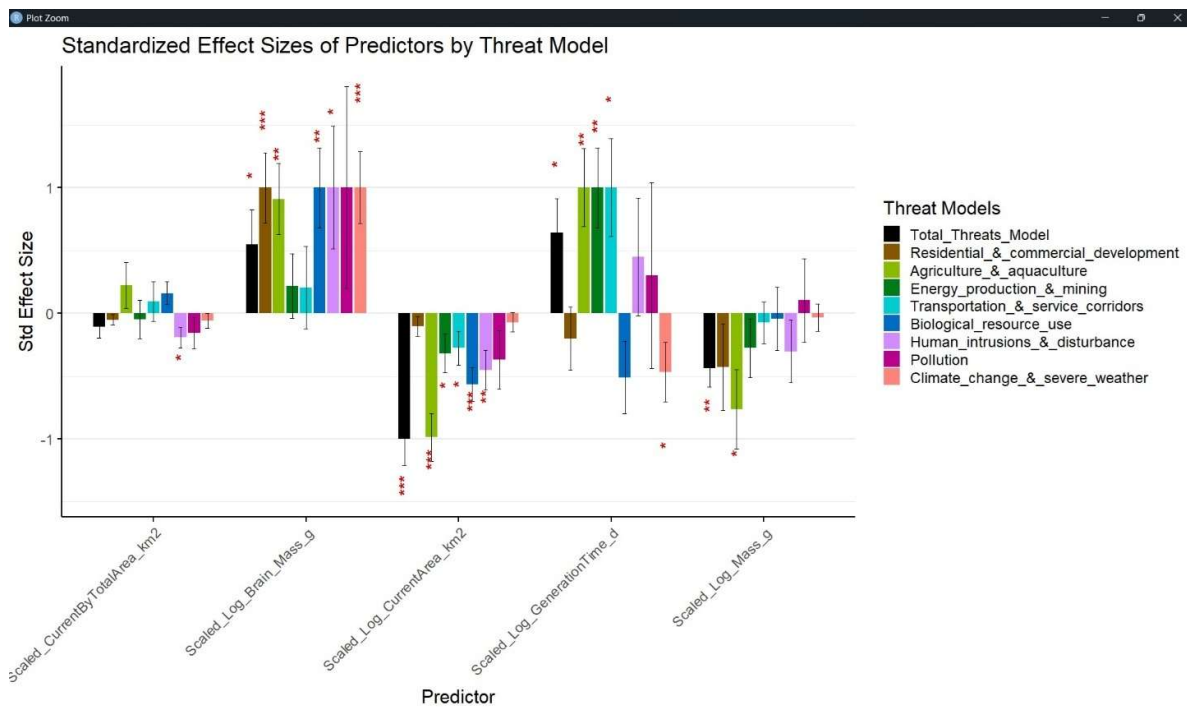


**Figure 1:** Effect sizes of biological trait predictors across IUCN threat models. Bars represent regression coefficients ( $\pm$  SE) from phylogenetic logistic regression models. Asterisks indicate significance: \*\*\* $p < 0.001$ , \*\* $p < 0.01$ , \* $p < 0.05$ . Colours represent different threat models; the black bar indicates the Total Threat Model.

## 2.6 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 (Figure 1) and the standardized effect size plot (Figure 2).



**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.

### 3. Results

This chapter presents the outcomes of the phylogenetic logistic regression analyses, that was conducted to evaluate the influence of key biological traits on the extinction risk of Nigerian mammal species across diverse anthropogenic threat categories. We report the effect sizes, standard error and statistical significance of five trait variables across the aggregated Total Threats Model and the 8 IUCN threat-specific models. We also report the standardized data. Results are supported by quantitative data and visualized through comparative plots of model outputs.

#### 3.1 Trait Effects Across Threat Models

Among all the models we evaluated, the Total Threat Model (Figure 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. Generation time showed a positive and statistically significant relationship with extinction risk in this model. Additionally, body mass exhibited a significant negative effect under cumulative threats. These results are visualized in Figure 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.

#### 3.2 Standardized Effects of Predictors Across Threat Models

To compare the influence of traits across threat categories, we standardized effect sizes and standard error variables from phylogenetic logistic regression models. Figure 2 presents these standardized coefficients across nine IUCN threat categories.

##### 3.2.1 Key Findings

Brain Mass was the most consistent and influential predictor across models (Figure 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<sup>2</sup>) exhibited consistently negative effects and was highly significant in the Total Threats Model, Agriculture & Aquaculture, Biological Resource Use and Human Intrusions. These results highlight that species with limited geographic ranges may be particularly susceptible to a variety of threats.

Generation Time showed strong positive and statistically significant associations in the Total Threats Model as well as in Energy Production & Mining, Agriculture & Aquaculture and Transportation & Service Corridors, implying that species with longer life cycles and slower reproduction may be more at risk under rapid anthropogenic change.

Body Mass showed a consistent negative effect in the Total Threats Model, and was statistically significant, contrasting with weaker or non-significant effects across most threat-specific models. 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 Figures 1 and 2, providing both standardized and raw perspectives. Figure 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. Figure 2 complements this by presenting fully standardized coefficients, allowing a direct comparison of trait influence across different threat contexts on a common scale. Together, these visualizations emphasize the consistent role of traits like brain mass and geographic range in predicting extinction risk, while also revealing variation in trait importance depending on the specific threat type.

Across threat models, both raw and standardized results revealed consistent trait-risk associations. Brain Mass was the strongest and most reliable predictor of extinction risk, with significant positive effects across threats such as urban development, agriculture, biological resource use and climate change. Standardized models confirmed their dominant influence, showing the highest scaled effect sizes. Generation Time was also a significant positive predictor, including in the Total Threats Model, and in several contexts such as agriculture and transportation infrastructure, though effects varied across models. Current Area (km<sup>2</sup>) consistently exhibited strong negative effects in both raw and scaled analyses, reinforcing the vulnerability of range-restricted species. Body Mass showed a significant negative effect in the Total Threats Model and the Agriculture & Aquaculture, but otherwise displayed weak, non-significant or marginal effects across all models, suggesting limited predictive power under most threat conditions, even in agriculture, where it reached significance only modestly.

## 4. 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, Climate Change & Severe Weather and the Total Threats Model (Figure 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). Brain mass and geographic range size remained the most influential predictors, reinforcing their central role in driving extinction risk across threat types, as seen in the Total Threats Model (black bar in Figure 1). This aggregate model serves as a benchmark for comparing how trait effects vary under specific threats.

A longer generation time predicted higher extinction risk under threats such as Total Threats Model, Agriculture & Aquaculture, and Energy Production & Mining (Figure 1). This aligns with life-history theory, which suggests that slow-reproducing species recover more slowly from population declines (Gaillard *et al.*, 2000; Robbins & 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). In the Total Threats Model (black bar in Figure 1), generation time also showed a statistically significant and positive effect, indicating that species with slower reproductive rates are at heightened risk. In contrast, body mass was negatively associated with extinction risk and reached statistical significance, suggesting that smaller-bodied species may be more vulnerable overall.

Body mass displayed weak or non-significant negative effects in most models in our findings (Figure 1), reaching marginal significance in Agriculture & Aquaculture. However, in the Total Threats Model, body mass was significantly and negatively associated with extinction risk, contrasting with expectations that larger species are universally more vulnerable. 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, 2024), our findings suggest that in Nigeria, this relationship is less robust than for brain size or range extent. This weak association between large 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 & 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). While larger mammals generally have larger brains due to allometric scaling,

extinction risk analyses often find that relative brain size (known as brain size relative to body size) is more informative than the raw brain size alone. This relative measure is referred to as called encephalization. And here is why larger brain mass may predict extinction risk independently of body mass. In this study, we used raw brain mass data alongside body mass to model extinction risk. The significant predictive power of brain mass independent of body mass suggests that relative brain size or encephalization may influence extinction vulnerability (Kruska, 2005).

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 (Figure 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 (Montero-Botey *et al.*, 2024; Luiselli *et al.*, 2019).

#### **4.1 Trait Sensitivity under Human Threats**

Our study reveals that direct human-induced threats, such as hunting, agriculture and urban development have stronger and more consistent links to species traits than indirect and environmental threats like pollution or climate change. Among the traits analyzed, brain size emerged as the most robust predictor of extinction risk under human threats, with significantly high effect sizes in agriculture, biological resource use, urban development, and human disturbance (Figure 2). This suggests that cognitively complex mammals, particularly primates and carnivores, are especially vulnerable to human exploitation and land-use pressures (Chichorro *et al.*, 2019; Estrada *et al.*, 2017).

The geographic range also consistently showed strong negative effects under human threats (Figure 2), highlighting that species with restricted distributions are highly sensitive to localized habitat loss and fragmentation, especially from agriculture and logging (Maxwell *et al.*, 2016; Luiselli *et al.*, 2019; Montero-Botey *et al.*, 2024). These species often lack the ecological flexibility necessary to adapt or disperse in response to rapid habitat changes caused by human activities. Generation time further contributed to risk under human-driven pressures, with slow-reproducing species showing reduced capacity to recover from disturbances (Gaillard *et al.*, 2005; Chichorro *et al.*, 2022). Their low reproductive output limits population rebound in response to threats such as hunting or land clearance.

In contrast, under climate change, species with larger brain mass and shorter generation times were more at risk. This is possibly due to physiological or ecological sensitivity of these highly cognitive species (Figure 1 and 2) to environmental variability (Gonzalez-Voyer *et al.*, 2016). While under pollution, none of the traits significantly predicted extinction risk, suggesting that these threats may operate through more complex or indirect mechanisms (Rhind, 2009).

These findings indicate that human threats are more trait-selective, affecting species in predictable ways based on intrinsic biological characteristics. Conservation planning should therefore focus on trait-sensitive species, particularly those with large brains, small ranges, and slow reproduction, that are disproportionately impacted by human activities in Nigeria (Maxwell *et al.*, 2016).

## 4.2 Conservation Implications

Our study has strong conservation relevance, particularly for regional biodiversity strategies in Nigeria:

- 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.

Trait-based models, as applied in this context, provide valuable predictive tools for informed conservation decision-making. They enable risk assessments based on intrinsic species characteristics, allowing for the early identification of at-risk taxa (Kumschick & Richardson, 2013).

## 4.3 Limitation

While this study provides valuable insights into the trait-based determination of extinction risk among Nigerian mammals, several limitations need to be mentioned. Foremost, 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). Third, geographic range data could not be computed for 17 species, primarily aquatic or semi-aquatic mammals, due to the absence of spatial polygons in the IUCN shapefile (Rondinini *et al.*, 2011). We retained these species in the dataset with a placeholder value of zero, which may affect the interpretation of range-related predictors. 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 *et al.*, 2016). Furthermore, the findings although regionally important, may have limited relevance elsewhere to other biodiversity hotspots unless local ecological and threat variables are taken into account (Purvis *et al.*, 2000).

## 5. 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. However, in the aggregate model, smaller body size emerged as a significant risk factor, suggesting that, contrary to global expectations, smaller mammals may be disproportionately impacted in Nigeria, perhaps due to indiscriminate hunting or niche vulnerability (Fa & Brown, 2009). 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 & 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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## **Appendix 1: Popular science summary**

### **Where Have All the Mammals Gone?**

#### **Inside Nigeria's Extinction Crisis, and What We Can Do About It**

##### **A Biodiversity Hotspot in Trouble**

Imagine taking a walk through the lush Nigerian rainforest, where elephants once roamed majestically and chimpanzees swung through the treetops, and been greeted with echoing silence in that same forest. In recent years, more and more mammals in Nigeria have begun to vanish. Not from the pages of a nature book, but from real life. More unraveling is the fact that behind every lost animal and every empty forest lies a deeper story. One that science can help us uncover. To understand why so many mammals are disappearing, we must first decode the hidden patterns that put them at risk.

##### **Cracking the Extinction Code through Research**

Globally, according to IUCN (2025), over 46,300 species are threatened with extinction and for mammals, about one in every four species faces the risk of extinction. But in Nigeria, where nature and people often collide, the situation is even more urgent. To explore patterns of extinction risk on the 314 Nigerian mammals, a study which involves analyzing the biological traits of mammalian species, with a special focus on Nigeria's mammals was launched, reflecting trends already observed on a global scale. Nigeria as a country is part of the Guinean Forests of West Africa, one of the world's richest ecosystems. Sadly, it's also one of the most threatened. Some mammals like chimpanzees, elephants, and western gorillas are more at risk because species with small geographic ranges, large bodies, and slow reproduction are hit hardest by human-driven change, which is the focus of this study.

##### **Data with a Purpose**

This study used versatile computer-based statistical tools to analyze the traits of Nigerian mammals and the threats they face from human activity, in order to identify patterns in the data. By modeling how biological characteristics like brain size, body size, reproduction rate, and habitat need interact with threats such as agriculture, human intrusions, and climate change, we seek to determine which species are most at risk and why. In conservation initiatives, knowing where to start is key. Should we prioritize big mammals in forest zones? Or fast-declining species in farming areas? This study work aims to answer just that.

##### **What the Results Reveal**

What our ongoing study uncovered is both eye-opening and deeply concerning: not all mammals are equally vulnerable, and the traits that define a species (like its brain size, body size, reproductive rate, and how much land it needs) can predict how likely it is to disappear. For instance, species with larger brains, like chimpanzees, are more often threatened by urban development and climate change - possibly because their intelligence ties them closely to complex habitats now in decline. Those with smaller home ranges or slower reproduction cycles, such as gorillas and pangolins, were more at risk from agriculture and infrastructure, where rapid land-use changes outpace their ability to adapt or recover.

## **Why This Matters Now**

These patterns offer a predictive lens for identifying which species are most likely to decline. Each increase in extinction risk signals a weakening of ecosystem's health. Mammals help maintain forests, control pests, and spread seeds. Nigeria holds immense biodiversity, but it's vanishing. By identifying the traits that predict extinction risk, this study helps ensure conservation efforts are strategic and timely. With this knowledge in hand, we can do more than sound the alarm. We can act. Equipped with data, we have the chance to shape a different future. One where future generation will walk through those forests, not in silence, but in wonder.

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