Historical shifts, geographic biases, and biological constraints shape mammal taxonomy

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Short running title:

Temporal trends in mammal alpha taxonomy

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Abstract

Species descriptions in taxonomy have become increasingly comprehensive, yet disparities persist across taxa and regions. We assess temporal trends in mammal species descriptions (1990–2022) using four proxies of comprehensiveness—counts of examined specimens and compared taxa, number of pages (only from the Methods/Results sections), and number of evidence lines (i.e., analytical tools and techniques). Using generalised linear models, we assessed how these proxies are explained by factors associated with species' biology, geography, and taxonomic practice. Most new species derive from tropical regions, particularly rodents and bats, reflecting global discovery hotspots. Descriptions have grown more rigorous over time, with expanded specimen sampling, broader taxonomic comparisons, and integrative methods. However, disparities emerge along geographic and biological axes: temperate-region descriptions incorporate more evidence lines, while small-bodied and tropical species (especially bats) remain understudied due to sampling biases and resource limitations. Body size inversely correlates with description length, as smaller species often require advanced diagnostics. Species-rich genera show greater comprehensiveness, likely due to heightened diagnostic scrutiny, though bats exhibit the opposite trend, possibly due to taxon-specific sampling challenges. Our findings highlight progress in taxonomic rigor but underscore persistent gaps tied to geography, body size, and accessibility of analytical tools. Addressing these disparities requires targeted investments in local capacity, equitable collaboration, and accessible methodologies to strengthen global taxonomic infrastructure and support conservation priorities.

Keywords: Taxonomy, Linnean shortfall, Mammalia, species descriptions, taxonomic practice.

Introduction

Species represent fundamental units in biodiversity science (Braby, Hsu, and Lamas 2024), where their names constitute testable hypotheses subject to revision in light of new data (Bremer et al. 1990; Gippoliti, Farina, and Andreone 2024; Raposo et al. 2017; Streicher et al. 2023). Although taxonomic science is dynamic and an absolute nomenclatural stability is clearly undesirable (Dominguez and Wheeler 1997; Dubois 2007), avoiding unnecessary nomenclatural changes in species identities can increase usability of biodiversity databases and improve scientific communication, data sharing, and conservation planning (Bertrand and Härlin 2006; Hamdan et al. 2024; Mahony et al. 2024; Sullivan et al. 2023). Following the development and popularization of integrative taxonomy, contemporary species descriptions often show increasing robustness—i.e., incorporating more comprehensive diagnostic criteria (Guedes et al. 2024; Poulin and Presswell 2016; Sangster and Luksenburg 2015)—and reduced synonymisation rates (Alroy 2002; Baselga et al. 2008; Guedes et al. 2025; Solow, Mound, and Gaston 1995), contrasting with older descriptions, which generally relied on simpler diagnostics (Guedes et al. 2020; Poulin and Presswell 2016; Sangster and Luksenburg 2015). Understanding how temporal trends in species description comprehensiveness are related to improved sampling and analytical frameworks help to inform best practices that can strengthen taxonomic science.

Comprehensive descriptions can help mitigate common pitfalls in taxonomic practices (Braby et al. 2024; Dayrat 2005; Wüster et al. 2021), such as oversplitting due to insufficient diagnostic criteria and failure to accurately distinguish natural variation within species (Isaac, Mallet, and Mace 2004), or undersplitting resulting from overlooked phenotypic or genetic divergence (Chek, Austin, and Lougheed 2003; Hendrixson and Bond 2005; Mutanen et al. 2016). While the accumulated evidence highlights temporal shifts in taxonomic practices (Guedes et al. 2024; Padial and De la Riva 2020; Sangster and Luksenburg 2015), recent studies also reveal pronounced spatial variation (Freeman and Pennell 2021; Padial and De la Riva 2020; De Queiroz 2007). A well-documented latitudinal taxonomic bias exists, wherein biodiversity-rich but resource-limited regions (e.g., the Tropics) often exhibit lower taxonomic resolution compared to temperate, high-income regions (Diniz Filho et al. 2023; Freeman and

Pennell 2021; Guedes et al. 2025). This spatial variation likely emerges from differences in access to resources and tools, though international collaborations and open-access data initiatives have the potential to mitigate these imbalances (Carneiro et al. 2025; Nakamura et al. 2023). Addressing these gaps is critical to ensuring robust taxonomic frameworks that support downstream research on fields dependent on taxonomic data (Diniz Filho et al. 2023; Lessa et al. 2024).

Because citation-based metrics are poor proxies of the comprehensiveness of taxonomic publications (Pyke 2014; Valdecasas 2011; Valdecasas, Castroviejo, and Marcus 2000), more direct metrics are needed to investigate trends in the robustness of species descriptions and to inform whether many nomenclatural changes are likely to occur in the future across organismal groups. Using metrics like page counts and the number of evidence lines or number of techniques adopted (e.g., morphometrics, cytogenetics, internal anatomy, molecular analysis) in descriptions, studies have generally observed an increase in comprehensiveness of descriptions across taxa (e.g., Benton 2008; Guedes et al. 2024; Pante, Schoelinck, and Puillandre 2015; Poulin and Presswell 2016; Sangster and Luksenburg 2015). Here, we investigate how several proxies of comprehensiveness in species description have changed over time and assess their potential determinants.

We focus our assessment on recent mammals, a group with a well-established alpha taxonomy. Although future additions to mammalian species counts may be small compared to vertebrates like amphibians and reptiles (Moura and Jetz 2021), there are still likely hundreds of species awaiting discovery and description (Parsons et al. 2022). We explore whether temporal variation is evident across four proxies of comprehensiveness in species descriptions, namely: (1) the number of specimens used to describe the new taxa, (2) count of taxa to which the new species is compared, (3) page counts, and (4) number of evidence lines used in the description. We examine whether variability in these proxies is related to species' biology, geography, and taxonomic practice. Additionally, we inspect how accessibility to specific resources and tools is associated with the internationalization of species descriptions. Given that many mammalian taxa still lack comprehensive taxonomic studies (Feijó and Brandão 2022), and that most formal descriptions represent the splitting of one species into many (Burgin et al. 2018; Isaac et al. 2004), it is likely that several taxonomic changes lie ahead. Our

findings can inform the development of protocols and practices that ultimately increase species description comprehensiveness and improve mammal data usage in biodiversity research (Mahony et al. 2024).

Material and methods

Data collection

We examined the descriptions of 1,032 mammal species published between 1990 and 2022, covering 33 years of mammal discovery. Focusing on post-1990 descriptions minimize inconsistencies from historical variations in taxonomic standards, such as the cladistics and molecular systematics, ensuring comparable scientific and socioeconomic trends. We only considered "original" descriptions, disregarding redescriptions, revalidations, and other taxonomic works. Taxonomic nomenclature follows the December 2022 version of the Mammal Diversity Database (MDD 2022).

For each species in our database, we extracted four proxies for the species description comprehensiveness: (1) number of specimens - as type-specimens plus all referred specimens of the new species used to obtain diagnostic traits (type-series size and all referred specimens were highly correlated, Pearson's $r = 0.60$, $p < 0.001$); (2) number of taxa compared - the count of close-related species directly compared with the new species; (3) number of pages - by dividing each page into quadrants and including only the Methods/Results sections. For studies including multi-species descriptions/redescriptions, we divided page counts by the number of species described/redescribed. Our fourth proxy was represented by the (4) number of evidence lines, scored from only one line of evidence to nine lines of evidence based on the presence or absence of the analysed character in the formal description: (i) dentition (e.g. dental formula, tooth shape, etc), (ii) internal soft anatomy (e.g. internal morphology of the stomach, glans, etc.), (iii) external qualitative morphology (e.g. comparison of head and tail shapes), (iv) microscopic-based trichology, (v) coloration patterns, (vi) karyotype, (vii) external morphometry (e.g., head-body length, hind foot length, forearm length), (viii) osteological morphometry (from teeth, skull, mandible and other skeleton parts), and (ix) DNA (e.g. allozyme, mtDNA, nucDNA, multiLoci). These proxies

showed low multicollinearity (Variance Inflation Factor, VIF < 1.5; Table S1) and limited pairwise correlations (Spearman's *r* correlation range = 0.03-0.37; Fig. S1), indicating they capture relatively distinct aspects of description comprehensiveness.

To represent potential determinants of species description comprehensiveness, we used the seven variables: (1) year of species description; (2) number of authors; (3) average number of countries per author, the country counts derived from authors affiliations were divided by author counts to avoid sampling effects associated with multiauthored works (see Fig. S2 for pairwise correlation between authors and countries counts); (4) maximum body mass, obtained from original descriptions and from Moura et al. (2024), (5) per-genus species richness based on the year of species descriptions (i.e., for each species, we tallied the total number of currently accepted species described in the same genus until their year of description); (6) absolute latitude of type-locality; and whether description was based on (7) taxonomic revision, which was considered as such only if the work explicitly mentioned the term "revision" (or similar) in its title, abstract, keywords, or main text. To allow cross-group comparisons, we also recorded data on taxonomic ranks.

Statistical analyses

Temporal trends in our proxies of the species description comprehensiveness (number of lines of evidence, number of pages, number of specimens, and number of taxa compared) were investigated using Spearman's (r_s) correlation between the year of publication and annual means for the metrics analysed across species described in each year. We assessed multicollinearity among continuous predictors using the Variation Inflation Factors (VIF; Mansfield and Helms 1982), where strong multicollinearity is often attributed to variables holding VIF > 10 (Kutner et al. 2005). All variables in our analysis had VIF values below 2 (Table S2), so none were excluded. We inspected the multicollinearity of the predictor.

We assessed potential determinants of species description comprehensiveness, using generalised linear models (GLMs; Zuur et al. 2009). We used a negative binomial error distribution to analyse the number of specimens and number of taxa compared, both of which are count data. The number of pages was calculated as a continuous variable, so we applied a $\log_{10}$-transformation and modelled it using a GLM with a Gaussian error

distribution. Although the number of evidence can be considered a count variable, given its hump-shaped distribution (Fig. S1), we used both negative binomial and Gaussian distributions, comparing model fit and selecting the one with the lowest AIC values (Burnham and Anderson 2002). Each response variable was modelled against year of species description, number of authors (log_{10}-transformed), average number of countries per author (log_{10}-transformed), body mass (log_{10}-transformed), per-genus species richness (log_{10}-transformed), and occurrence of taxonomic revision. Continuous predictors were *z*-transformed before modelling, allowing comparisons of their effect sizes. Because of varying amounts of missing data among response and predictor variables, GLMs were performed with datasets differing slightly in the number of modelled species: number of lines of evidence (n = 820 species); number of pages (n = 807), number of specimens (n = 805); and number of taxa compared (n = 810). All analyses were performed in the R software version 4.3.1 (R Core Team 2023).

All models were fitted using the package *MASS* (Venables and Ripley 2002). We assessed explained variation through Nagelkerke's pseudo-R^2 for negative binomial models (response variables 'number of taxa compared' and 'number of specimens') and the coefficient of determination (R^2) for the Gaussian model (response variables 'number of evidence' and 'number of pages'), both computed with the R package *performance* (Lüdecke et al. 2021). We assessed the necessity of phylogenetic regression models by investigating the phylogenetic autocorrelation of model residuals through Moran's *I* correlograms, computed across 14 distance classes (Revell 2010). Correlograms were derived from the average results of 100 fully sampled phylogenies for mammals (Upham, Esselstyn, and Jetz 2019), with trees trimmed to include only modelled species. Phylogenetic autocorrelation analyses were conducted with the R packages *phylobase* (Bolker et al. 2020) and *phylosignal* (Keck et al. 2016).

To further investigate if accessibility of costly analytical tools is reflected across international collaboration, we applied a Kruskal-Wallis analysis to test whether the average number of countries per authors differed among descriptions using (i) molecular biology, (ii) taxonomic review, or (iii) other evidence lines. *Post-hoc* comparisons were conducted using Dunn's test, with pairwise contrasts adjusted for multiple testing using the Bonferroni correction method (Bonferroni 1936). All analyses were conducted using

the *rstatix* R package (Kassambara 2023). See Data Availability section for raw data and R code.

Results

Most mammal species described between 1990 and 2022 were from Africa, South America, Southeast Asia, and islands near Australia (Fig. 1). The Afrotropical realm stands out in terms of primate descriptions, whereas the few descriptions from the Nearctic were mostly from rodents and Eulipotyphla (e.g., hedgehogs, moles, true shrews). Of the 1032 species described, 40.8% were rodents (n = 421) and 27.1% were bats (n = 280)—a trend observed globally as well as across most biogeographic realms. Descriptive statistics for comprehensiveness metrics across all mammals, rodents, bats, and when considering mammals excluding bats and rodents, are summarized in Table 1.

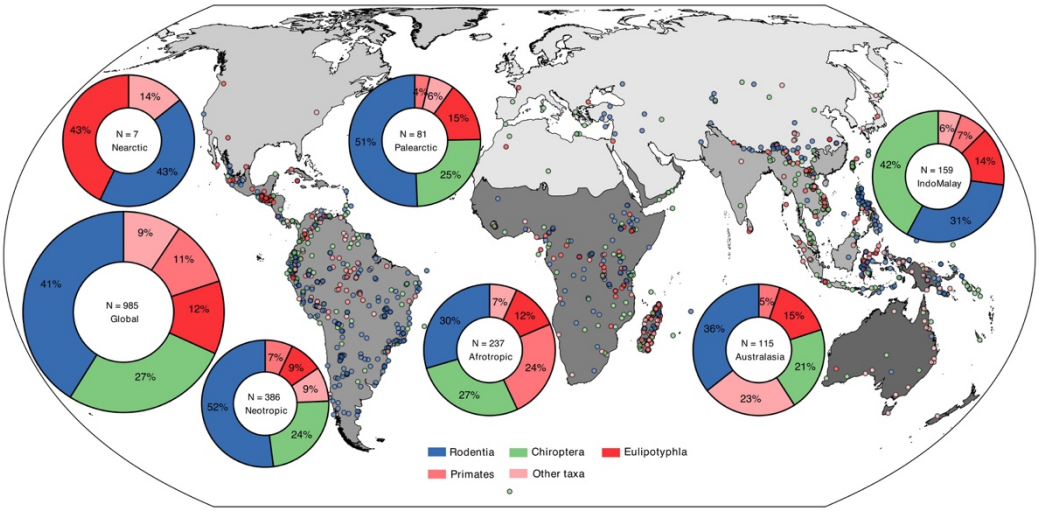

Figure 1. Global distribution of mammal species described between 1990 and 2022. Each point on the map represents a species' type locality, while donut charts indicate the proportion of species described within each taxonomic order. Points are coloured according to their respective taxonomic order, with rodents in blue, bats in green, and the different shades of red representing other mammals. To improve visualization, taxonomic orders holding less than 5% of species descriptions were grouped under 'Other taxa' label in the donut charts. The total sample size (N) is lower than the 1,032 species described during this period due to missing type-locality data for some species.

Table 1. Descriptive statistics for metrics of species descriptions' comprehensiveness. For each group, we report the median and the range (minimum–maximum) for the number of evidence lines, number of specimens, number of pages, and number of taxa compared.

	All mammals	**Non-bats & non-rodents**	**Bats**	**Rodents**
N. of evidence lines	5 (1–8)	4 (1–7)	5 (1–7)	5 (1–8)
N. of specimens	8 (1–409)	7 (1–345)	7 (1–327)	9 (1–409)
N. of pages	7.3 (0.23–179)	5.5 (0.23–48.2)	8 (0.8–179)	8.1 (1–130)
N. of taxa compared	5 (1–77)	4 (0–46)	5 (1–45)	5 (1–77)

Temporal trends in mammal description comprehensiveness

The annual mean number of evidence lines used in species descriptions increased when analyzing all mammals (rs = 0.67; $p < 0.001$), non-bats & non-rodent mammals (rs = 0.45; p = 0.03), bats (rs = 0.60; p = 0.001) and rodents (rs = 0.53; p = 0.007; Fig 2a). There was no change in the number of pages over time (Fig. 2b), but an increase in the number of specimens when considering all mammals together (rs = 0.47; $p < 0.05$, Fig. 2c) and non-bats & non-rodent mammals (rs = 0.45; p = 0.03). The number of taxa compared also increased for all mammals combined (rs = 0.59; p = 0.001, Fig. 2d), non-bats & non-rodent mammals (rs = 0.51; p = 0.01) and for bats separately (rs = 0.59; $p <$ 0.002), but not for rodents (rs = 0.24; p = 0.9). In addition, the incorporation of molecular analyses in species descriptions has grown over time, with a noticeable increase in the proportion of taxa described annually using molecular data (Figs S3-S4).

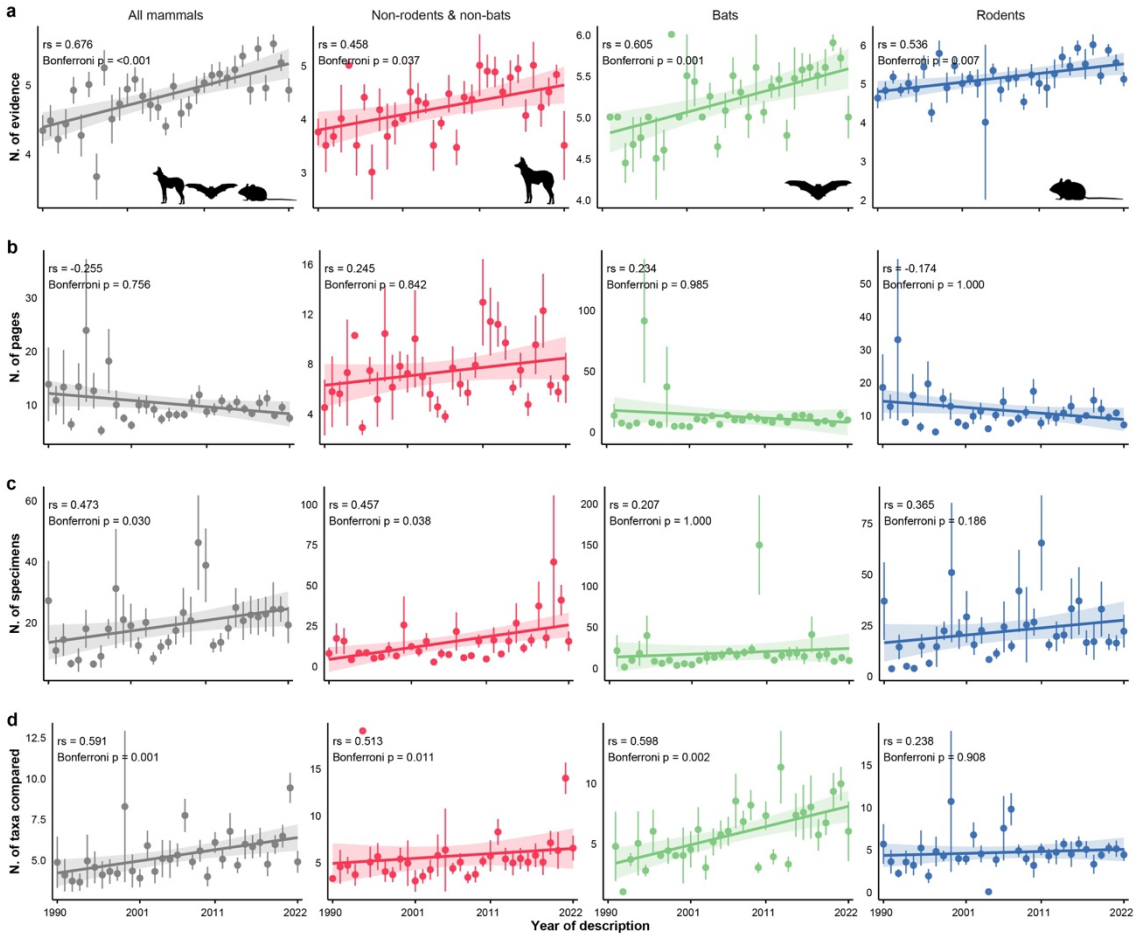

Figure 2. Variation in proxies of mammal species descriptions comprehensiveness over time (1990–2022). Panels show overall trends for all mammals (gray), non-rodents and non-bats (red), bats (green), and rodents (blue). Proxies include the (a) number of evidence used in species descriptions, (b) number of pages in taxonomic description papers, (c) number of specimens examined in species descriptions, and (d) number of taxa compared to distinguish new species. rs denotes the Spearman's correlation between the year of description and annual means for each variable. We applied Bonferroni corrections to p-values to account for multiple comparisons. Vertical lines represent standard errors, and shaded areas around the regression lines represent 95% confidence intervals.

Internationalization of mammal descriptions

We found a temporal decrease in the average number of countries per author for all taxonomic groups, except bats (Fig. 3). In addition, this 'internationalisation indicator' differed across descriptions using particular analytical tools, with studies using molecular biology and taxonomic review showing lower values of average number of countries per

author. In bats and rodents, only molecular-based descriptions involved fewer countries relative to other lines of evidence.

The use of molecular data in descriptions varies across mammalian orders, with Primates (105 species), Didelphimorphia, Carnivora, Macroscelidea, Peramelemorphia, and Artiodactyla frequently incorporating genetic evidence, while Dasyuromorphia (8 species) lacked such data entirely. International collaborations were common in molecular-based descriptions, except in Lagomorpha, with three descriptions associated with a single country (Fig. 4a). Taxonomic revisions contributed substantially to new species descriptions in Pilosa, Monotremata, and Carnivora (> 50%), but were rare in species-rich groups like Rodentia and Chiroptera and absent in depauperate orders (e.g., Peramelemorphia, Paucituberculata, Microbiotheria, Macroscelidea, Lagomorpha, and Hyracoidea). While international collaboration in revision-based descriptions was idiosyncratic, primates and afrosoricids exhibited broader multinational involvement (Fig. 4b).

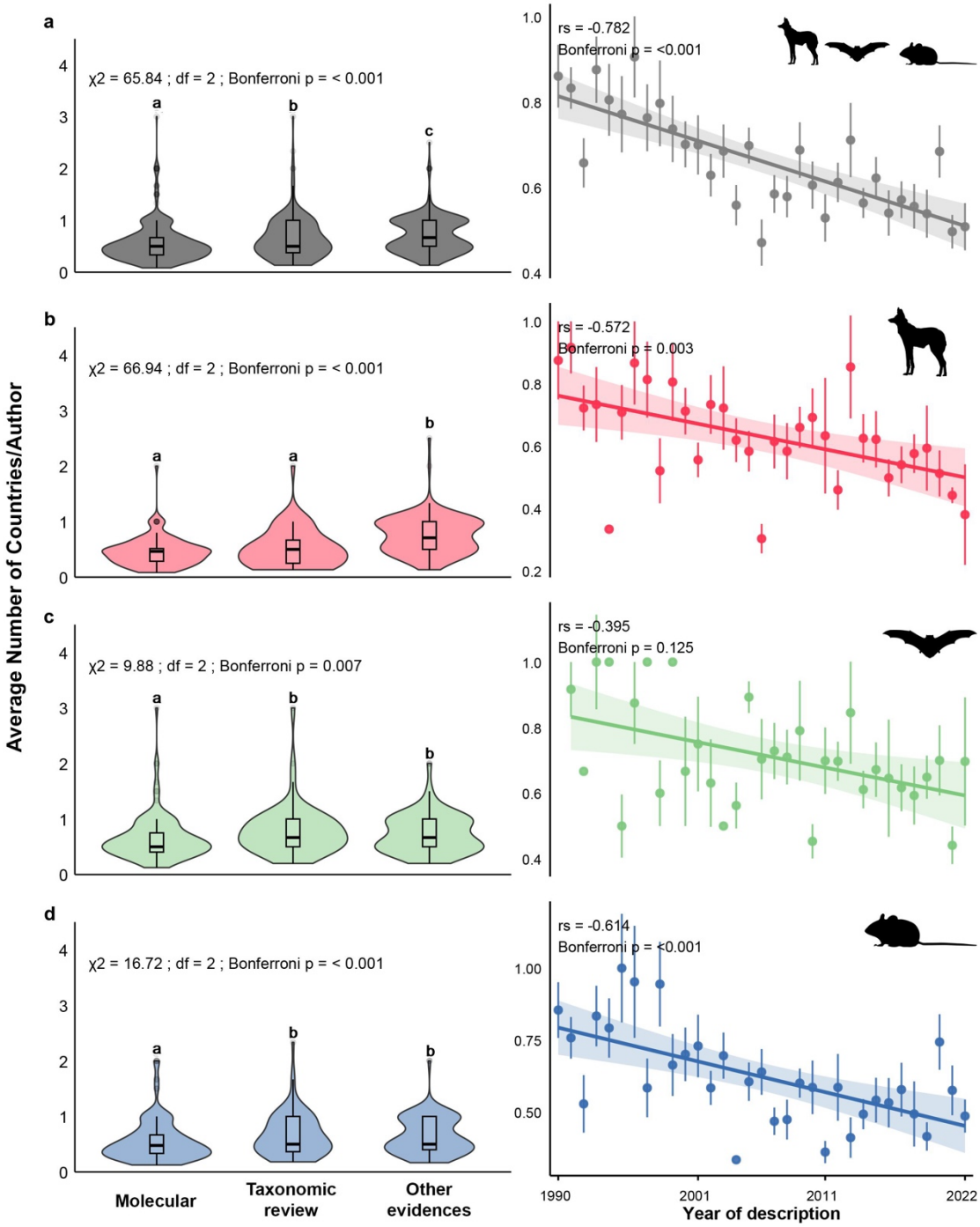

Figure 3. Average number of countries per author involved in mammal species descriptions across different lines of evidence and over time. Patterns are shown for (a) all mammals, (b) non-bats and non-rodents, (c) bats, and (d) rodents. 'Other evidences' refers to descriptions that do not include molecular diagnoses and were not derived from taxonomic revisions. Molecular approaches exhibit different levels of internationalization compared to taxonomic reviews and other evidence types across mammals, bats, and rodents. In the violin plot, post-hoc comparisons were performed using estimated marginal means, with pairwise contrasts adjusted for multiple testing using the Bonferroni method. Groups that do not share letters are significantly different from each

other.

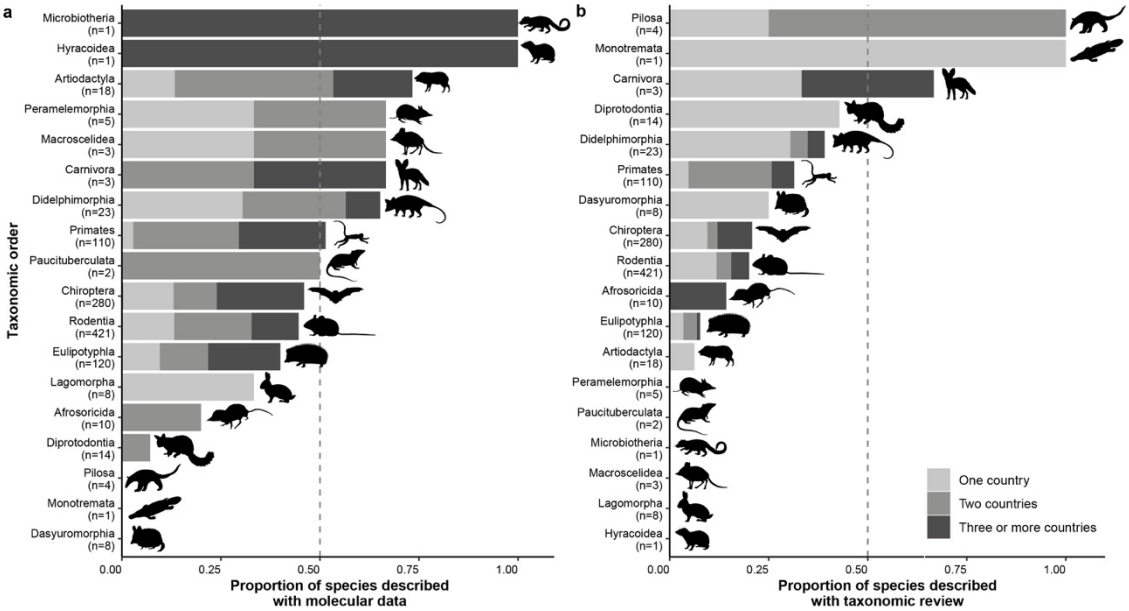

Figure 4. Proportion of species descriptions using (a) molecular analysis or (b) taxonomic review for each mammal order from 1990–2022. The bars indicate the proportion of the total number of species described per order over this period. The different shades of gray indicate the proportion of these descriptions involving one, two, and three or more countries.

Determinants of comprehensiveness in mammal descriptions

GLMs explained 6-37% of the variation in taxonomic comprehensiveness metrics (Fig. 5). Across all four proxies tested, the number of taxa compared emerged as the best-explained one for descriptions in all mammals and bats, whereas the number of specimens was the most explained metric in rodents and non-bats & non-rodent mammals. We did not find phylogenetic structure in GLM residuals, as indicated by phylogenetic correlograms (Fig. S5).

We found the year of description, number of species/genus, and absolute latitude among the most important predictors of species description comprehensiveness. Recent descriptions used more evidence, referred specimens, compared taxa, and (to some extent) more pages across all taxonomic groups, although such effect was less pronounced in bats overall (Fig. 5). Species-rich genera correlated with more specimens and compared taxa overall, except for bat specimens. Our results revealed a latitudinal

gradient, with the number of evidence lines decreasing in mammal descriptions from tropical regions. We also observed fewer specimens in descriptions of non-rodent and non-bat species towards the Tropics.

Other predictors affected only some taxonomic groups. For instance, we found fewer evidence lines and pages in descriptions of small-sized mammals that are neither rodents nor bats. In bats, fewer specimens were used to describe small-sized species, particularly if such descriptions were produced via taxonomic review. However, for non-flying mammals, the taxonomic reviews tended to promote descriptions with more evidence lines and to some extent, more pages.

The two remaining predictors, number of authors and average number of countries per author (an indicator of internationalisation), showed more contrasting trends across taxonomic groups and proxies of description comprehensiveness. Non-rodent and non-bat species had fewer lines of evidence and specimens in multi-authored descriptions. In contrast, bat descriptions with more authors included more evidence, and international collaborations had limited influence on description comprehensiveness, as descriptions of non-rodent mammals with multinational authorship consistently included fewer specimens.

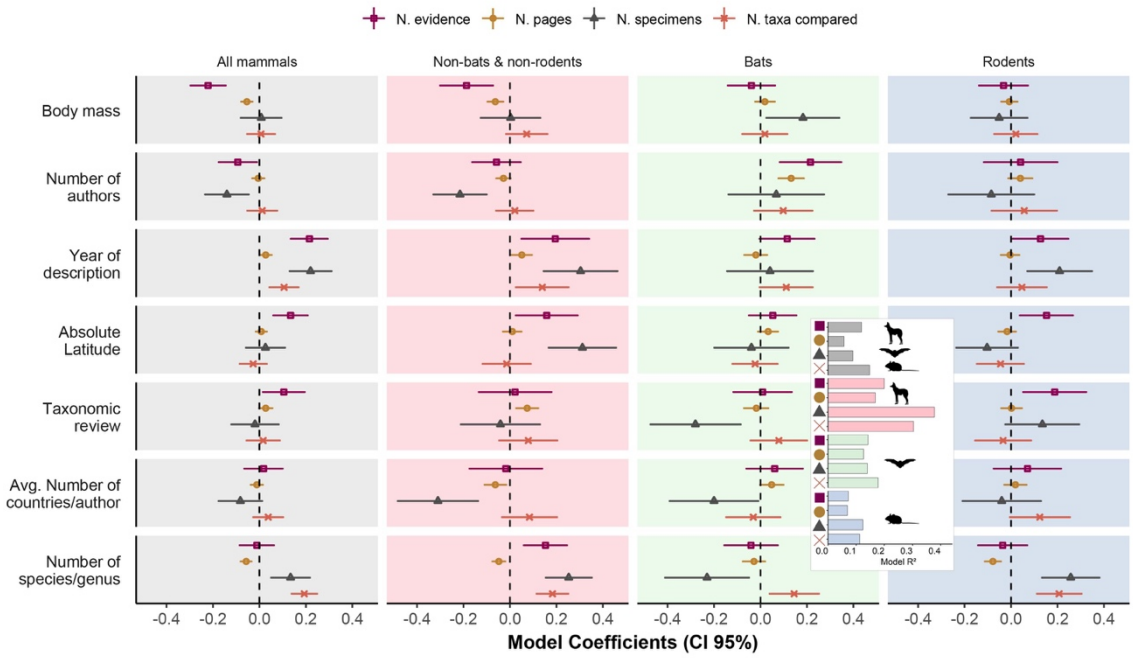

Figure 5. Influence of putative drivers on proxies of mammal species description comprehensiveness. Standardized coefficients from the generalized linear models fit to

all species and for bats and rodents separately are shown. Horizontal lines denote the 95% confidence intervals around each coefficient. Predictors with significant effect sizes (p-value < 0.05) are those whose horizontal lines do not cross 0. Explained variation is presented (Model R^2) as Nagelkerke's pseudo-R^2 for negative binomial models (Number of taxa compared and Number of specimens) and as the coefficient of determination (R^2) for the Gaussian model (Number of evidence and Number of pages).

Discussion

Most new mammal species described between 1990 and 2022 come from tropical regions, particularly rodents and bats. This pattern aligns with mammal discovery hotspots (Moura and Jetz 2021; Parsons et al. 2022) and corresponds to the highest diversity of both orders in these regions (Abreu et al. 2024; MDD 2025). Although the rate of new mammal descriptions remains slower than in ectothermic tetrapods (Moura et al. 2018), hundreds of species await formal descriptions (Moura and Jetz 2021; Parsons et al. 2022), with 68.8% increase in recognized species since the 1980s (~65 new species/year; Burgin et al. 2025). Many additions result from taxonomic splits, reflecting taxonomic uncertainties often rooted in species descriptions of limited comprehensiveness, likely due to the historical unavailability or accessibility of tools that are now commonly used in taxonomic research (Guedes et al. 2024; Poulin and Presswell 2016; Sangster and Luksenburg 2015). We find a clear temporal progression toward more rigorous practices in mammal descriptions, including an increased use of multiple evidence lines, expanded sampling of referred specimens, and broader taxonomic comparisons (Fig. 2). Our results reveal substantial heterogeneity in determinants of species description comprehensiveness, likely associated with taxon-specific sampling challenges.

The increase over time in proxies of mammal species descriptions comprehensiveness has mirrored trends observed across various taxa (Guedes et al. 2024; Poulin and Presswell 2016; Sangster and Luksenburg 2015). While this pattern aligns with the principles of integrative taxonomy (Dayrat 2005; Will, Mishler, and Wheeler 2005), it also shows that many taxonomists were already applying integrative approaches before the formalization of the concept (Valdecasas, Williams, and Wheeler 2008). The higher comprehensiveness of recent descriptions can be attributed to technological advancements and reduced costs, which have democratized access to analytical tools (Guedes et al. 2024; Nakamura et al. 2023; Trisos, Auerbach, and Katti 2021), like micro-

CT scanning, DNA sequencing, and automated platforms for taxonomic analysis (e.g., Blackburn et al. 2024; Grenié et al. 2023; Thomer, Twidale, and Yoder 2018). Taken together, these technological advances have accelerated species descriptions and expanded the scope and depth of taxonomic knowledge, contributing to a more comprehensive understanding of biodiversity. Despite improvements in access to analytical tools, disparities still persist, as evidenced by a greater number of evidence lines in descriptions from temperate regions (Fig. 5), where wealthy economies predominate relative to low latitudes.

While descriptions of new mammal species now involve more authors and countries overall (Fig. S6), the growth in authorship size has outpaced international collaboration (Fig. 3). Consequently, we find a lower average number of countries per author in recent descriptions, which is also noticeable across molecular-based descriptions. These findings may relate to novel standards in authorship criteria of recent descriptions (Allen, O'Connell, and Kiermer 2019; Lin 2024). For instance, more collectors of mammal type-specimens have authored recent descriptions (Fig. S7). This suggests that recent species descriptions may be based on newly collected specimens obtained through projects led by these collectors, or that there is an increasing recognition of the contributions made by fieldwork personnel. In addition, the somewhat limited internationalisation of molecular-based descriptions corroborates DNA sequencing in taxonomic research, which is nowadays more affordable by researchers in biodiversity-rich regions in the Global South. For instance, the Human Genome Project (1990-2003) required 3 US$ billions, whereas advances like next−generation sequencing reduced costs to less than $1,000 per genome (Schmidt and Hildebrandt 2017; Wetterstrand 2025). This shift is evident in the rising prevalence of molecular-based diagnoses in mammal descriptions (Figs S4-S5).

Among the most consistent findings of this study is the higher comprehensiveness of descriptions made within speciose genera. On the one hand, this finding may reflect a sampling effect, as species-rich genera inherently necessitate more extensive within-group comparisons as additional species accumulate over time (Fig. 2). On the other hand, alpha taxonomy is inherently comparative, and distinguishing closely related species becomes particularly challenging in species-rich genera (Gaston, Blackburn, and Loder 1995), where greater phenotypic and genetic variation may require more specimens to

accurately delineate species. Surprisingly, bats exhibited the opposite pattern (fewer specimens in species-rich genera). It is possible that taxon-specific sampling challenges explain divergent patterns of specimen acquisition. Our dataset shows that 70% of bat species in the five richest bat genera - *Myotis*, *Murina*, *Rhinolophus*, *Miniopterus*, and *Hipposideros* - are echolocating and have body masses below the median of 10 g. This pattern is likely attributable to size-dependent sampling bias in mist-netting, where mesh dimensions favour the capture of larger individuals, and the echolocating frequency of each species may influence the effectiveness of different mist-net types (Ferreira et al. 2021; Francis 1989). Consequently, the species-rich genera are likely under-sampled, which may explain their limited representation in bat species descriptions. These size-related constraints in bat sampling align with the higher frequency of taxonomic revisions in well-sampled (mostly large-sized) species, with less than one-fifth of bats above median body mass described in taxonomic reviews.

Species descriptions of larger mammals contain fewer evidence lines and are shorter than those of smaller species, especially in non-flying mammals. While larger species' morphologies are typically diagnosable without advanced imaging, smaller species frequently require (Ziegler and Sagorny 2021). Thus, body size shows a negative relationship with evidence lines, contrasting to its positive associations with species description probability and data availability (Meiri 2018; Moura and Jetz 2021). The inverse association between body mass and description length appears to be mediated through the number of evidence lines. That is, small species demand more pages to document their additional evidence lines, a pattern supported by the moderate but significant correlation between page count and evidence lines (Fig. S1). Notably, body mass influenced specimen availability only in bats, once again reflecting taxon-specific sampling challenges. Unlike bats, which face size-biased mist-netting limitations, non-flying mammals (especially rodents) are more efficiently collected through passive methods like pitfalls and baited live traps (Tobler et al. 2008), with minimal size-related bias (Bovendorp, MCCleery, and Galetti 2017; Williams and Braun 1983). These sampling limitations result in fewer specimens of bats relative to non-flying mammals, as evidenced by GBIF's global holdings of preserved specimens (1.16 million bats versus 3.6 million rodents and 1.89 million other non-flying mammals; GBIF 2025), although

these figures may also reflect the global distribution of known species by order (MDD 2025).

Overall, our study highlights the significant progress in the comprehensiveness of mammal species descriptions since 1990, driven by technological advancements and the broader adoption of integrative taxonomic practices. However, persistent disparities rooted in socioeconomic inequalities, taxon-specific sampling biases, and the broader taxonomic impediment (i.e., systemic barriers limiting both taxonomic output and end-user reliability; Ebach, Valdecasas, and Wheeler 2011) continue to shape taxonomic output. Bats and other small-bodied tropical mammals face compounded challenges, from methodological constraints to underrepresentation in either molecular diagnoses or revisionary studies. We reveal that variation in taxonomic practices mirrors well-documented latitudinal gaps in taxonomic resolution (Freeman and Pennell 2021; Guedes et al. 2025). Addressing these gaps requires targeted investments in building local capacity and inclusive collaboration frameworks to ensure more comprehensive species descriptions (Carneiro et al. 2025; Nakamura et al. 2023; Trisos et al. 2021). In the absence of such interventions, the interoperability and integration of taxonomic data risk being delayed (Sandall et al. 2023), thereby undermining subsequent conservation and research efforts.

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Data Availability Statement

The R-script and raw dataset used in the analyses of this study will be made available at Zenodo Digital Repository after potential acceptance. Meanwhile, reviewers can access the data from https://github.com/jhonny-guedes/mammal_desc_trends

Disclosure Statement

The authors report there are no competing interests to declare.

References

Abreu, E. F., D. Casali, R. Costa-Araújo, G. S. T. Garbino, G. S. Libardi, D. Loretto, A. C. Loss, M. Marmontel, L. M. Moras, M. C. Nascimento, M. L. Oliveira, S. E. Pavan, and F. P. Tirelli. 2024. "Lista de Mamíferos Do Brasil (2024-1) [Data Set]."

Allen, Liz, Alison O'Connell, and Veronique Kiermer. 2019. "How Can We Ensure Visibility and Diversity in Research Contributions? How the Contributor Role Taxonomy (CRediT) Is Helping the Shift from Authorship to Contributorship." *Learned Publishing* 32(1):71–74. doi: 10.1002/leap.1210.

Alroy, John. 2002. "How Many Named Species Are Valid?" *Proceedings of the National Academy of Sciences of the United States of America* 99(6):3706–11. doi: 10.1073/pnas.062691099.

Baselga, A., J. M. Lobo, J. Hortal, A. Jiménez-Valverde, and J. F. Gómez. 2008. "Assessing Alpha and Beta Taxonomy in Eupelmid Wasps: Determinants of the Probability of Describing Good Species and Synonyms." *Journal of Zoological Systematics and Evolutionary Research* 48(1):40–49. doi: 10.1111/j.1439-0469.2009.00523.x.

Benton, Michael J. 2008. "Fossil Quality and Naming Dinosaurs." *Biology Letters* 4(6):729–32. doi: 10.1098/rsbl.2008.0402.

Bertrand, Yann, and Mikael Härlin. 2006. "Stability and Universality in the Application of Taxon Names in Phylogenetic Nomenclature" edited by M. Lee. *Systematic Biology* 55(5):848–58. doi: 10.1080/10635150600960061.

Blackburn, David C., Doug M. Boyer, Jaimi A. Gray, Julie Winchester, John M. Bates,

Stephanie L. Baumgart, Emily Braker, Daryl Coldren, Kevin W. Conway, Alison Davis Rabosky, Noé de la Sancha, Casey B. Dillman, Jonathan L. Dunnum, Catherine M. Early, Benjamin W. Frable, Matt W. Gage, James Hanken, Jessica A. Maisano, Ben D. Marks, Katherine P. Maslenikov, John E. McCormack, Ramon S. Nagesan, Gregory G. Pandelis, Heather L. Prestridge, Daniel L. Rabosky, Zachary S. Randall, Mark B. Robbins, Lauren A. Scheinberg, Carol L. Spencer, Adam P. Summers, Leif Tapanila, Cody W. Thompson, Luke Tornabene, Greg J. Watkins-Colwell, Luke J. Welton, and Edward L. Stanley. 2024. "Increasing the Impact of Vertebrate Scientific Collections through 3D Imaging: The OpenVertebrate (OVert) Thematic Collections Network." *BioScience* 74(3):169–86. doi: 10.1093/biosci/biad120.

Bolker, Ben, Marguerite Butler, Peter Cowan, Damien de Vienne, Dirk Eddelbuettel, Mark Holder, Thibaut Jombart, Steve Kembel, Francois Michonneau, David Orme, Brian C. O'Meara, Emmanuel Paradis, Jim Regetz, and Derrick Zwickl. 2020. "Phylobase: Base Package for Phylogenetic Structures and Comparative Data."

Bonferroni, C. 1936. "Teoria Statistica Delle Classi e Calcolo Delle Probabilita." *Pubblicazioni Del R Istituto Superiore Di Scienze Economiche e Commericiali Di Firenze* 8:3–62.

Bovendorp, Ricardo S., Robert A. MCCleery, and Mauro Galetti. 2017. "Optimising Sampling Methods for Small Mammal Communities in Neotropical Rainforests." *Mammal Review* 47(2):148–58. doi: 10.1111/mam.12088.

Braby, Michael F., Yu-Feng Hsu, and Gerardo Lamas. 2024. "How to Describe a New Species in Zoology and Avoid Mistakes." *Zoological Journal of the Linnean Society*. doi: 10.1093/zoolinnean/zlae043.

Bremer, K., B. Bremer, P. Karis, and M. Källersjö. 1990. "Time for Change in Taxonomy." *Nature* 434:202–202.

Burgin, Connor J., Jocelyn P. Colella, Philip L. Kahn, and Nathan S. Upham. 2018. "How Many Species of Mammals Are There?" *Journal of Mammalogy* 99(1):1–14. doi: 10.1093/jmammal/gyx147.

Burgin, Connor J., Jelle S. Zijlstra, Madeleine A. Becker, Heru Handika, Jesse M. Alston, Jane Widness, Schuyler Liphardt, David G. Huckaby, and Nathan S. Upham. 2025. "How Many Mammal Species Are There Now? Updates and Trends

in Taxonomic, Nomenclatural, and Geographic Knowledge."

Burnham, Kenneth P., and David A. Anderson. 2002. *Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach*. 2nd ed. edited by K. P. Burnham and D. A. Anderson. Fort Collins, CO: Springer.

Carneiro, Céline M., Analisa Shields-Estrada, Alexandra E. Boville, Gabriela Alves-Ferreira, Tianyi Xu, Ryan L. Wong Arnott, Chloé M. Allen-Love, Micaela Puertas, John J. Jacisin, Hannah Chapman Tripp, Edmund W. Basham, Kelly R. Zamudio, and Anat M. Belasen. 2025. "Toward a Global Science of Conservation Genomics: Coldspots in Genomic Resources Highlight a Need for Equitable Collaborations and Capacity Building." *Molecular Ecology*. doi: 10.1111/mec.17729.

Chek, Andrew A., James D. Austin, and Stephen C. Lougheed. 2003. "Why Is There a Tropical–Temperate Disparity in the Genetic Diversity and Taxonomy of Species?" *Evolutionary Ecology Research* 5:69–77.

Dayrat, Benoît. 2005. "Towards Integrative Taxonomy." *Biological Journal of the Linnean Society* 85(3):407–15. doi: 10.1111/j.1095-8312.2005.00503.x.

Diniz Filho, Jose Alexandre F., Lucas Jardim, Jhonny J. M. Guedes, Leila Meyer, Juliana Stropp, Livia Estéfane Fernandes Frateles, Rafael B. Pinto, Lucía G. Lohmann, Geiziane Tessarolo, Claudio J. B. De Carvalho, Richard J. Ladle, and Joaquin Hortal. 2023. "Macroecological Links between the Linnean, Wallacean, and Darwinian Shortfalls." *Frontiers of Biogeography* 15(2):1–11. doi: 10.21425/F5FBG59566.

Dominguez, Eduardo, and Quentin D. Wheeler. 1997. "Forum – Taxonomic Stability Is Ignorance." *Cladistics* 13(4):367–72. doi: 10.1111/j.1096-0031.1997.tb00325.x.

Dubois, Alain. 2007. "Naming Taxa from Cladograms: Some Confusions, Misleading Statements, and Necessary Clarifications." *Cladistics* 23(4):390–402. doi: 10.1111/j.1096-0031.2007.00151.x.

Ebach, Malte C., Antonio G. Valdecasas, and Quentin D. Wheeler. 2011. "Impediments to Taxonomy and Users of Taxonomy: Accessibility and Impact Evaluation." *Cladistics* 27(5):550–57. doi: 10.1111/j.1096-0031.2011.00348.x.

Feijó, Anderson, and Marcus Vinicius Brandão. 2022. "Taxonomy as the First Step towards Conservation: An Appraisal on the Taxonomy of Medium- and Large-Sized Neotropical Mammals in the 21st Century." *Zoologia (Curitiba)* 39:e22007.

doi: 10.1590/s1984-4689.v39.e22007.

Ferreira, Diogo F., Crinan Jarrett, Patrick Jules Atagana, Luke L. Powell, and Hugo Rebelo. 2021. "Are Bat Mist Nets Ideal for Capturing Bats? From Ultrathin to Bird Nets, a Field Test" edited by A. Baird. *Journal of Mammalogy* 102(6):1627–34. doi: 10.1093/jmammal/gyab109.

Francis, C. M. 1989. "A Comparison of Mist Nets and Two Designs of Harp Traps for Capturing Bats." *Journal of Mammalogy* 70(4):865–70. doi: 10.2307/1381730.

Freeman, Benjamin G., and Matthew W. Pennell. 2021. "The Latitudinal Taxonomy Gradient." *Trends in Ecology and Evolution* 36(9):778–86. doi: 10.1016/j.tree.2021.05.003.

Gaston, Kevin J., Tim M. Blackburn, and Natasha Loder. 1995. "Which Species Are Described First?: The Case of North American Butterflies." *Biodiversity and Conservation* 4:119–27.

GBIF. 2025. "GBIF Home Page." Retrieved June 30, 2025 (https://www.gbif.org).

Gippoliti, Spartaco, Simone Farina, and Franco Andreone. 2024. "Lost Species, Neglected Taxonomy, and the Role of Natural History Collections and Synonymization in the Identification of the World's Forgotten Biodiversity." *Nature Conservation* 56:119–26. doi: 10.3897/natureconservation.56.132036.

Grenié, Matthias, Emilio Berti, Juan Carvajal-Quintero, Gala Mona Louise Dädlow, Alban Sagouis, and Marten Winter. 2023. "Harmonizing Taxon Names in Biodiversity Data: A Review of Tools, Databases and Best Practices." *Methods in Ecology and Evolution* 14(1):12–25. doi: 10.1111/2041-210X.13802.

Guedes, Jhonny J. M., Renato N. Feio, Shai Meiri, and Mario Ribeiro Moura. 2020. "Identifying Factors That Boost Species Discoveries of Global Reptiles." *Zoological Journal of the Linnean Society* 190(4):1274–84. doi: 10.1093/zoolinnean/zlaa029.

Guedes, Jhonny J. M., Mario R. Moura, Lucas Jardim, and José Alexandre F. Diniz-Filho. 2025. "Global Patterns of Taxonomic Uncertainty and Its Impacts on Biodiversity Research." *Systematic Biology* In Press. doi: 10.1093/sysbio/syaf010.

Guedes, Jhonny J. M., H. Valentim, L. R. Mendonça, R. Chen-Zhao, J. A. F. Diniz-Filho, and M. R. Moura. 2024. "Temporal Trends in Global Reptile Descriptions over Three Decades [Dataset]." *Zenodo*. doi:

https://doi.org/10.5281/zenodo.13485016.

Hamdan, Breno, Sandro L. Bonatto, Dennis Rödder, Victor Corrêa Seixas, Rogério Mercês Ferreira Santos, Diego José Santana, Larissa Gonçalves Machado, Jessica Matos Kleiz-Ferreira, Marco A. de Freitas, Rodrigo Castellari Gonzalez, Thabata Cavalcante, Moisés Barbosa de Souza, Cristiane Barros Régis, Daniel Silva Fernandes, Hugo Fernandes-Ferreira, and Russolina Benedeta Zingali. 2024. "When a Name Changes Everything: Taxonomy and Conservation of the Atlantic Bushmaster (Lachesis Daudin, 1803) (Serpentes: Viperidae: Crotalinae)." *Systematics and Biodiversity* 22(1). doi: 10.1080/14772000.2024.2366215.

Hendrixson, Brent E., and Jason E. Bond. 2005. "Testing Species Boundaries in the Antrodiaetus Unicolor Complex (Araneae: Mygalomorphae: Antrodiaetidae): 'Paraphyly' and Cryptic Diversity." *Molecular Phylogenetics and Evolution* 36(2):405–16. doi: 10.1016/j.ympev.2005.01.021.

Isaac, Nick J. B., James Mallet, and Georgina M. Mace. 2004. "Taxonomic Inflation: Its Influence on Macroecology and Conservation." *Trends in Ecology & Evolution* 19(9):464–69. doi: 10.1016/j.tree.2004.06.004.

Kassambara, Alboukadel. 2023. "Rstatix: Pipe-Friendly Framework for Basic Statistical Tests, R Package Version 0.7.2."

Keck, François, Frédéric Rimet, Agnès Bouchez, and Alain Franc. 2016. "Phylosignal: An R Package to Measure, Test, and Explore the Phylogenetic Signal." *Ecology and Evolution* 6(9):2774–80. doi: 10.1002/ece3.2051.

Kutner, Michael H., Christopher J. Nachtsheim, John Neter, and William Li. 2005. *Applied Linear Statistical Models*. 5th ed. New York: McGraw-Hill Irwin.

Lessa, Thainá, Juliana Stropp, Joaquín Hortal, and Richard J. Ladle. 2024. "How Taxonomic Change Influences Forecasts of the Linnean Shortfall (and What We Can Do about It)?" *Journal of Biogeography*. doi: 10.1111/jbi.14829.

Lin, Zhicheng. 2024. "Modernizing Authorship Criteria and Transparency Practices to Facilitate Open and Equitable Team Science." *Accountability in Research* 1–24. doi: 10.1080/08989621.2024.2405041.

Lüdecke, Daniel, Mattan Ben-Shachar, Indrajeet Patil, Philip Waggoner, and Dominique Makowski. 2021. "Performance: An R Package for Assessment, Comparison and Testing of Statistical Models." *Journal of Open Source Software*

6(60):3139. doi: 10.21105/joss.03139.

Mahony, Stephen, Rachunliu G. Kamei, Rafe M. Brown, and Kin Onn Chan. 2024. "Unnecessary Splitting of Genus-Level Clades Reduces Taxonomic Stability in Amphibians." *Vertebrate Zoology* 74:249–77. doi: 10.3897/vz.74.e114285.

Mansfield, Edward R., and Billy P. Helms. 1982. "Detecting Multicollinearity." *The American Statistician* 36(3):158–60. doi: 10.1080/00031305.1982.10482818.

MDD. 2022. "Mammal Diversity Database." *Zenodo*. Retrieved (https://www.mammaldiversity.org/).

MDD. 2025. "Mammal Diversity Database, Version 2.2." *Zenodo*. Retrieved (https://www.mammaldiversity.org/).

Meiri, Shai. 2018. "Traits of Lizards of the World: Variation around a Successful Evolutionary Design." *Global Ecology and Biogeography* 27(10):1168–72. doi: 10.1111/geb.12773.

Moura, Mario Ribeiro, Karoline Ceron, Jhonny J. M. Guedes, Rosana Chen-Zhao, Yanina V Sica, Julie Hart, Wendy Dorman, Julia M. Portmann, Pamela González-del-Pliego, Ajay Ranipeta, Alessandro Catenazzi, Fernanda P. Werneck, Luis Felipe Toledo, Nathan S. Upham, João Filipe Riva Tonini, Timothy J. Colston, Robert Guralnick, Rauri C. K. Bowie, Robert Alexander Pyron, and Walter Jetz. 2024. "A Phylogeny-Informed Characterisation of Global Tetrapod Traits Addresses Data Gaps and Biases." *PLoS Biology* 22(7):e3002658. doi: 10.1371/journal.pbio.3002658.

Moura, Mario Ribeiro, Henrique C. Costa, Marco A. Peixoto, André L. G. Carvalho, Diego J. Santana, and Heraldo L. Vasconcelos. 2018. "Geographical and Socioeconomic Determinants of Species Discovery Trends in a Biodiversity Hotspot." *Biological Conservation* 220:237–44. doi: 10.1016/j.biocon.2018.01.024.

Moura, Mario Ribeiro, and Walter Jetz. 2021. "Shortfalls and Opportunities in Terrestrial Vertebrate Species Discovery." *Nature Ecology & Evolution* 5(5):631–39. doi: 10.1038/s41559-021-01411-5.

Mutanen, Marko, Sami M. Kivelä, Rutger A. Vos, Camiel Doorenweerd, Sujeevan Ratnasingham, Axel Hausmann, Peter Huemer, Vlad Dincă, Erik J. van Nieukerken, Carlos Lopez-Vaamonde, Roger Vila, Leif Aarvik, Thibaud Decaëns,

Konstantin A. Efetov, Paul D. N. Hebert, Arild Johnsen, Ole Karsholt, Mikko Pentinsaari, Rodolphe Rougerie, Andreas Segerer, Gerhard Tarmann, Reza Zahiri, and H. Charles J. Godfray. 2016. "Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera." *Systematic Biology* 65(6):1024–40. doi: 10.1093/sysbio/syw044.

Nakamura, Gabriel, Bruno Eleres Soares, Valério D. Pillar, José Alexandre Felizola Diniz-Filho, and Leandro Duarte. 2023. "Three Pathways to Better Recognize the Expertise of Global South Researchers." *Npj Biodiversity* 2(1):17. doi: 10.1038/s44185-023-00021-7.

Padial, José M., and Ignacio De la Riva. 2020. "A Paradigm Shift in Our View of Species Drives Current Trends in Biological Classification." *Biological Reviews*. doi: 10.1111/brv.12676.

Pante, E., C. Schoelinck, and N. Puillandre. 2015. "From Integrative Taxonomy to Species Description: One Step Beyond." *Systematic Biology* 64(1):152–60. doi: 10.1093/sysbio/syu083.

Parsons, Danielle J., Tara A. Pelletier, Jamin G. Wieringa, Drew J. Duckett, and Bryan C. Carstens. 2022. "Analysis of Biodiversity Data Suggests That Mammal Species Are Hidden in Predictable Places." *Proceedings of the National Academy of Sciences* 119(14). doi: 10.1073/pnas.2103400119.

Poulin, Robert, and Bronwen Presswell. 2016. "Taxonomic Quality of Species Descriptions Varies over Time and with the Number of Authors, but Unevenly among Parasitic Taxa." *Systematic Biology* 65(6):1107–16. doi: 10.1093/sysbio/syw053.

Pyke, Graham H. 2014. "Evaluating the Quality of Taxonomic Publications: A Simple Alternative to Citations and Effort." *BioScience* 64(11):961–62.

De Queiroz, Kevin. 2007. "Species Concepts and Species Delimitation." *Systematic Biology* 56(6):879–86. doi: 10.1080/10635150701701083.

R Core Team. 2023. "R: A Language and Environment for Statistical Computing." *R Foundation for Statistical Computing*.

Raposo, Marcos A., Renata Stopiglia, Guilherme Renzo R. Brito, Flávio A. Bockmann, Guy M. Kirwan, Jean Gayon, and Alain Dubois. 2017. "What Really Hampers Taxonomy and Conservation? A Riposte to Garnett and Christidis (2017)."

Zootaxa 4317(1):179–84.

Revell, Liam J. 2010. "Phylogenetic Signal and Linear Regression on Species Data." *Methods in Ecology and Evolution* 1:319–29. doi: 10.1111/j.2041-210X.2010.00044.x.

Sandall, Emily L., Aurore A. Maureaud, Robert Guralnick, Melodie A. McGeoch, Yanina V. Sica, Matthew S. Rogan, Douglas B. Booher, Robert Edwards, Nico Franz, Kate Ingenloff, Maisha Lucas, Charles J. Marsh, Jennifer McGowan, Stefan Pinkert, Ajay Ranipeta, Peter Uetz, John Wieczorek, and Walter Jetz. 2023. "A Globally Integrated Structure of Taxonomy to Support Biodiversity Science and Conservation." *Trends in Ecology & Evolution* 38(12):1143–53. doi: 10.1016/j.tree.2023.08.004.

Sangster, George, and Jolanda A. Luksenburg. 2015. "Declining Rates of Species Described per Taxonomist: Slowdown of Progress or a Side-Effect of Improved Quality in Taxonomy?" *Systematic Biology* 64(1):144–51. doi: 10.1093/sysbio/syu069.

Schmidt, Bertil, and Andreas Hildebrandt. 2017. "Next-Generation Sequencing: Big Data Meets High Performance Computing." *Drug Discovery Today* 22(4):712–17. doi: 10.1016/j.drudis.2017.01.014.

Solow, Andrew R., Laurence A. Mound, and Kevin J. Gaston. 1995. "Estimating the Rate of Synonymy." *Systematic Biology* 44(1):93–96.

Streicher, Jeffrey W., John J. Wiens, Merlijn Jocqué, Uri O. García-Vázquez, and Eric N. Smith. 2023. "Molecular Phylogenetic Analyses Reveal Both Underestimation and Overestimation of Species Diversity in Northern Rain Frogs (Craugastor)." *Journal of Vertebrate Biology* 72(23072). doi: 10.25225/jvb.23072.

Sullivan, Kathryn A., Erika M. Tucker, Nicolas J. Dowdy, Julie M. Allen, Vijay Barve, James H. Boone, Sarah E. Bush, Neal L. Evenhuis, Michael Hastriter, Jessica E. Light, Teresa Mayfield-Meyer, Barry M. OConnor, Jorrit H. Poelen, Gabor R. Racz, Katja C. Seltmann, and Jennifer M. Zaspel. 2023. "Building a Community-Based Taxonomic Resource for Digitization of Parasites and Their Hosts" edited by J. Lozier. *Insect Systematics and Diversity* 7(6). doi: 10.1093/isd/ixad023.

Thomer, Andrea K., Michael Bernard Twidale, and Matthew J. Yoder. 2018. "Transforming Taxonomic Interfaces." *Proceedings of the ACM on Human-*

Computer Interaction 2(CSCW):1–23. doi: 10.1145/3274442.

Tobler, Mathias W., S. E. Carrillo-Percastegui, R. Leite Pitman, R. Mares, and G. Powell. 2008. "An Evaluation of Camera Traps for Inventorying Large- and Medium-Sized Terrestrial Rainforest Mammals." *Animal Conservation* 11(3):169–78. doi: 10.1111/j.1469-1795.2008.00169.x.

Trisos, Christopher H., Jess Auerbach, and Madhusudan Katti. 2021. "Decoloniality and Anti-Oppressive Practices for a More Ethical Ecology." *Nature Ecology & Evolution* 5(9):1205–12. doi: 10.1038/s41559-021-01460-w.

Upham, Nathan S., Jacob A. Esselstyn, and Walter Jetz. 2019. "Inferring the Mammal Tree: Species-Level Sets of Phylogenies for Questions in Ecology, Evolution, and Conservation." *PLoS Biology* 17(12):1–44. doi: 10.1371/journal.pbio.3000494.

Valdecasas, Antonio G. 2011. "An Index to Evaluate the Quality of Taxonomic Publications." *Zootaxa* 62(2925):57–62. doi: 10.11646/zootaxa.2925.1.6.

Valdecasas, Antonio G., Santiago Castroviejo, and Leslie F. Marcus. 2000. "Reliance on the Citation Index Undermines the Study of Biodiversity." *Nature* 403(6771):698. doi: 10.1038/35001751.

Valdecasas, Antonio G., David Williams, and Quentin D. Wheeler. 2008. "'Integrative Taxonomy' Then and Now: A Response to Dayrat (2005)." *Biological Journal of the Linnean Society* 93(1):211–16. doi: 10.1111/j.1095-8312.2007.00919.x.

Venables, W. N., and B. D. Ripley. 2002. *Modern Applied Statistics with S.* Fourth Edi. New York: Springer.

Wetterstrand, K. A. 2025. *DNA Sequencing Costs: Data from the NHGRI Genome Sequencing Program (GSP)*.

Will, Kipling W., Brent D. Mishler, and Quentin D. Wheeler. 2005. "The Perils of DNA Barcoding and the Need for Integrative Taxonomy." *Systematic Biology* 54(5):844–51. doi: 10.1080/10635150500354878.

Williams, Daniel F., and Suzanne E. Braun. 1983. "Comparison of Pitfall and Conventional Traps for Sampling Small Mammal Populations." *The Journal of Wildlife Management* 47(3):841. doi: 10.2307/3808622.

Wüster, Wolfgang, Scott A. Thomson, Mark O'shea, and Hinrich Kaiser. 2021. "Confronting Taxonomic Vandalism in Biology: Conscientious Community Self-Organization Can Preserve Nomenclatural Stability." *Biological Journal of the*

Linnean Society 133(3):645–70. doi: 10.1093/biolinnean/blab009.

Ziegler, Alexander, and Christina Sagorny. 2021. "Holistic Description of New Deep Sea Megafauna (Cephalopoda: Cirrata) Using a Minimally Invasive Approach." *BMC Biology* 19(1):81. doi: 10.1186/s12915-021-01000-9.

Zuur, Alain F., Elena N. Ieno, Neil J. Walker, Anatoly A. Saveliev, and Graham M. Smith. 2009. *Statistics for Biology and Health*. Springer.

Figure legends

Figure 1. Global distribution of mammal species described between 1990 and 2022. Each point on the map represents a species' type locality, while donut charts indicate the proportion of species described within each taxonomic order. Points are coloured according to their respective taxonomic order, with rodents in blue, bats in green, and the different shades of red representing other mammals. To improve visualization, taxonomic orders holding less than 5% of species descriptions were grouped under 'Other taxa' label in the donut charts. The total sample size (N) is lower than the 1,032 species described during this period due to missing type-locality data for some species.

Figure 2. Variation in proxies of mammal species descriptions comprehensiveness over time (1990–2022). Panels show overall trends for all mammals (gray), non-rodents and non-bats (red), bats (green), and rodents (blue). Proxies include the (a) number of evidence used in species descriptions, (b) number of pages in taxonomic description papers, (c) number of specimens examined in species descriptions, and (d) number of taxa compared to distinguish new species. rs denotes the Spearman's correlation between the year of description and annual means for each variable. We applied Bonferroni corrections to p-values to account for multiple comparisons. Vertical lines represent standard errors, and shaded areas around the regression lines represent 95% confidence intervals.

Figure 3. Average number of countries per author involved in mammal species descriptions across different lines of evidence and over time. Patterns are shown for (a) all mammals, (b) non-bats and non-rodents, (c) bats, and (d) rodents. 'Other evidences' refers to descriptions that do not include molecular diagnoses and were not derived from taxonomic revisions. Molecular approaches exhibit different levels of internationalization compared to taxonomic reviews and other evidence types across mammals, bats, and rodents. In the violin plot, post-hoc comparisons were performed using estimated marginal means, with pairwise contrasts adjusted for multiple testing using the Bonferroni method. Groups that do not share letters are significantly different from each other.

Figure 4. Proportion of species descriptions using (a) molecular analysis or (b) taxonomic review for each mammal order from 1990–2022. The bars indicate the proportion of the total number of species described per order over this period. The different shades of gray indicate the proportion of these descriptions involving one, two, and three or more countries.

Figure 5. Influence of putative drivers on proxies of mammal species description comprehensiveness. Standardized coefficients from the generalized linear models fit to all species and for bats and rodents separately are shown. Horizontal lines denote the 95% confidence intervals around each coefficient. Predictors with significant effect sizes (p-value < 0.05) are those whose horizontal lines do not cross 0. Explained variation is presented (Model R^2) as Nagelkerke's pseudo-R^2 for negative binomial models (Number of taxa compared and Number of specimens) and as the coefficient of determination (R^2) for the Gaussian model (Number of evidence and Number of pages).