


## DATA ARTICLE OPEN ACCESS

# TetraDENSITY 2.0—A Database of Population Density Estimates in Tetrapods

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**Received:** 21 July 2024 | **Revised:** 27 September 2024 | **Accepted:** 7 October 2024

**Handling Editor:** Adam Conan Algar

**Funding:** The authors received no specific funding for this work.

**Keywords:** abundance | amphibians | birds | density | mammals | reptiles

## ABSTRACT

**Motivation:** Population density is a fundamental parameter in ecology and conservation, and taxonomic and geographic patterns of population density have been an important focus of macroecological research. However, population density data are time-consuming and costly to collect, so their availability is limited. Leveraging decades of research, TetraDENSITY 1.0 was developed as a global repository containing over 18,000 population density estimates for > 2100 terrestrial vertebrate species, aiding researchers in investigating patterns of population density, its intrinsic and extrinsic drivers, and for developing predictive models. Here we present a substantially expanded version of the database, which now includes marine tetrapods and encompasses over 54,300 estimates for 3717 species associated with error estimates and geographical coordinates when available, hence enabling meta-analytical approaches and better spatial matching of estimates with environmental conditions.

**Main Types of Variables Contained:** Population density estimates and associated errors, time and location of data collection, taxonomic information, estimation method.

**Spatial Location:** Global.

**Time Period and Grain:** 1925–2024.

**Major Taxa and Level of Measurement:** Amphibia, Reptilia, Aves and Mammalia. Estimates reported at the population level.

**Software Format:** .csv.

## 1 | Introduction

Population density is a critical piece of information for ecology and conservation, as it provides insights into species' spatial requirements, their relative abundance in a community, their population dynamics and, ultimately, their extinction risk (Brown, Mehlman, and Stevens 1995; Sanderson 2006; Santini et al. 2019,

2022; Wang et al. 2021; Callaghan et al. 2024). However, obtaining absolute population densities can be both costly and time-consuming; robust density estimates can require long field seasons, substantial costs for personnel, travel and equipment (e.g., Barea-Azcón et al. 2007; Liberg et al. 2012). Additionally, since density estimates are an instantaneous representation of a given period in time, they have limited temporal validity for

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management purposes. Decades of field research have produced thousands of estimates for thousands of species; capitalising on the vast amounts of density estimates available in the literature can allow researchers to generalise knowledge to investigate the drivers of population density across taxa and environmental gradients (Currie and Fritz 1993; Pettorelli et al. 2009; Santini, Isaac, and Ficetola 2018; Santini et al. 2023), identify biases in available knowledge and temporal trends in the data (Santini et al. 2021), assess the consistency of different methodologies to estimate density (Murphy et al. 2022), and make predictions for conservation and global change analyses (Santini, Butchart et al. 2019; Wang et al. 2021; Broekman et al. 2022; Pranzini, Bertolino, and Santini 2023). Furthermore, density estimates can be used for coarse approximation of population size over large areas for pragmatic conservation-oriented goals (Fechter and Storch 2014; Galaverni et al. 2016; Lewis et al. 2017; sRedList 2023).

The TetraDENSITY database was developed to address this challenge and provide researchers and conservationists with a tool to better understand the distribution and abundance of terrestrial vertebrates across the world (Santini, Isaac, and Ficetola 2018). TetraDENSITY is a comprehensive collection of global tetrapod population density estimates. The first version of the database contained 18,246 population density estimates for 2101 species of mammals, birds, reptiles, and amphibians.

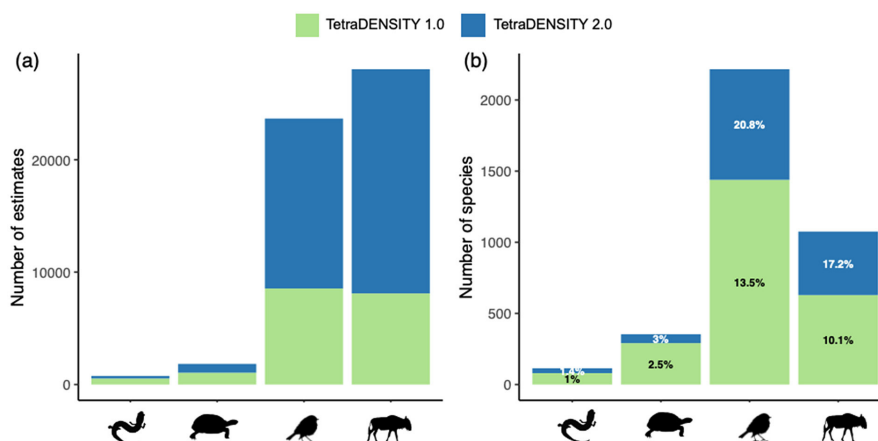
Since its release, the TetraDENSITY database has been used in various research areas, such as testing macroecological and conservation hypotheses (Santini et al. 2019; Sykes et al. 2020; Santini and Isaac 2021; Street et al. 2023), conducting macro-evolutionary analyses (Pie, Caron, and Divieso 2021), identifying the macroecological factors influencing population density (Santini et al. 2018, 2022, 2023; Gonzalez-Suarez et al. 2021), evaluating the impact of anthropogenic changes on the environment (Tucker et al. 2021), or estimating allometric relationships (Santini and Isaac 2021; Mason et al. 2022; Witting 2023). Additionally, TetraDENSITY has been used for developing predictive models (Santini et al. 2018, 2022) that have been applied in the fields of conservation assessments (Santini et al. 2019; Broekman et al. 2022; van Eeden and Dickman 2023; Cazalis

et al. 2024), global change biology (Wang et al. 2021), and planning of protected areas (Wolff et al. 2023).

Since the publication of the first version, the database continued to expand. Now TetraDENSITY has more than doubled, and includes marine tetrapods. The updated database now comprises 54,323 estimates for 3717 extant species (Figure 1). Additionally, the new version also includes error estimates from the original studies when made available. This opens the door to meta-analytical approaches where uncertainty in the original estimates is accounted for (Gurevitch et al. 2018). For studies conducted over large areas, when possible, the database now reports the longitudinal and latitudinal extent, which allows to better match the estimates with potential drivers at the right spatial scale (e.g., environmental and anthropogenic conditions). Finally, we revised the classification of sampling methods, increasing the number of method families and standardising the classes for better comparability.

## 2 | Methods

The expansion of our database was made feasible through various means. Firstly, over the years we received automatic notifications from Google Scholar that alerted us to new publications containing the keyword 'population density' and 'abundance'. These publications were periodically inspected and used for collecting additional data where relevant. By reviewing these papers, we also uncovered prior studies that were not included in our database, triggering a snowball-type of data gathering process. Additionally, we have been personally contacted by authors who have published new papers, colleagues who have come across estimates in their own research, or authors who could not find certain species or studies in the initial version of our database and have provided us with the missing references. Furthermore, we have been able to conduct more targeted data collections with the help of Bachelor, Master and Erasmus+ students who have focused their dissertations on specific species or systems. To mitigate the effect of several publication biases (see discussion), we collected estimates from scientific journals, technical reports, and dissertations.



**FIGURE 1** | Comparison of the first and second version of the database in terms of (a) number of population density estimates and (b) number of species. Percentage values in panel b indicate completeness compared to the total number of species per Class according to Catalogue of Life. Animal silhouettes retrieved from [PhyloPic.org](https://www.phylopic.org/).

Data were collected following the same procedure described in Santini, Isaac, and Ficetola (2018). For amphibians, we only collected data for terrestrial species and life stages, excluding breeding aggregations (e.g., counts of breeding individuals/egg clutches per pond) which are the most common in the literature. Similarly, we did not collect densities in lakes for entirely aquatic amphibians and freshwater turtles, nor bird breeding aggregations (e.g., nest colonies), which is typical for pelagic birds. All these estimates are in fact very much dependent on temporary aggregations or fine scale habitat features (e.g., perimeter–area ratio and depth of water bodies, coastline width, etc.) which makes it hard to use in any comparative analysis. We also excluded all density estimates expressed as linear densities (e.g., n/km) which are common for semi-aquatic species (e.g., otters).

From each paper, we recorded the species name, the density estimate, the year of data collection, the coordinates of the locality, the locality name, the period of the year (month(s) season), habitat type and sampling method (Table 1). Where possible, we collected individual estimates for different years, habitat types, or locations, and did not record the overall average estimate. We recorded the species name as reported in the original study, but also provide the name according to the Catalogue of Life taxonomy for comparability. In fact, the taxonomy of some species remains ambiguous or has changed over time, so the same species can be reported under different names across studies. The area over which population density is estimated can introduce biases (Blackburn and Gaston 1996; Gaston, Blackburn, and Gregory 1999), which arises from the perimeter–area ratio in relation to the species density (i.e., the change in ratio between the number of animals only intersecting the study area and those whose home range is entirely included in the study area). Therefore, when possible we collected the plot size, size of the strip transects, area used to place traps or camera traps, etc. The definition of this parameter depends on the method used (Table 1).

The coordinates are often reported by the original studies but no information is generally provided for the precision of such coordinates. When provided, we collected the coordinates and reconverted them into decimal degrees. When not provided, we obtained the most precise coordinates as possible from maps displayed in the study, or reported toponyms. For studies spanning over vast areas, we reported the longitudinal and latitudinal extreme values, which allows one to associate estimate with the conditions within that spatial window.

Habitat type is inconsistently described across papers, so it remains a qualitatively descriptive field that cannot be used for comparative analyses, but can provide study specific information for filtering or more systematic classifications into broader categories depending on the needs in more taxon-specific analyses. The time of the year the study was conducted was also recorded, but the level of detail varies from months to entire seasons.

When key information (sampling period and study site coordinates) could not be retrieved from the paper (e.g., sampling year) we directly contacted the corresponding author to gather the missing information.

The methods used to estimate density are extremely diversified, and a number of variants exist for each method. Here we classified the methods into 10 broad categories: Census, Counts, Distance sampling, Corrected distance sampling, Encounter models, Home range extrapolation, Mark Recapture, Spatial capture recapture, Mixture models, and Minimum numbers known to be alive. Each category can be further split into further sub-categories. A description of all categories and sub-categories is provided in Tables 1 and 2, respectively.

Data are not always provided as values in the papers, in many instances are provided as part of figures. In these cases, we extracted the data using WebPlot-Digitiser v. 4 Desktop (<https://automeris.io/v4/>; Rohatgi 2010). Most of the references were in English, but the database also includes a minority of studies published in Spanish, Portuguese, French, German, Italian, Chinese and Greek. This was possible thanks to language knowledge of the coauthors. For Chinese papers we conducted an independent search using the China National Knowledge Infrastructure database (CNKI, <https://cnki.net/>) using the following search string: (((TI=('种群密度'+'种群多度'+'种群数量'+'空间标记-重捕模型'+'标记重捕'+'标志重捕'+'距离取样'+'随机遭遇模型'+'Mark-recapture'+'Capture-Recapture'+'population census'+'transect'+'point count'+'random encounter models'+'territory mapping'+'N-mixture') AND AB=(carnivores + rodent + ungulate + birds + reptiles + snake + lizard + amphibians + amphibia + frog)) OR (KY=('种群密度'+'种群多度'+'种群数量'+'标记重捕'+'标志重捕'+'距离取样'+'空间标记-重捕模型'+'随机遭遇模型'+'Mark-recapture'+'population census'+'transect'+'point count'+'random encounter models'+'territory mapping'+'N-mixture') AND AB=(carnivores + rodent + ungulate + birds + reptiles + snake + lizard + amphibians + amphibia + frog))) OR AB=('头/km'+'只/km'+'头/hm'+'只/hm'+'头/ha'+'只/ha')) NOT TKA %=(疫+病+防治+菌群+正常组+模型组+小鼠+养殖+载畜). The search returned 1408 unique publications. We then reviewed titles, abstracts and full texts of the 300 most recent publications (published between 2018 and 2024), selecting 52 papers. Due to time constraints of our Chinese-speaking coauthor, we were unable to expand the search further.

Since data collection can come with compilation errors, we have implemented two periodic checks along the period of data collection. First, we plotted species  $\log_{10}$ -body mass by  $\log_{10}$ -population density and inspected outliers (Figure S1). Body mass—density relationship is indeed well established in the literature (Damuth 1981, 1987; White et al. 2007), so important deviations from the expected relationship may point to compilation errors. While most outliers are just natural outliers, a minority of cases pointed to compilation errors and were fixed. The second check concerned the spatial coordinates, which can be switched or miss a negative sign. We compared the reported country of occurrence with the country where coordinates would fall. This check resulted in some estimates falling in the oceans or in different countries. These studies were inspected in more detail. While in some instances, the discrepancies were due to approximations in the coordinates along the coastline, or across country borders, we identified multiple errors in the original data collection that were fixed. Data gathering for version 2.0 of TetraDENSITY ended in

**TABLE 1** | Metadata of the TetraDENSITY 2.0.

Field	Description	Type	N
Collector	Person who collected the data	Character	54,323
Class	Taxonomic class	Character	54,323
Order	Taxonomic order	Character	54,323
Species COL	Binomial standardised using Catalogue of Life	Character	54,278
Species_rep	Binomial reported in the study	Character	54,323
Subspecies_rep	Subspecies	Character	2706
Year	Sampling year(s). Expressed as a range when the sampling occurred over multiple years	Character	53,139
X	Central longitude of the study area (decimal degrees)	Numerical	54,226
Y	Central latitude of the study area (decimal degrees)	Numerical	54,226
X <sub>min</sub>	Westernmost longitude of the study area	Numerical	2847
X <sub>max</sub>	Easternmost longitude of the study area	Numerical	2847
Y <sub>min</sub>	Northernmost latitude of the study area	Numerical	2847
Y <sub>max</sub>	Southernmost latitude of the study area	Numerical	2847
Site	Name of the study site (also reporting region, island name, etc.)	Character	50,313
Country	Name of the country	Character	53,391
Sampling_area	The smallest sampling unit. If data were collected over the whole study area (e.g., mark-recapture, census) it corresponds to the study area. If data were collected within smaller areas (e.g., plots, strip transects) it corresponds to their size	Numerical	30,391
Sampling_area_unit	Unit measurement of the sampling area	Character	30,391
Density	Population density estimate	Numerical	54,323
Density_unit	Unit measurement for the population density estimate	Character	54,323
SE	Standard error of the density estimate	Numerical	3617
SD	Standard deviation of the density estimate	Numerical	458
CI90	90% confidence intervals of the density estimate	Numerical	110
CI95	95% confidence intervals of the density estimate	Numerical	4682
CV	Coefficient of variation of the density estimate expressed as percentage	Numerical	3321
Method	Sampling method category: Census = Any count that assumes all individuals were counted (e.g., aerial census); Counts = any incomplete count extrapolated on a larger area (e.g., strip transect counts, plot counts); Distance_sampling = Estimates based on distance sampling methods (e.g., line transects or point counts); Distance_sampling_corrected = Distance sampling estimates where $g(0) \neq 1$ , i.e. detectability at distance = 0 can be lower than 1 (e.g., aquatic mammals); Encounter_Models = Camera-trap models based on animal movement and frequency of encounters; Home_range = Density estimated as the inverse of the home range area (1/home range area), in some cases accounting for group size, home range overlap, etc.; Mark_recapture = Any estimate obtained on mark-recapture methods (genetic, camera traps, classical, etc.); Spatial_Capture_Recapture = Capture-recapture approaches modelling the spatial heterogeneity in detectability of individuals as a function of the distance from their activity centers; Mixture_Models = Models combining a model for probability of detection and one for estimating abundance from count data; Minimum_Number_Alive = any estimate based on the minimum number of animals observed (e.g., trapping studies)	Character	51,326

(Continues)



**TABLE 1** | (Continued)

Field	Description	Type	N
Method2	Sub-category of method as reported in Table 2	Character	29,483
Notes_method	Free-format field where additional notes related to the method are reported	Character	11,690
Habitat	Descriptive field of the habitat type	Character	
Season	Period of sampling expressed in seasons (e.g., Dry seasons, Fall) or months (e.g., February—April). If both are available, only months are reported	Character	36,441
Native	Indicates if the species is native to the area	Boolean	54,323
Notes	Additional useful notes that do not fit in other fields	Character	13,116
Reference	Reference of the study reported in APA format	Character	54,323

July 2024. A description of all variables included is presented Table 1, and the database is accessible at <https://doi.org/10.6084/m9.figshare.26342614>. A full list of data sources is provided in Appendix S1.

### 3 | Results

We gathered data from a total of 2734 studies. Compared to the first version, TetraDENSITY 2.0 expanded in terms of number of estimates (Amphibians = 40.6%, Reptiles = 73.8%, Birds = 56.5%, Mammals = 40.6%, Figure 1a) and species (Amphibians = 42.5%; Reptiles = 21.3%, Birds = 54.0%, Mammals = 70.9%, Figure 1b) for the four classes, totalling 54,323 density estimates for 3717 species (Figure 1).

Data are also highly heterogeneous across taxonomic groups (Figure 2a), with a minority of data belonging to amphibians (1.4%), followed by reptiles (3.4%), birds and mammals (43.6% and 51.7%, respectively). Within amphibians, 69.5% of the records belonged to Anura, and 30.5% to Caudata, whereas no estimates were found for Gymnophiona. In reptiles, 74.7% to Squamata and 24.9% to Testudines. Birds' estimates mostly consisted in Passeriformes (65.4%), followed by Piciformes (6.4%), Anseriformes (4.9%), Galliformes (4.2%), and Columbiformes (3.2%), all other orders made less than 3% of the data. Within mammals, most data belonged to Cetartiodactyla (both ungulates and cetaceans, 40.8%), followed by Rodentia (14.9%), Carnivora (14.0%), and Primates (13.4%), Lagomorpha (4.9%) and Proboscidea (4.8%), all other orders made less than 3% of the total.

Data span from early 20th century up to 2024, but are mostly available from 1975 onwards with a peak around 2000–2010 (Figure 2b). Methods are unequally distributed across the four classes (Figure 2c). Amphibians are mostly estimated using simple counts, mark-recapture, minimum number known to be alive, and Mixture model approaches. Reptiles mostly using simple counts, distance sampling and mark-recapture methods. Birds were estimated mostly using census (territory mapping), simple counts, and distance sampling techniques. Mammals were the most diverse in terms of methodological approaches, with a large proportion of studies employing distance sampling, census (mostly aerial surveys), simple counts, and mark-recapture and a minority using minimum number known to be

alive, and spatial capture recaptures. Other method classes were more rarely used (Figure 2c).

Estimates are widely distributed globally (Figure 3), but their relative abundance is highly heterogeneous, with Europe, United States and Brazil holding a substantial portion of the estimates. Furthermore, geographic biases are highly heterogeneous between groups, with amphibian data mostly present in Europe, United States, central and South America (Figure 3a), reptile data largely present in islands but missing in several continental areas (Figure 3b), birds and mammals (Figure 3c,d) more widely distributed but with substantially more estimates in Africa and India for mammals (Figure 3d).

Across the terrestrial realm, the environmental space (obtained through a principal component analysis) is widely covered with the exception of very cold regions (Antarctica, Figure 4a). Across the marine realm, most estimates are present nearby the coasts, but span the full temperature gradient (Figure 4b).

### 4 | Discussion

TetraDENSITY 2.0 is a substantial improvement compared to its first version both in terms of data quantity, comprehensiveness and standardisation of the reported information. While the database spans across a wide range of taxa globally, a number of taxonomic, spatio-temporal and environmental biases are evident. Such biases are due to a number of factors including biases in research efforts, relevance of population density estimates for conservation and management, publication biases, diverse accessibility to papers, search engine algorithms behaviour, and costs.

Birds and mammals have traditionally received more research attention than herptiles (Bonnet, Shine, and Lourdaïs 2002; Clark and May 2002). Additionally, absolute estimates of population density are way more common in birds and mammal research than in herpetological research, where relative indices are more commonly applied. Moreover, most herps live at high population density, making abundance a less relevant parameter than occurrence in conservation with respect to endotherms (i.e., ectotherm species achieve large populations in small areas). Within endotherms, some species are more relevant for management (e.g., problematic species like wild boars) and conservation

**TABLE 2** | Method categories and subcategories with the respective explanations.

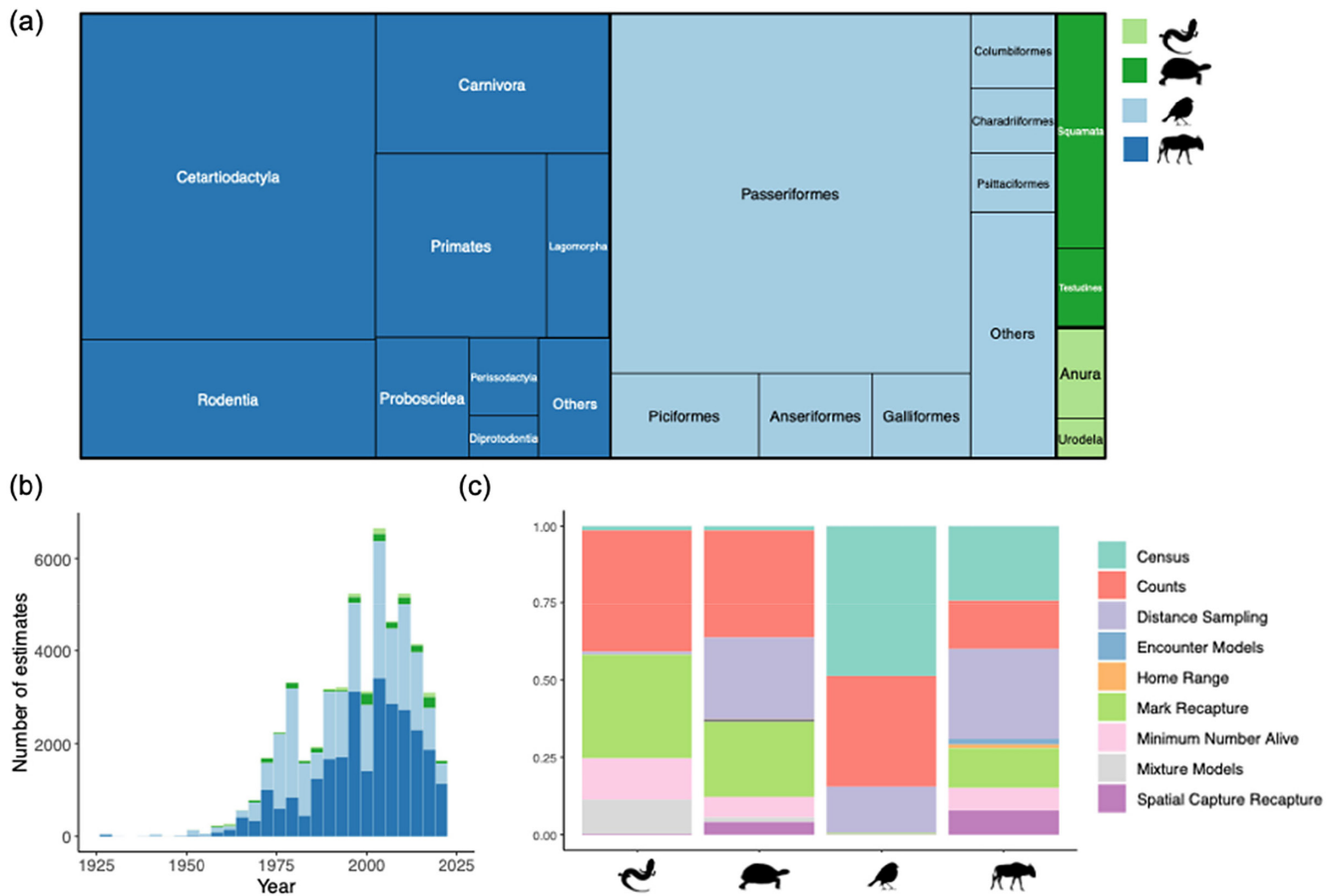
Method	Method2	Method2 explanation
Census	Territory mapping	Mapping the bird territories through repeated visits or acoustic surveys
Counts	Direct	Counts on live animals
	Indirect	Counts on animal cues
	Direct/Indirect	Counts on both live animals and cues
Distance_Sampling	Line transects	Distance sampling on line transects
	Point counts	Distance sampling on point transects (visual and acoustic)
	Line/point transects	Distance sampling on both line and point transects
	CTDS	Camera Traps-Distance Sampling
Distance_Sampling_corrected	Line transects	Distance sampling on line transects
	Point transects	Distance sampling on point transects (visual and acoustic)
	MRDS	Mark-recapture distance sampling
Encounter_Models	REM	Random Encounter Model
	REST	Random Encounter and Staying Time model
	STE	Space-To-Event model
	TTE	Time-To-Event model
Home_Range	/	No further subdivisions (details in Notes_method)
Mark_Recapture	/	No further subdivisions (details in Notes_method)
Minimum_Number_Alive	/	No further subdivisions (details in Notes_method)
Mixture_Models	NM	N-Mixture models
	RN	Royle-Nichols models
Spatial_Capture_Recapture	SC	Spatial Counts model
	SECR	Spatially-Explicit Capture Recapture
	USCR	Unmarked Spatial Capture Recapture

(e.g., tigers) and are more often targeted for population density studies. In birds, taxonomic bias is less acute because most studies do not target one single species. In contrast, studies on mammals diverge substantially in methods used for different species, hence studies normally report densities on one or few similar species.

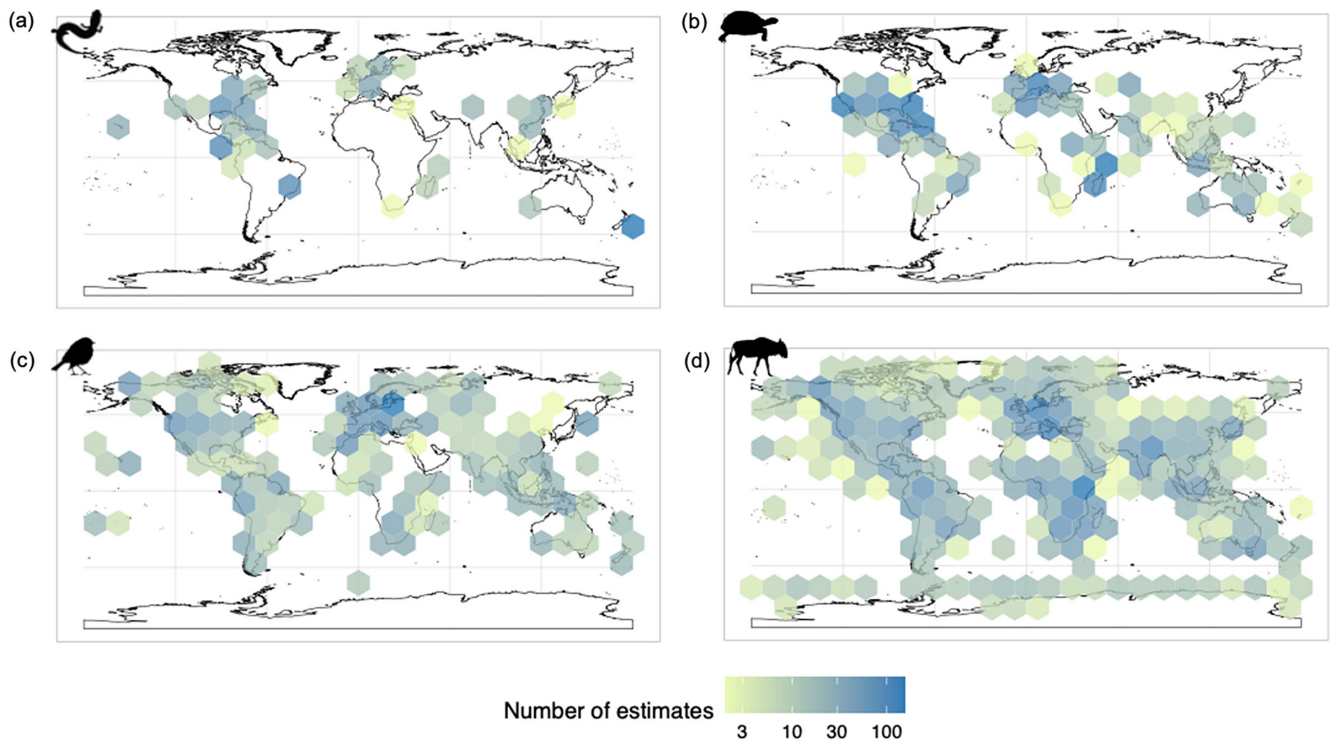
A further cause of taxonomic bias originates from the challenges of estimating density in certain taxa. Two notable examples are bats and snakes, which make about ~20% and > 30% of known mammals and reptiles, respectively. Despite their prevalence, relatively few density estimates for these taxa have been produced thus far. In bats, the difficulty lies in the complexity of density estimation. Recently developed methods based on

acoustic signals are promising, but at present are still sensitive to a number of hard-to-measure parameters, and still infrequently applied (e.g., Milchram et al. 2020; Hoggatt, Starbuck, and O'Keefe 2024). Snakes, on the other hand, show exceptionally low densities among reptiles, and are extremely elusive. Traditional methods used to estimate the density of other reptiles (e.g., transect counts) are generally impractical for snakes. While more intense and expensive mark-recapture studies are possible, the low research interest and funding compared to other elusive and rare taxa (e.g., mammals) results in snake density estimates being quite rarely produced.

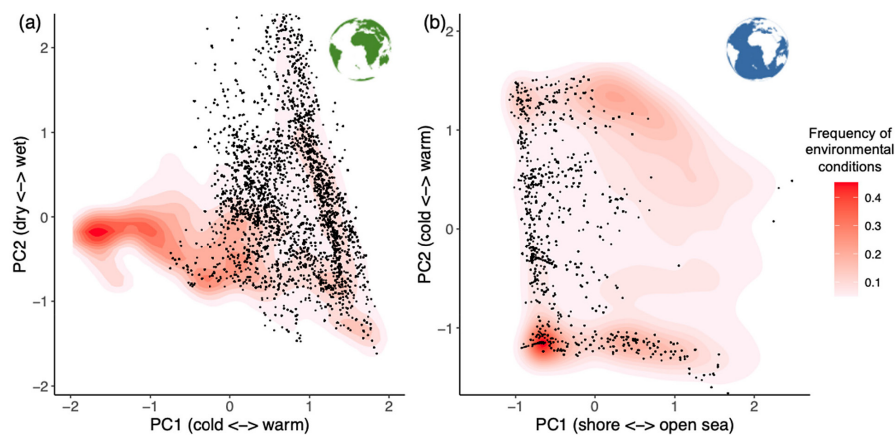
Another source of bias concerns scientific production. In the current panorama where articles are screened by editors also in



**FIGURE 2** | (a) Treeplot depicting the relative proportion of estimates belonging to different taxonomic orders of the four tetrapod classes. (b) Temporal distribution of the population estimates in the database per taxonomic class. (c) Relative abundance of different methods per taxonomic class. Distance sampling and corrected distance sampling method classes are aggregated for simplicity. Animal silhouettes retrieved from [Phylopic.org](https://www.phylopic.org/).



**FIGURE 3** | Geographic distribution of population density estimates in the database divided per (a) amphibians, (b) reptiles, (c) birds and (d) mammals. Hexagons' colour represent total number of estimates in the region. Animal silhouettes retrieved from [PhyloPic.org](https://www.phylopic.org/).



**FIGURE 4** | Environmental coverage of the population density estimates in the database for the (a) terrestrial and (b) marine realms. Colour shading indicate the density of those conditions globally, while points indicate the conditions associated to the population density estimates. A principal component analysis was performed on all bioclimatic variables (Fick and Hijmans 2017) for the terrestrial realm, and mean surface temperature, distance from shore, and bathymetry for the marine realm (Basher, Bowden, and Costello 2018). The two principal axes are plotted with label indicating in brackets the variable with the highest loading.

terms of potential citations, it is more and more difficult to publish density estimates for non-charismatic species than charismatic species (Prokop et al. 2022). Furthermore, the study of less charismatic species, or less relevant from a conservation or managerial perspective, is less likely to receive fundings (Mammola et al. 2023).

Moreover, researchers in developing countries may find more difficult to publish in high-impact journals. However, search engine algorithms give more visibility to well-cited papers in higher impact journals than non- (or little) cited papers in lower impact journals. To mitigate these biases, we did not apply any filter to journals (e.g., based on IF or their inclusion in Web of Science) and included also technical reports and dissertations reporting unpublished data.

Further biases derive from the heterogeneous reporting of data across publications. In many cases, population density is estimated and analysed, but not reported or detailed in the paper. This contributes to the temporal bias, since more and more journals require all data to be made available (Jenkins et al. 2023). Especially in low-ranked journals, key ancillary information is highly incomplete, such as the months and years of sampling, or the exact location of the study. When possible, we mitigated this problem by contacting the original authors to gather missing information.

Publications in different languages pose additional barriers. Regions with less data are in most cases areas where language follow non-Roman like Russian, Greek, Arabic, Chinese, Japanese, Korean, etc. We were able to partially address this limitation through ad hoc search in Chinese. A clear geographic bias in our dataset remains for Eastern Russia, which might also reflect the limited accessibility to remote areas (Weiss et al. 2018).

Over time, ecological research has received more attention and funding, and an increasing number of methods have been developed to estimate the density of more elusive species. This has led to a surge in the number of estimates produced over time. However, such temporal bias has been further exacerbated by

the limited accessibility to old publications. Accessibility also explains part of the geographic bias: many regional journals publishing data on local wildlife are not accessible to institutions in other regions due to lack of subscriptions. A notable example are many Australian journals belonging to CSIRO publishing. When possible we attempted emailing authors to access newly published papers, but this was not possible for older publications.

An additional source of bias to consider is that some studies are significantly more expensive and time consuming than others, and less likely to receive appropriate fundings (as we also mentioned in relation to non-charismatic species). Methods for obtaining density estimates varies enormously across species, from simple plot and transect counts over small areas that can be conducted by few persons over short times, to mark-recapture estimates based on camera traps or genetic analyses spanning over entire regions for several years. Since most of the research in tropical countries is still conducted by institutions in developed countries (Trisos, Auerbach, and Katti 2021), costs are also expected to vary geographically, with higher costs to study distant countries to the research institution.

Although these sources of bias lead to a non-homogeneous geographic distribution of collected estimates, data are well-distributed across different climates from an environmental space perspective (Figure 4). Individually, herptiles cover a more limited range of environmental conditions, which however reflects their biology (e.g., thermoregulation strategies and susceptibility to dehydration in amphibians). This, along with their distribution across the body mass gradient (Figure S1), suggests a limited extent of environmental and functional biases in macroecological analyses.

Despite these limitations, by accounting for sampling biases in modelling studies (e.g., Isaac et al. 2014) while being transparent with limitations (Boyd et al. 2022), one can still extract valuable information from these data. TetraDENSITY 2.0 has the potential to foster macroecological and conservation research by elucidating



the drivers of population density and resulting patterns, and inform conservation plans. Additional data collection in the future can further contribute to these efforts, and recent AI-developments can further accelerate the production of new estimates by assisting researchers on specific tasks (e.g., Vélez et al. 2022; Henrich et al. 2023). Although further testing and improvements are needed, artificial intelligence has the potential to facilitate, assist, and accelerate biodiversity data collection in the future, and might ultimately help achieving more comprehensive and up-to-date database in the future (Gougherty and Clipp 2024).

## Authors Contribution

L.S. conceived the original idea, L.S., V.Y.M.A., C.K., D.F., N.P., C.V., T.Z., S.J.G., D.M. and L.P. collected the data, L.S. and A.Z. revised the classification of the methods, L.S., A.Z. and D.M. revised and harmonised data collected for the first version of the database, L.S. wrote the first version of the paper, all authors revised the paper.

## Acknowledgements

We thank Adam C. Aglar and an anonymous referee for providing constructive comments that helped improving the manuscript. We also thank Ana Benítez-López for suggesting papers for data collection, Fabio Rivellini and G. Boratto for minor contributions to the data collection, and all colleagues who have got in contact over the years to inform us about missing papers in TetraDENSITY 1.0 or new published papers.

## Conflicts of Interest

The authors declare no conflicts of interest.

## Data Availability Statement

The database is available at <https://doi.org/10.6084/m9.figshare.26342614>.

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## Supporting Information

Additional supporting information can be found online in the Supporting Information section.