DATA ARTICLE

HomeRange: A global database of mammalian home ranges

Maarten Jaap Erik Broekman ⓘ | **Selwyn Hoeks** ⓘ | **Rosa Freriks** |
Merel M. Langendoen | **Katharina M. Runge** | **Ecaterina Savenco** | **Ruben ter Harmsel** |
Mark A. J. Huijbregts ⓘ | **Marlee A. Tucker** ⓘ

Department of Environmental Science,
Radboud Institute of Biological and
Environmental Sciences, Radboud
University, Nijmegen, The Netherlands

Correspondence
Marlee A. Tucker, Department of
Environmental Science, Radboud Institute
of Biological and Environmental Sciences,
Radboud University, Nijmegen, The
Netherlands.
Email: marlee.tucker@ru.nl

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Abstract

Motivation: Home range is a common measure of use of space by animals because it provides ecological information that is useful for conservation applications. In macroecological studies, values are typically aggregated to species means to examine general patterns of use of space by animals. However, this ignores the environmental context in which the home range was estimated and does not account for intraspecific variation in home range size. In addition, the focus of macroecological studies on home ranges has historically been biased towards terrestrial mammals. The use of aggregated numbers and the terrestrial focus limit our ability to examine home-range patterns across different environments, their variation in time and variation between different levels of organization. Here, we introduce *HomeRange*, a global database with 75,611 home-range values across 960 different species of mammals, including terrestrial, aquatic and aerial species.

Main types of variables contained: The dataset contains estimates of home ranges of mammals, species names, methodological information on data collection, method of home-range estimation, period of data collection, study coordinates and name of location, in addition to species traits derived from the studies, such as body mass, life stage, reproductive status and locomotor habit.

Spatial location and grain: The collected data are distributed globally. Across studies, the spatial accuracy varies, with the coarsest resolution being 1°.

Time period and grain: The data represent information published between 1939 and 2022. Across studies, the temporal accuracy varies; some studies report start and end dates specific to the day, whereas for other studies only the month or year is reported.

Major taxa and level of measurement: Mammalian species from 24 of the 27 different taxonomic orders. Home-range estimates range from individual-level values to population-level averages.

Software format: Data are supplied as a comma-delimited text file (.csv) and can be loaded directly into R using the "HomeRange" R package (https://github.com/SHoeks/HomeRange).

Maarten Jaap Erik Broekman and Selwyn Hoeks shared lead authorship.

1 | INTRODUCTION

Home range is the area that animals use to secure resources for reproduction and survival (Burt, 1943) and is a reflection of how animals interact with their environment (Börger et al., 2008) and their energetic constraints (Boratyński, 2020; Enriquez-Urzelai & Boratyński, 2022). Home range is commonly estimated because it provides ecological information on use of space by animals, resource use (Butler et al., 2020; Ofstad et al., 2019), predation (Messinger et al., 2019), the distribution of organisms and populations (Wang & Grimm, 2007) and their social interactions (Olejarz et al., 2022). The information derived from home ranges is also useful for conservation managers, such as for controlling invasive species (Hradsky et al., 2019), identifying areas that are commonly used by multiple species and ensuring that protected areas are large enough to support species (Di Franco et al., 2018). Home range is therefore a valuable and widely used metric of space use by animals.

Home ranges are commonly measured for individuals at a specific location. In macroecological studies, these values are often converted to a single mean per species to examine general patterns of space use by animals (Kelt & Van Vuren, 2001; Lindstedt et al., 1986). However, the use of single home-range values per species ignores the environmental context in which the home range was estimated and does not account for intraspecific variation in home-range size, which might be large for several species (Naidoo et al., 2012; Snider et al., 2021; Walton et al., 2017). Currently, there are several datasets that report species-level home-range values for mammals (Jones et al., 2009; Kelt & Van Vuren, 2001; Soria et al., 2021). Additionally, these databases focus almost exclusively on terrestrial mammals, excluding the full diversity of mammals. Moreover, even within terrestrial mammals, home-range sizes for the majority of species are still missing within these datasets [e.g., the COMBINE dataset (Soria et al., 2021) reports home-range values for only 13% of species of mammal]. Therefore, our ability to examine home-range patterns within and across mammalian taxa is limited.

To fill these data gaps, we compiled the *HomeRange* database, consisting of home-range values for mammal species (n = 960) across 24 orders collected from the literature. We included all home ranges reported by each study and indicated the level at which the home range was estimated (e.g., home range for a single individual, mean home range of multiple individuals, combined home range for multiple group-living individuals). We also provided methodological and geographical information for each home-range value. Variations in home-range size have consequences for individuals (e.g., survival), populations (e.g., declines) and ecosystems (e.g., trophic structure). Therefore, examining how home-range size varies across time, space and species is important for understanding these ecological processes.

2 | DATA COLLECTION

2.1 | Literature search

We collected home-range data from the scientific literature (peer-reviewed papers), theses (master's and PhD), secondary sources (e.g., books) and grey literature (e.g., government reports) for mammals using Web of Science. In contrast to regular literature searches that use a single search string to collect papers, we applied a search string per species name using an automated search method. For the list of species names, we relied on the list of mammals provided by the International Union for Conservation of Nature (IUCN, 2017). We iterated over all species (n = 6296) and made a search inquiry using the following parameters:

TI = ("scientific name" OR "common name") OR AB = ("scientific name" OR "common name")

AND

ALL = ("home-range" OR "home range" OR "home-ranges" OR "home ranges" OR "space use" OR "space-use")

OR

ALL = ("polygon" OR "kernel" OR "convex" OR "brownian bridge movement model")

Using a PYTHON (v.3.9.6) script and the Selenium WebDriver, these searches were automated in a "for loop". In each iteration, the "scientific name" and "common name" were inserted by the entry in the species list. The search hits per search inquiry were stored in a .csv file and merged after completion of the script. The first full search was completed in October 2020. A second search was completed in April 2022 to include new papers published during the initial data-collection process. We also collected data from the papers included in the Kelt and Van Vuren (2001) and panTHERIA (Jones et al., 2009) databases, in addition to papers from the review by Heit et al. (2021). Please note that the data from these databases and the review were extracted following the same procedure applied to all other papers. In total, this resulted in 9043 potentially useful papers (Figure 1). All papers collected were used in the following screening step.

2.2 | Paper screening

All 9043 papers were screened by title and abstract using the "metagear" package (Lajeunesse, 2015) in R (v.3.6.3). If the abstract
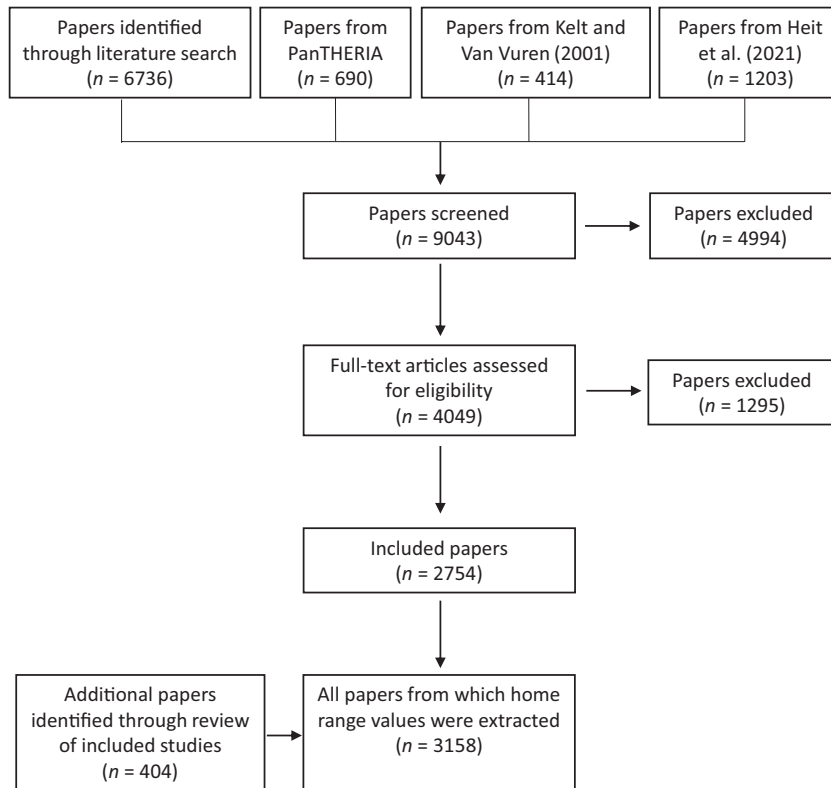
FIGURE 1 Diagram detailing the procedure for identifying and including papers with home-range values

was not available by this method or did not provide enough information from which to judge the paper, the full text was downloaded. The screening process resulted in 4049 papers for which the full text was inspected. Of these 4049 papers, 1295 papers were not included in the *HomeRange* database, because the paper could not be accessed, the paper provided very limited methodological information, the paper reported only home-range values from other studies or the paper was a duplicate. By inspecting the full text of the papers, we were also able to identify 404 additional papers with home-range values that were not yet in our database. Therefore, our final database contains home-range values from 3158 different papers (Figure 1).

2.3 | Data extraction

From each study included in our final publication list ($n = 3158$), we extracted all home-range values reported in the paper. If the reported home-range value was based on multiple home-range estimates (mean or median of multiple home ranges), we recorded (when possible) the variation in home-range estimates (e.g., standard deviation, quantiles), in addition to the number of individuals and home-range values included. We also extracted information concerning the study duration, geographical location, characteristics of the studied individuals (e.g., sex, life stage, body weight), tracking method, home-range estimation method, isopleth size and the number of spatial data points included in the home-range estimate (see Table 1).

2.4 | Data harmonization and verification

All home-range values and the measures of the variation in home-range values were converted to square kilometres. For individuals for which the age was given, but not the life stage (e.g., juvenile, adult), we used the age of sexual maturity from the COMBINE dataset (Soria et al., 2021) to classify individuals as adult or immature. Scientific species names were corrected to match the most recent taxonomy of the IUCN Red List (v.2022-1). To verify that the reported species name was correct, we checked whether the reported location of a study occurred within the geographical range of the given species from the IUCN. We corrected the species name or the longitude and latitude when there was a mismatch between the reported species name and the IUCN range of that species. We also checked whether the reported location occurred within the specified country and corrected the country name or the longitude and latitude when there was a mismatch. Finally, we identified potentially incorrect home-range and body mass values. For home-range values, we exposed potentially incorrect values by calculating the .05 and .95 quantiles of the species-specific home-range values and flagging the values that deviated by more than one order of magnitude from these quantiles, and by comparing the extracted home-range values wih the home ranges from the COMBINE dataset (Soria et al., 2021) and flagging the values from studies for which >70% of home-range values differed by at least one order of magnitude from the home-range values from COMBINE (including only home-range values for which the isopleth was >75%). For body mass, the extracted values were compared with the adult body mass from the COMBINE

TABLE 1 Description of the key parameters in the dataset

Variable	Definition	Number of data
Species	Scientific name of the species	75,611
Ind_ID	Unique identifier of the individual, population or group of individuals for which home range was estimated	51,351
Home_Range_km2	Area of home range (in square kilometres)	75,611
HR_level	Categorical value indicating whether the reported home-range value is the home range of a single individual (individual), a group of individuals (group) or the mean/median home-range value of multiple individuals (population)	75,605
HR_Span	Period over which home range was calculated	75,611
No_Individuals	Number of individuals that were included in the home-range estimation	72,678
No_HR	Number of home-range values included in the calculation of the reported mean or median home-range value	73,449
Sex	Sex of the individual(s) for which the home range was estimated	70,799
Life_Stage	Life stage of the individual(s) for which the home range was estimated	58,395
Reproductive_Status	Reproductive status of the individual(s) for which the home range was estimated	9755
Body_mass_kg	Body mass of the individual(s) as reported by the study (in kilograms)	20,061
Context	Categorical value indicating whether the home range was estimated in conditions deliberately changed by humans (Experiment) or not (Wild)	75,611
Locomotion	Locomotor habit of species: terrestrial, arboreal, semi-arboreal, fossorial, aerial, semi-aquatic or aquatic	75,611
Latitude/Longitude	Latitude and longitude of the study area (in decimal degrees)	74,613
Country	Name of the country in which the study area was located	75,573
dayStart	The first day from which data were collected for home-range calculation	17,671
monthStart	The first month from which data were collected for home-range calculation	65,385
yearStart	The first year from which data were collected for home-range calculation	73,688
dayEnd	The last day from which data were collected for home-range calculation	17,235
monthEnd	The last month from which data were collected for home-range calculation	64,934
yearEnd	The last year from which data were collected for home-range calculation	73,675
Tracking_Method	Method used to track the animal(s)	75,461
HR_Method	Method used to calculate the home range	74,832
Isopleth_Size	Percentage of locations used to estimate the home range	74,024
Mean_No_Locations_Used	Mean number of locations to estimate home-range values	51,985

dataset (Soria et al., 2021). Values that deviated by more than two orders of magnitude were flagged. All flagged values were checked manually, and erroneous values were corrected by inspecting the full text of the original source (i.e., values that were entered incorrectly in the dataset were modified, and possible outliers were retained when the values matched the original source). Most detected errors were associated with mistakes in units of measurement (e.g., grams vs. kilograms, or square kilometres vs. square metres).

2.5 | Data availability and access

The *HomeRange* database is available via github (https://github.com/SHoeks/HomeRange) or DRYAD (Tucker et al., 2022). We provide three data files. The first file contains the *HomeRange* database, including home-range values, location of study and associated variables (Table 1). The second file contains the metadata, with in-depth information on the variables in the database. The third file is a complete list of all the data sources used to compile the data.

In addition to the *HomeRange* database, we also provide an R package, which can be installed from: https://github.com/SHoeks/HomeRange. The *HomeRange* R package provides functions for downloading the latest version of the *HomeRange* database and loading it as a standard dataframe into R, plotting several statistics of the database and, finally, attaching species traits (e.g., species average body mass, trophic level) from COMBINE (Soria et al., 2021) for statistical analysis.

3 | RESULTS

The database contains 75,611 home-range values (Table 2) collected between 1936 and 2021 from 960 different species (including four hybrid species) and 24 different taxonomic orders

TABLE 2 Number of home-range estimates grouped by locomotion (based on the studies by Santini et al., 2022; Soria et al., 2021) and home-range level

Locomotion	Individual	Group	Population	Total
Aerial	1859 (71)	119 (20)	526 (73)	2504 (93)
Aquatic	2049 (30)	128 (12)	396 (28)	2573 (37)
Semi-aquatic	1056 (15)	46 (3)	456 (19)	1558 (19)
Arboreal	5228 (125)	2709 (124)	2584 (149)	10,521 (275)
Semi-arboreal	2164 (27)	1567 (36)	733 (27)	4464 (59)
Terrestrial	34,388 (301)	2408 (63)	15,315 (374)	52,111 (430)
Fossorial	1248 (28)	74 (5)	558 (46)	1880 (47)
All	47,992 (597)	7051 (263)	20,568 (716)	75,611 (960)

Note: The numbers in parentheses indicate the number of species.

(excluding Dermoptera, Notoryctemorphia and Paucituberculata). The body mass of the species in the database ranges from 4.15 g (*Amorphochilus schnablii*) to 1.49×10^5 kg (*Balaenoptera musculus*) (Figure 2). Most home ranges are for terrestrial species (68.9% of the home ranges and 45% of the species; Table 2). Most studies collected data for the white-tailed deer (*Odocoileus virginianus*; 101 studies), followed by the coyote (*Canis latrans*; 81 studies) and the red fox (*Vulpes vulpes*; 67 studies). The majority of data come from North America (21,342 home-range values from 1042 studies) and Europe (15,295 home-range values from 541 studies), whereas only a very limited number of studies come from Russia (678 home-range values from 18 studies) and Northern Africa (46 home-range values from 3 studies) (Figure 3).

The home-range values include the complete home range [i.e., the total area an individual uses to reproduce and survive (Burt, 1943)], defined using large isopleths (e.g., 95 or 100%), in addition to core areas of home ranges [i.e., the part of the home range in which the majority of activities take place (Samuel et al., 1985)], often defined using an isopleth size of 50% (Laver & Kelly, 2008). The home ranges cover time periods ranging from a single day to multiple years. In addition, home-range values are collected for individuals spanning a range of life stages and reproductive stages. The home-range values span 12 orders of magnitude, from 1×10^{-6} km² (a monthly home range for *Dicrostonyx groenlandicus*) to 1.9×10^6 km² (an annual home range for *Ursus maritimus*) (Figure 2).

4 | DISCUSSION

To the best of our knowledge, we have compiled the most comprehensive mammal home-range database to date. The data will facilitate the study of ecological theories, such as the allometric scaling of the use of space by animals, and could be used to study inextricable links with life-history optimization (White et al., 2022). It can also help to increase our understanding of the impact of external factors, such as the characteristics of the environment or anthropogenic pressures, on home-range patterns. *HomeRange* might also help to update current species-level home-range values and fill gaps in species trait databases. For example, species averages derived from the *HomeRange* dataset could be used to add home-range data for 463 species to the recently published COMBINE dataset (Soria et al., 2021).

Accuracy and precision of home-range estimates can depend greatly on the tracking method used, the home-range estimation method applied, the sample size (e.g., number of animals tracked) and the study duration. These factors relate directly to the species studied, geographical region and study year. For example, certain species and regions make sampling and tracking of animals easier than others, and studies published in recent years apply more modern tracking and home-range estimation methods. The *HomeRange* dataset includes data on these factors (see Table 1) that could be used to account for the resulting variation in home-range estimates.

Although the data points of *HomeRange* are distributed globally, there is a strong bias towards Europe and North America (see Figure 3). This can be explained by the known geographical patterns of ecological research (Martin et al., 2012) and by our search being constrained to literature written in English, with the exception of a small number of papers written in other languages (e.g., Dutch, German, French, Spanish). In our literature search, we applied a search string for each species independently, which made it possible to include papers that could otherwise be overlooked (e.g., when relying on a single search string and including terms such as "mammals", "ungulates" or "rodents"). Papers that did not include the species name (common or scientific) in the title or abstract might have been excluded from this search method. However, by including all the home-range-related data that could be extracted from the papers listed by Kelt & Van Vuren (2001), panTHERIA (Jones et al., 2009) and Heit et al. (2021) and by including additional papers found by inspecting the full text of the papers (see Figure 1), we aimed to compile the most complete database possible.

In conclusion, the *HomeRange* database provides an extensive number of home-range estimates quantified over multiple levels of organization, from population-level home ranges down to individual-level home ranges and from home ranges spanning days to multiple years. Given that the size of the home range is more than a product of the species studied and varies greatly because of individual-level variation and extrinsic factors or pressures (Duncan et al., 2015; Hirt et al., 2021; Tucker et al., 2014), *HomeRange* might provide important insights into patterns of animal movement across different environments, variation in time and variation between different levels of organization. Ultimately, this level of information might aid in the identification of potentially vulnerable species and regions and help conservation efforts.
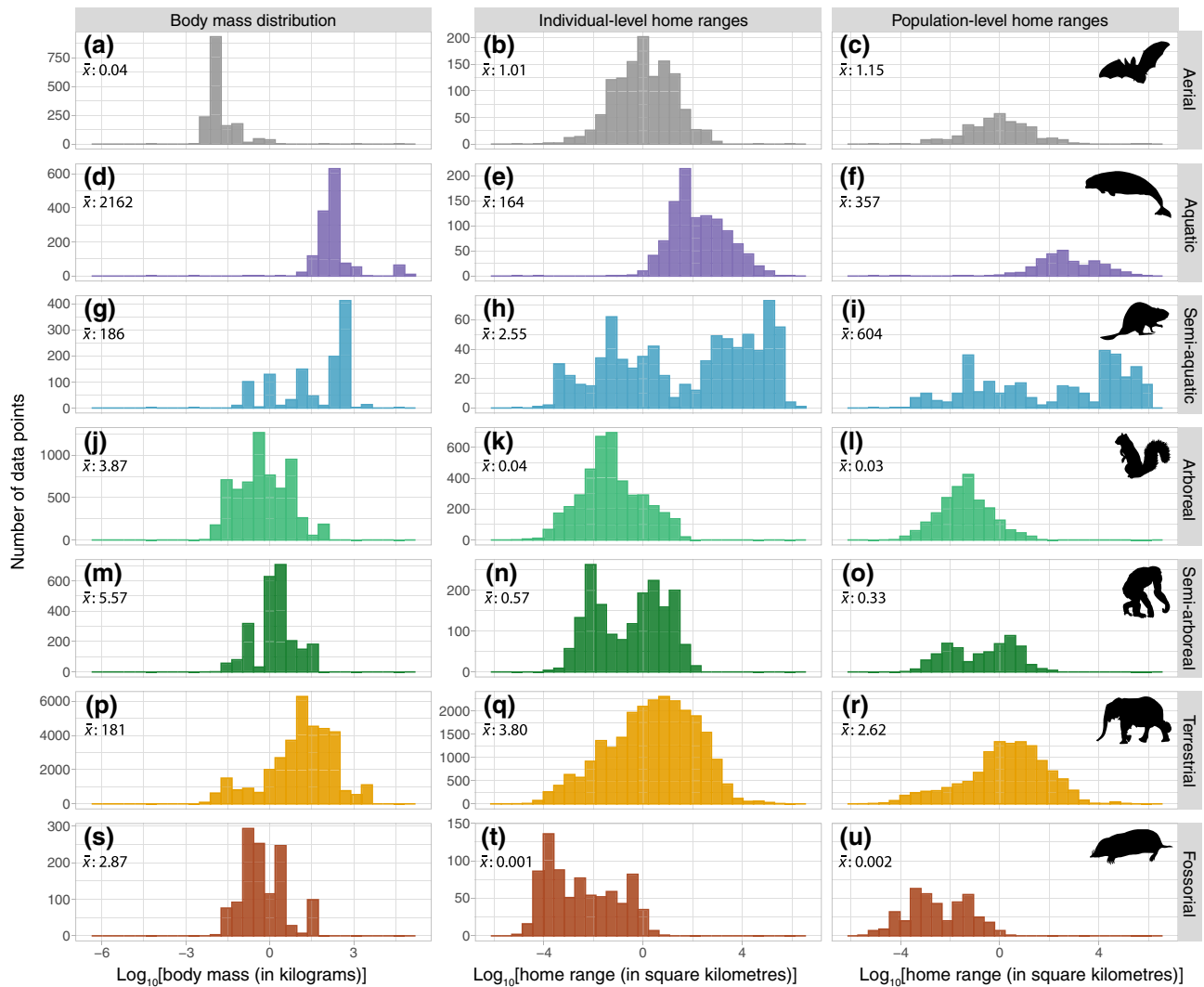
FIGURE 2 Distribution of (a,d,g,j,m,p,s) body mass, (b,e,h,k,n,q,t) individual and (c,f,i,l,o,r,u) population home-range entries with >90% isopleth across the different locomotion types (based on the studies by Santini et al., 2022; Soria et al., 2021). When body mass values were not available, we used species-level means from the study by Soria et al. (2021). $\bar{x}$ provides the mean of the distribution for body mass (in kilograms) and home range (in square kilometres)
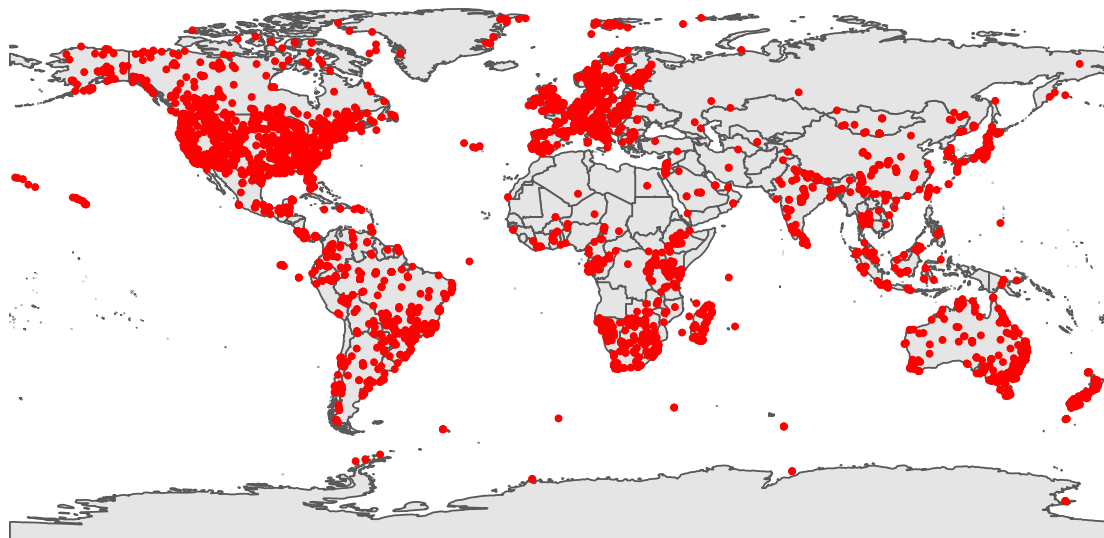

FIGURE 3 Distribution of the locations of the home-range studies included in the *HomeRange* database (n = 75,611)

CONFLICT OF INTEREST

The authors have no conflict of interest to declare.

DATA AVAILABILITY STATEMENT

The HomeRange database, metadata and R package can be accessed via https://github.com/SHoeks/HomeRange. The publication version of the data is archived on DRYAD and can be accessed via https://doi.org/10.5061/dryad.d2547d85x.

ORCID

Maarten Jaap Erik Broekman https://orcid.org/0000-0002-0565-5220

Selwyn Hoeks https://orcid.org/0000-0001-5619-3233

Mark A. J. Huijbregts https://orcid.org/0000-0002-7037-680X

Marlee A. Tucker https://orcid.org/0000-0001-7535-3431

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BIOSKETCHES

Maarten Broekman and **Selwyn Hoeks** are PhD candidates at the Radboud University in Nijmegen, The Netherlands. Maarten's research focuses on quantifying the effects of habitat conversion on biodiversity. Specifically, he studies terrestrial mammals at a global scale. Selwyn's research focuses on explaining ecosystem functioning using mechanistic modelling. His main interest is the importance of megafauna, in particular the role of large carnivores in maintaining ecosystem structure.