Rodent trapping studies can improve our understanding of the hazards of zoonotic pathogen spillover and novel zoonotic pathogen emergence.

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# Abstract

Rodents are important reservoirs of known zoonotic infectious diseases and novel zoonotic pathogens. Rodent reservoirs are globally distributed with West Africa containing multiple host species of zoonotic infectious diseases. Ongoing anthropogenic land use change alters the composition of rodent species assemblages which can alter the hazard of zoonotic disease spillover and emergence. Current global datasets to understand these hazards suffer from biases. Here, we synthesise data from 127 rodent trapping studies including over 72,000 individual rodent detections to understand the range and presence of important rodent reservoir species to quantify the bias in global datasets. We identify the rodent trapping studies are biased towards human dominated landscapes with important sampling biases across West Africa. We find that these rodent trapping studies can complement current global datasets on rodent population distributions which can minimise some of these observed biases. For four regionally important zoonotic infectious diseases we identify host-pathogen associations not included in a comprehensive global dataset. Rodent trapping studies can further enrich these resources through geolocating these associations and producing measures of pathogen prevalence within hosts. Finally, we find that for most of these diseases the proportion of a rodent hosts range that has been sampled remains small. Further rodent trapping studies are required to understand the true hazard of zoonotic spillover of these diseases across West Africa. Our results highlight that understanding rodent sampling bias is important when assessing the risk for zoonotic spillover events from rodents. The synthesis of contextually rich rodent trapping data contributes important information that is lacking in IUCN distribution maps and GBIF species presence data. We anticipate that this dataset can support the production of more complete understanding of the hazard of zoonotic spillover events.

# Introduction

Zoonotic infectious disease spillover events into human populations (animal-to-human transmission) can have important health and economic consequences at both the global and regional level (e.g. SARS-CoV-2 and Ebola virus disease) [1]. The number of zoonotic disease spillover events and the frequency of the emergence of novel zoonotic pathogens are predicted to increase under intensifying anthropenic pressure driven by increased human populations, urbanisation, climate change and wildlife defaunation [2–5]. West Africa is a nexus for these processes and a hotspot for both the risk of large epidemics of known zoonotic diseases and novel zoonotic pathogen emergence [2,6,7]. Two taxa - rodents (Rodentia) and bats (Chiroptera) - contribute the greatest number of predicted novel zoonotic pathogens and known zoonoses [8,9]. Of 2,220 extant rodent species, 244 (10.7%) are described as reservoirs of 85 zoonotic pathogens [7]. Specifically, West Africa has been identified as region at increased hazard for rodent-borne zoonotic disease spillover events under different projected future land-use change scenarios [4]. Currently within West Africa rodents are involved in the transmission of multiple zoonotic diseases with large burdens on human health, including, Lassa fever, Schistosomiasis, Leptospirosis and Toxoplasmosis [10,11].

Rodent species form diverse assemblages, which provide important and beneficial ecosystem services including pest regulation and seed dispersal [12]. The role of rodent species in zoonotic disease spillover or novel zoonotic pathogens emergence are examples of ecosystem disservices. Rodents typically demonstrate “fast” life histories [13] with traits such as early maturation and short gestation times further associated with being zoonotic reservoirs [8,14]. Rodent species with “fast” life histories thrive in human dominated landscapes, displacing species less likely to be reservoirs of zoonotic pathogens [15]. The widespread occurrence of reservoir species and their proximity to human activity make the description of rodent species assemblages and host-pathogen associations vitally important to understanding the hazard of zoonotic disease spillover and novel zoonotic pathogen emergence [7].

Despite the importance of understanding these complex systems, current evidence on host-pathogen associations is considerably affected by taxonomic and geographical sampling biases [9,16]. Studies identifying potential geographic hotspots of zoonotic disease spillover and novel pathogen emergence are based on global datasets of host species distributions and host-pathogen associations (e.g., IUCN, GBIF, GIDEON) which can result in biased hazard estimates [17,18]. For example, systematically increased sampling, over-representation of certain habitats and clustering around areas of high human population could lead to an apparent association between locations and hazard that is driven by these factors rather than underlying host-pathogen associations [9,19,20]. While other regions remain systematically undersampled (e.g., areas of sparse human populations), resulting in a reduced hazard of zoonotic spillover events or novel zoonotic pathogen emergence being attributed [21]. Predictions of zoonotic disease spillover and novel zoonotic pathogen emergence must account for these biases to understand the future hazard of zoonotic diseases [18].

Rodent trapping studies provide contextually rich information on when, where and under what conditions rodents were trapped, potentially enriching global datasets and mitigating against their inherent biases [22]. Rodent trapping provides a useful method to describe rodent population assemblages, their geographic distribution and host-pathogen associations beyond what is currently available in global datasets. Studies have been conducted in West Africa to investigate the distribution of rodent species, their species assemblages, the prevalence of known zoonoses within rodent hosts (e.g., Lassa fever, Schistosomiasis) and to identify novel zoonotic pathogens [23–25]. However, data from these studies have not previously been synthesised for inclusion in assessments of zoonotic disease spillover and novel zoonotic pathogen emergence.

Here, we synthesise rodent trapping studies conducted across West African from a search of literature between 1964-2019. First, we investigate the geographic biases in the rodent trapping dataset in relation to human population density and land use classification. Second, we compare this to global host datasets (IUCN and GBIF) to understand differences in reported host geographic distributions. Third, we compare identified host-pathogen associations with global datasets (CLOVER) to understand discrepencies in rodent host-pathogen associations and report the proportion positive for pathogens of interest. Finally, within our dataset we investigate the spatial extent of current host-pathogen sampling to identify areas of undersampling of pathogens within their host ranges. We expect that rodent trapping studies will provide an important additional source of high-resolution data that can be used to enrich global datasets to better understand the hazard of zoonotic disease spillover and novel zoonotic pathogen emergence across West Africa. We find that rodent trapping studies identify greater geographic ranges of important rodent hosts of zoonotic diseases than are reported from global datasets while also identifying locations and habitats in which further sampling is required. We also identify host-pathogen associations that are not reported in global host-pathogen association data, while identifying systematic undersampling for these pathogens across their host ranges.

# Methods

## Data sources

### Host and pathogen trapping data

We conducted a search in Ovid MEDLINE, Web of Science (Core collection and Zoological Record), JSTOR, BioOne, African Journals Online, Global Health and the pre-print servers, BioRxiv and EcoEvoRxiv for the following terms as keywords, no date limits were set: (1) Rodent OR Rodent trap\* AND (2) West Africa (or the individual countries).

We searched other resources including the UN Official Documents System, Open Grey, AGRIS FAO and Google Scholar using combinations of the above terms. Searches were run on 2021-03-01, returning studies conducted between 1964-2019.

We included studies if they met all of the following inclusion criteria; i) reported findings from trapping studies where the target was a small mammal, ii) described the type of trap used or the length of trapping activity or the location of the trapping activity, iii) included trapping activity from at least one West African country, iv) recorded the genus or species of trapped individuals, v) were published in a peer-reviewed journal or as a pre-print on a digital platform or as a report by a credible organisation. We excluded studies if they met any of the following exclusion criteria: i) reported data that were duplicated from a previously included study, ii) no full text available, iii) not available in English. One reviewer screened titles, abstracts and full texts against the inclusion and exclusion criteria. At each stage, a random subset (10%) was reviewed by a second reviewer.

We extracted data from eligible studies using a standardised tool that was piloted on 5 studies (Supplementary Table 1.). Data was abstracted into a Google Sheets document, which was archived on completion of data extraction [ref to zenodo]. Extracted variables included i) study identifiers; ii) study aims; iii) trapping methodology; iv) geolocation data; v) method of speciation; vi) trapping locations and dates; vii) trapped species; viii) number of trap-nights and ix) microorganisms/pathogens of interest. We summarised the number of studies, the year in which trapping occurred and the country in which they were conducted.

We extracted GPS locations for the most precise location presented, converting to decimal degrees as required. For studies not using standardised habitat recording (e.g., IUCN Habitat Classification Scheme (Version 3.1)), the explicit description of the habitat in which the trap was placed was extracted. For studies reporting multiple habitat types for a single trap, trap-line or trapping grid, a higher order classification of habitat type was recorded.

We mapped genus and species names to those in the Global Biodiversity Information Facility (GBIF) taxonomy [26]. We extracted information on the detection, non-detection and number of trapped individuals.

We extracted data on all pathogens assayed. The number of rodents tested and the number of positive or negative samples were recorded alongside the type of assay used. If studies reported indeterminate results this was noted. Pathogens were identified to species level, however, where an assay only allowed for attribution to a family of viruses or bacteria, the higher order grouping was used.

### Spatial covariates

Boundaries of countries and level-2 administrative regions were obtained from GADM 4.0.4 for the study region [27]. Land cover classification in 2005, the median year in which trapping activity occurred, was obtained from Copernicus climate change service at ~300m resolution [28]. Proportion of land cover type within a level-2 administrative region was calculated. Human population density for 2005 was obtained from SEDAC at ~ 1km resolution, with median population density within each region extracted [29].

### Rodent species ranges and presence

Rodent species distributions were obtained as shapefiles from the IUCN redlist, shapefiles were cropped to the study region [30]. Rodent presence locations were obtained from GBIF as point data limited to the study region [31].

### Host pathogen associations

CLOVER a synthesis of four host-pathogen datasets (GMPD2, EID2, HP3 and Shaw 2020) was released in 2021 and represents a comprehensive global repository of host-pathogen associations for Bacteria, Viruses, Helminth, Protozoa and Fungi [32]. Data were obtained from an archived version of the dataset [33]. The dataset was limited to species trapped within our included studies, no spatial subsetting was possible.

## Included studies

We identified 4,282 relevant citations, with 126 rodent trapping studies included (Supplementary Table 2.). The earliest trapping studies were conducted in 1964, with increasing numbers of studies being performed annually. The median year of first trapping activity was 2005, with the median length of trapping activity being 1 year (IQR 0-2 years) (Supplementary Figure 1.). Studies were conducted in 14 West African countries with no studies reported from Gambia or Togo, at 1,331 sites (Figure 1A.). A minority (31, 25%) of studies trapped at a single study site, with 46 (37%) trapping at between two and five sites, the remaining 49 studies (38%) trapped at between six and 93 study sites. There were 581,426 reported trap nights, with 384,983 trap nights imputed for studies with no recording of trapping effort (Figure 1B.).

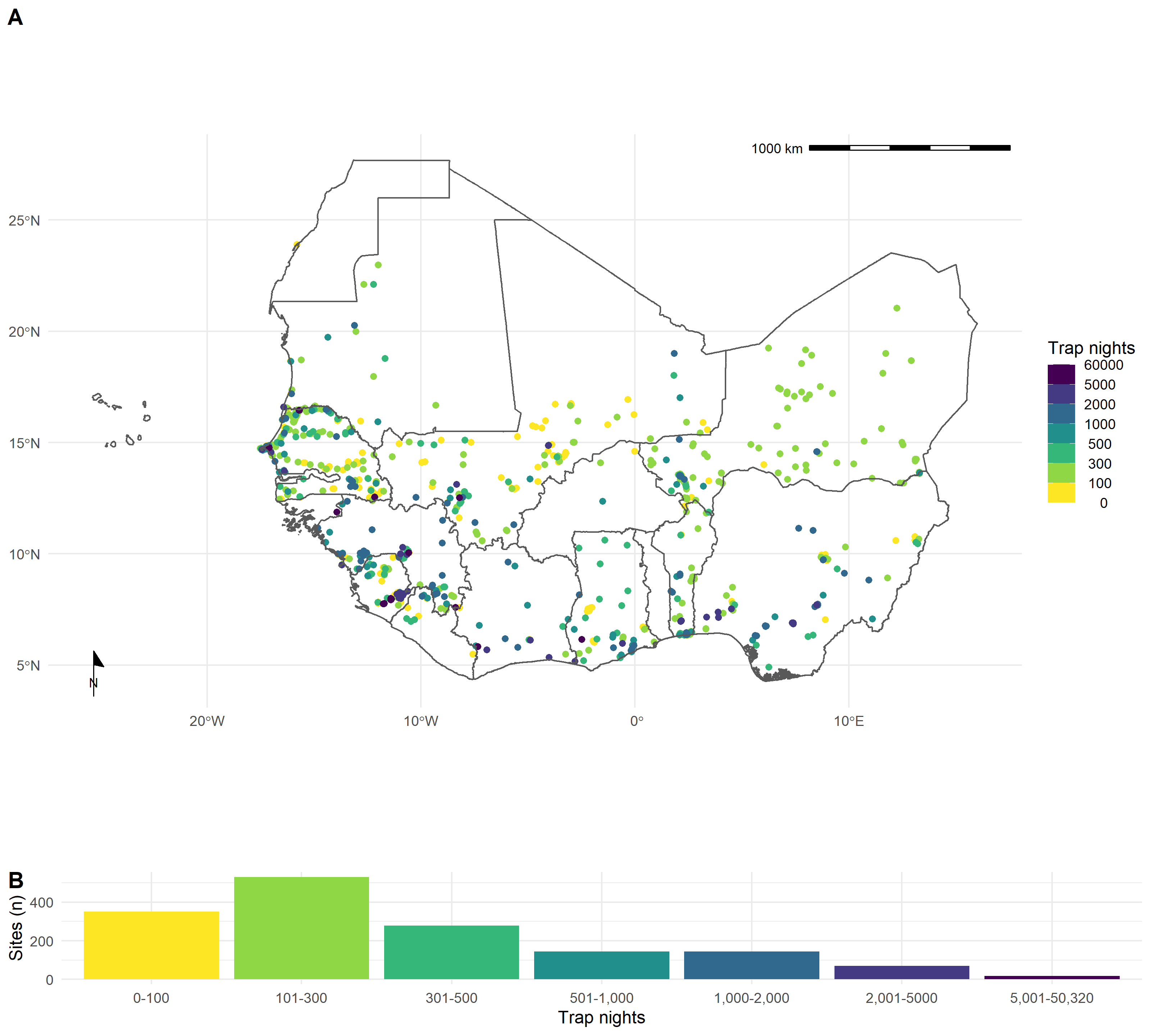


Figure 1: A) The location of trapping sites in West Africa. No sites were recorded from Togo or Gambia. There is important heterogeneity observed in the coverage of each country by trap night (colour) and location of sites. For example, Senegal, Mali and Sierra Leone have generally good coverage compared to Guinea and Burkina Faso. B) The distribution of trap nights performed at each study site on a log scale with a median of 244 trap nights (IQR 115-494) performed at each site

Within the included studies trap success varied importantly between traps placed in or around buildings (13%, IQR 6-24%) compared to other habitats (3%, IQR 1-9%). In total 73,164 small mammals were trapped with 62,574 (85%) identified to species level and 7,760 (11%) identified to genus. The majority of the 140 identified species were Rodentia (110, 76%) and Soricomorpha (30, 21%), of which Muridae (82, 73%) were the most common family.

62 studies tested for 32 microorganisms, defined to species or genus level that are known or potential pathogens. Most studies tested for a single microorganism (39, 62%). The most frequently assayed microorganisms were *Lassa mammarenavirus* or Arenaviridae (27, 43%), *Borrelia sp.* (8, 13%), *Bartonella sp.* (4, 6%) and *Toxoplasma gondii* (4, 6%). Most studies used Polymerase Chain Reaction to detect microorganisms (32, 52%), with fewer studies using molecular based tests (11, 18%) or histological or direct visualisation assays (8, 13%). From 32,014 individual rodent samples we produced 339 host-pathogen pairs. With *Rattus rattus*, *Mus musculus*, *Mastomys erythroleucus*, *Mastomys natalensis* and *Arvicanthis niloticus* being assayed for at least 18 microorganisms.

Further descriptive information from the included studies including geolocated trapping of species, their detection and non-detection alongside microorganism data has been made available online [34].

## Analysis

### What is the extent of spatial bias in the rodent trapping data?

We used the GPS coordinates of trapping locations and the number of trap nights to calculate trapping effort (trap night density) within level-2 administrative regions in West Africa. We imputed trap nights for studies with missing records using the number of trapped rodents and median trap success rate from studies reporting trapping effort stratified by habitat type. We calculated the proportion of land cover classes within each of these level-2 administrative, comparing surveyed regions to non-surveyed regions.

To better understand the potential bias associated with studies for zoonotic disease spillover or novel zoonotic pathogen emergence we limited further analyses to zoonotic pathogen studies only. We used a Generalised Additive Model (GAM) incorporating a spatial interaction term to investigate the association between number of trap nights, proportion of urban, cropland and forest land classification and human population density [35]. The model was constructed in *mgcv* using the R statistical programme [36,37]. Selection of the most parsimonious model was based on the adjusted-R2 and Deviance explained for each model. We performed sensitivity analysis by removing sites with imputed trapping effort. The final selected model structure was specified as:

The model identified locations of high and low trapping effort relative to land use classification, with proportion urban land very highly correlated with human population density (*r* = 0.835, 95% C.I. 0.82-0.85, *p* < 0.001). Model inference was limited to regions around observed trap sites.

### What is the difference between global datasets rodent host distributions and distributions from trapping studies?

We assessed the taxonomic coverage of the trapped taxa and for the seven species with the most trap locations (*M. natalensis*, *R. rattus*, *M. erythroleucus*, *M. musculus*, *A. niloticus*, *Praomys daltoni* and *Cricetomys gambianus*) we mapped the detection and non-detection of rodent species and compared this to detection data obtained from GBIF and species ranges from IUCN [30,31]. We identified rodent locations from GBIF and the rodent trapping studies within and outside the IUCN expected range. We located these to level-2 administrative regions to calculate the discrepencies between observed detections and non-detections with IUCN distributions.

### Are rodent trapping derived host-pathogen associations present in global zoonoses datasets?

For studies investigating rodent zoonoses we produced host-pathogen pairs. For each host-pathogen pair we compared our records with those available in CLOVER, reporting concordance and discordance. For host-pathogen pairs with assay results consistent with acute or prior infection we calculate the proportion positive and identify those absent from CLOVER. We expand the analysis to host-pathogen pairs with pathogens identified to genus level in Supplementary Figure 4.

### What is the spatial extent of pathogen testing within a hosts range?

For the four pathogens sampled at the most locations (Borreliaceae, Leptospiraceae, *Lassa mammarenavirus* and *Toxoplasma gondii*) we identify their potential host species. For the five species with most spatially complete sampling we associate their sampling locations with level-2 administrative regions and compare this to their IUCN range and rodent trapping detection range to calculate a measure sampling coverage.

# Results

## What is the extent of spatial bias in the rodent trapping data?

Trap sites were situated in 273 of 1,414 (19.3%) level-2 administrative regions in 14 West African nations. The areas with highest trap night density included the capital and large cities of Niger (Niamey), Sierra Leone (Freetown), Senegal (Dakar), Mali (Bamako), Ghana (Accra), Côte d’Ivoire (Abidjan), and Benin (Cotonou). Outside of these cities, regions in, Northern Senegal, Southern Guinea, Edo and Osun States in Nigeria and Eastern Sierra Leone had the highest density of trap nights (Figure 1A.).

Trapping sites were biased towards human modified landscapes (i.e., cropland, grassland and mosaic habitats), with under-representation of forest and bare habitats. However, urban habitats were comparitively undersampled (Supplementary Figure 2.).

Trapping effort, measured through trap nights, was biased with increased effort in areas with higher proportion of urban land use and no-significant association with proportion of forest cover. The spatial term shows trapping bias towards increased effort in Northern Senegal, Eastern Sierra Leone, Eastern Guinea and coastal regions of Nigeria, Benin and Ghana, in contrast South-East Nigeria, Northern Nigeria and Liberia had relatively lower trapping effort (Figure 2). The most parsimonious GAM model (adjusted R2 = 0.523, Deviance explained = 61%) included terms for coordinates, proportion urban coverage and proportion tree coverage, model selection is shown in Supplementary Tables 3.1-3.4. In sensitivity analysis excluding sites with imputed trap nights reduced contributing data, however, Mauritania, Northern Senegal and Sierra Leone remained as regions trapped at higher rates with Nigeria being trapped at lower than expected rates (Supplementary Figure 3.).

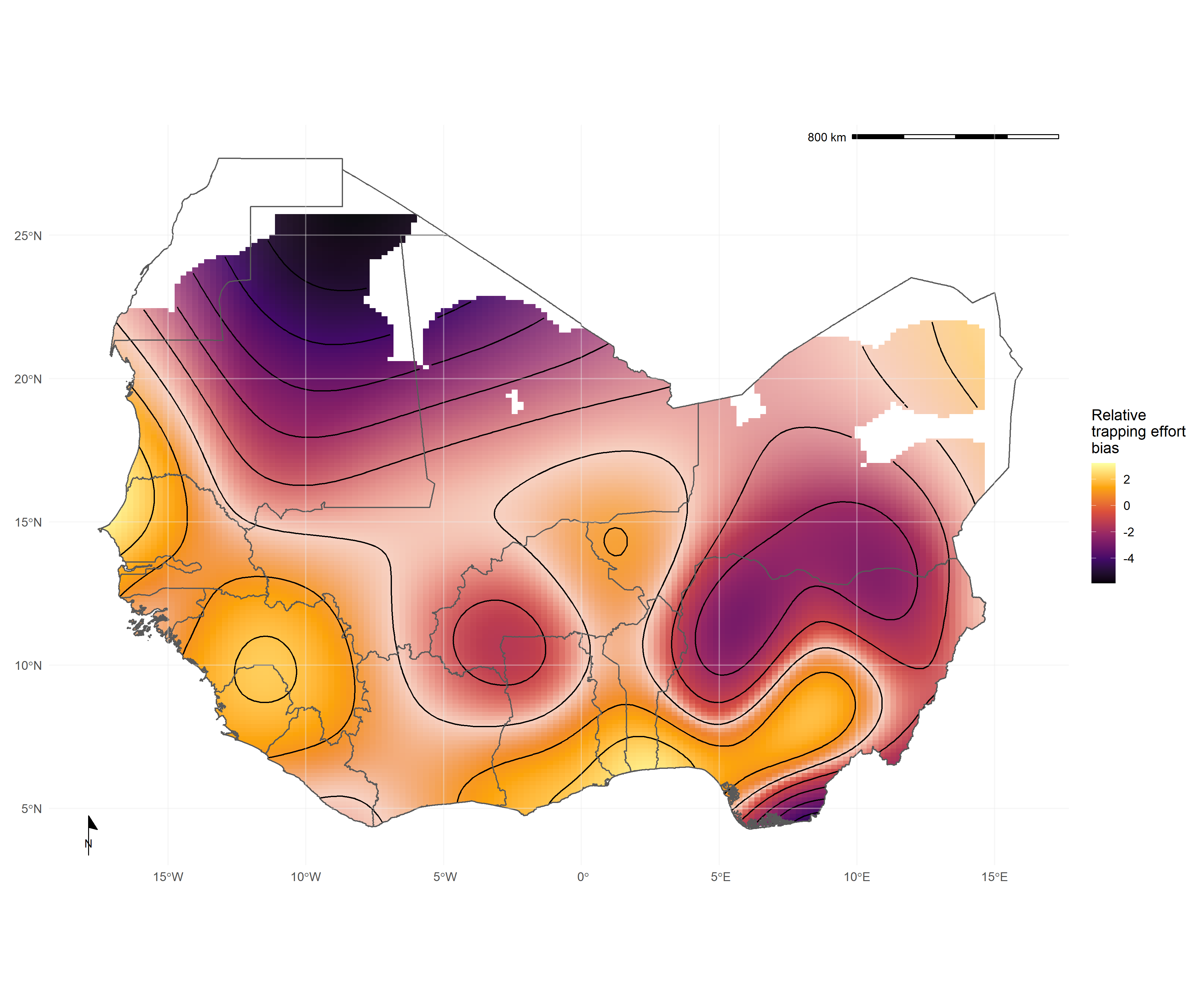


Figure 2. Relative trapping effort bias across West Africa from included studies adjusted for proportion urban land cover and proportion tree cover. Predictions are limited to areas around trap sites (coloured areas), uncertainty in the estimate of bias is represented by colour transparency/pallor. Purple regions represent areas with higher than expected trapping effort, yellow regions represent areas lower than expected trapping effort

## What is the difference between global datasets rodent host distributions and distributions from trapping studies?

For our species of interest, except *C. gambianus*, trapping studies provided more distinct locations of detection and non-detection than were available from GBIF. For the West African endemic species IUCN ranges showed generally good concordance to both trapping studies and GBIF, although the range of *A. niloticus* and *P. daltoni* are greater than expected. The invasive species *R. rattus* and *M. musculus* are present in a much larger range than is expected (Figure 3A. and 3B.).

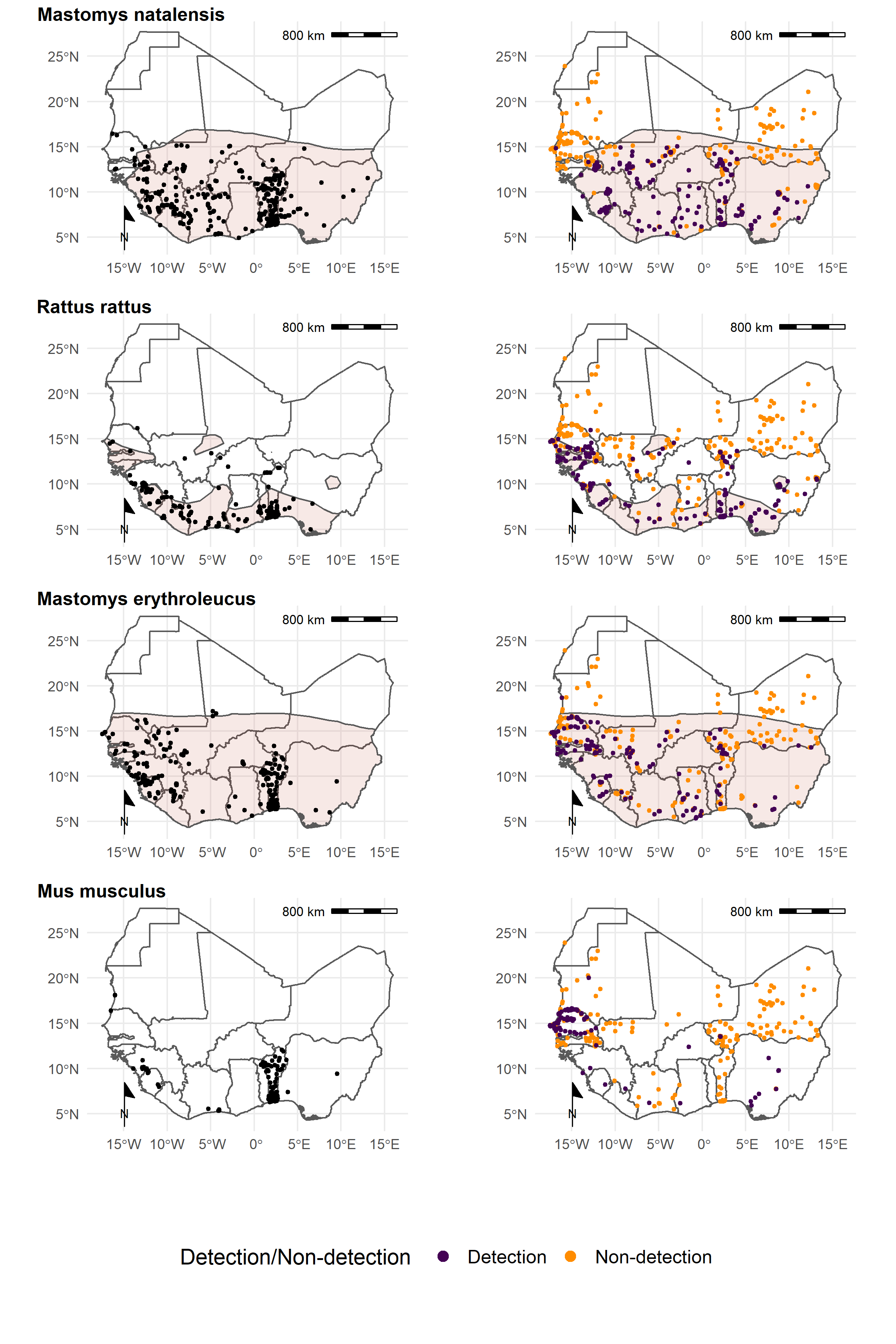


Figure 3A. Each row corresponds to a single rodent species. L) Presence recorded in GBIF overlaid on IUCN species range (red-shaded area). R) Detection and non-detection from rodent trapping studies overlaid on IUCN species ranges. M. musculus has no range in West African in IUCN data.

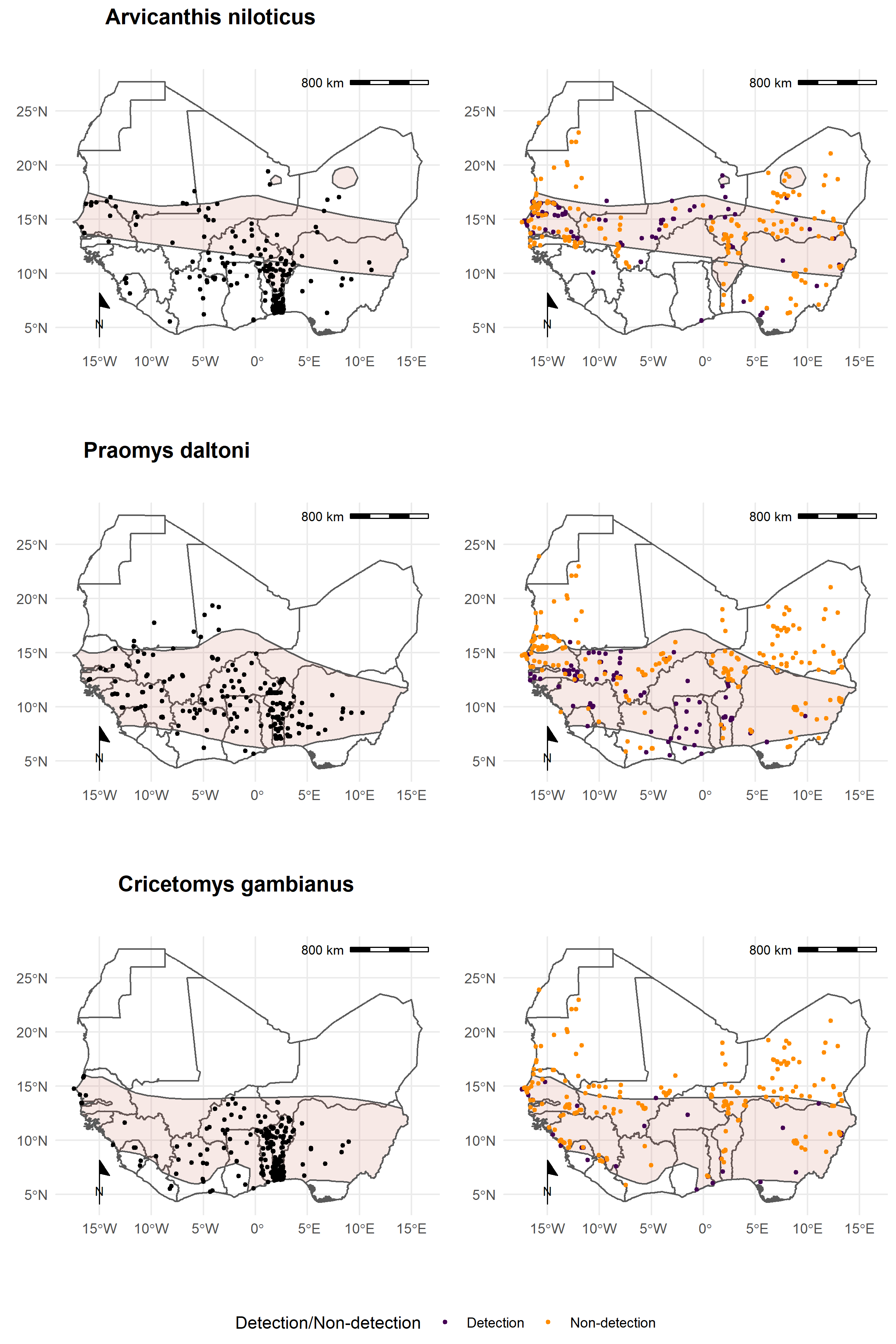


Figure 3B. Each row corresponds to a single rodent species. L) Presence recorded in GBIF overlaid on IUCN species range (red-shaded area). R) Detection and non-detection from rodent trapping studies overlaid on IUCN species ranges.

We identified the proportion of a rodent’s expected range in which detections and non-detections occurred (Table 1.). GBIF sampling occurred over > 15% of a rodent’s expected range with detections occurring outside of IUCN ranges for all species, most noticeably for *A. niloticus* and *P. daltoni*. Trapping studies occurred over > 13% for all species except *C. gambianus* with detections occurring outside of IUCN ranges most noticeably for *A. niloticus* and *R. rattus*. Combining GBIF and trapping data increased coverage by a mean of 9% of the species range suggesting limited overlap between the regions studied. Non-detections of rodents occurred across large areas of their ranges with *A. niloticus* and *M. erythroleucus* not being detected in >15% of their expected range, suggestive of substantial heterogeneity fo presence across their range.

**Table** : Table 1: Comparison of IUCN, GBIF and rodent trapping ranges for the 7 species trapped at the most sites.

|  | IUCN | GBIF | | Trapping studies | | | Combined |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Range   (1,000 km2) | Area inside range (1,000 km2) (% of IUCN) | Area outside range   (1,000 km2) | Detection area  inside range (1,000 km2) (% of IUCN) | Area outside range   (1,000 km2) (% of IUCN) | Non-detection area  inside range (1,000 km2) (% of IUCN) | Detection area  inside range (1,000 km2) (% of IUCN) |
| *Mastomys natalensis* | 3,257.11 | 6.83 (0.21%) | 0.19 | 4.4 (0.14%) | 0.17 | 3.12 (0.1%) | 12.73 (0.33%) |
| *Rattus rattus* | 1,018.71 | 2.61 (0.26%) | 0.52 | 2.42 (0.24%) | 1.21 | 1.3 (0.13%) | 5.72 (0.48%) |
| *Mastomys erythroleucus* | 3,735.48 | 4.48 (0.12%) | 0.04 | 3.24 (0.09%) | 0.12 | 4.35 (0.12%) | 11 (0.2%) |
| *Mus musculus* |  |  | 2.15 |  | 1.85 |  | 3.94 |
| *Arvicanthis niloticus* | 1,829.14 | 1.69 (0.09%) | 2.41 | 1.98 (0.11%) | 0.34 | 3.09 (0.17%) | 5.96 (0.2%) |
| *Praomys daltoni* | 2,657.77 | 4.03 (0.15%) | 0.29 | 2.03 (0.08%) | 0.15 | 2.78 (0.1%) | 8.21 (0.22%) |
| *Cricetomys gambianus* | 2,475.97 | 5 (0.2%) | 0.17 | 0.75 (0.03%) | 0.06 | 2.99 (0.12%) | 8.37 (0.23%) |

## Are rodent trapping derived host-pathogen associations present in global zoonoses datasets?

When limited to confirmed pathogens and classification of both pathogen and host to species level we identified 21 host-pathogen pairs among 11 rodent and 6 pathogen species (Figure 4.). We identified negative associations, through entirely negative assays, for 41 host-pathogen pairs among 31 rodent and 7 pathogen species. CLOVER contained 8 (38%) of our identified host-pathogen associations and positive associations for 6 (15%) of the negative associations.

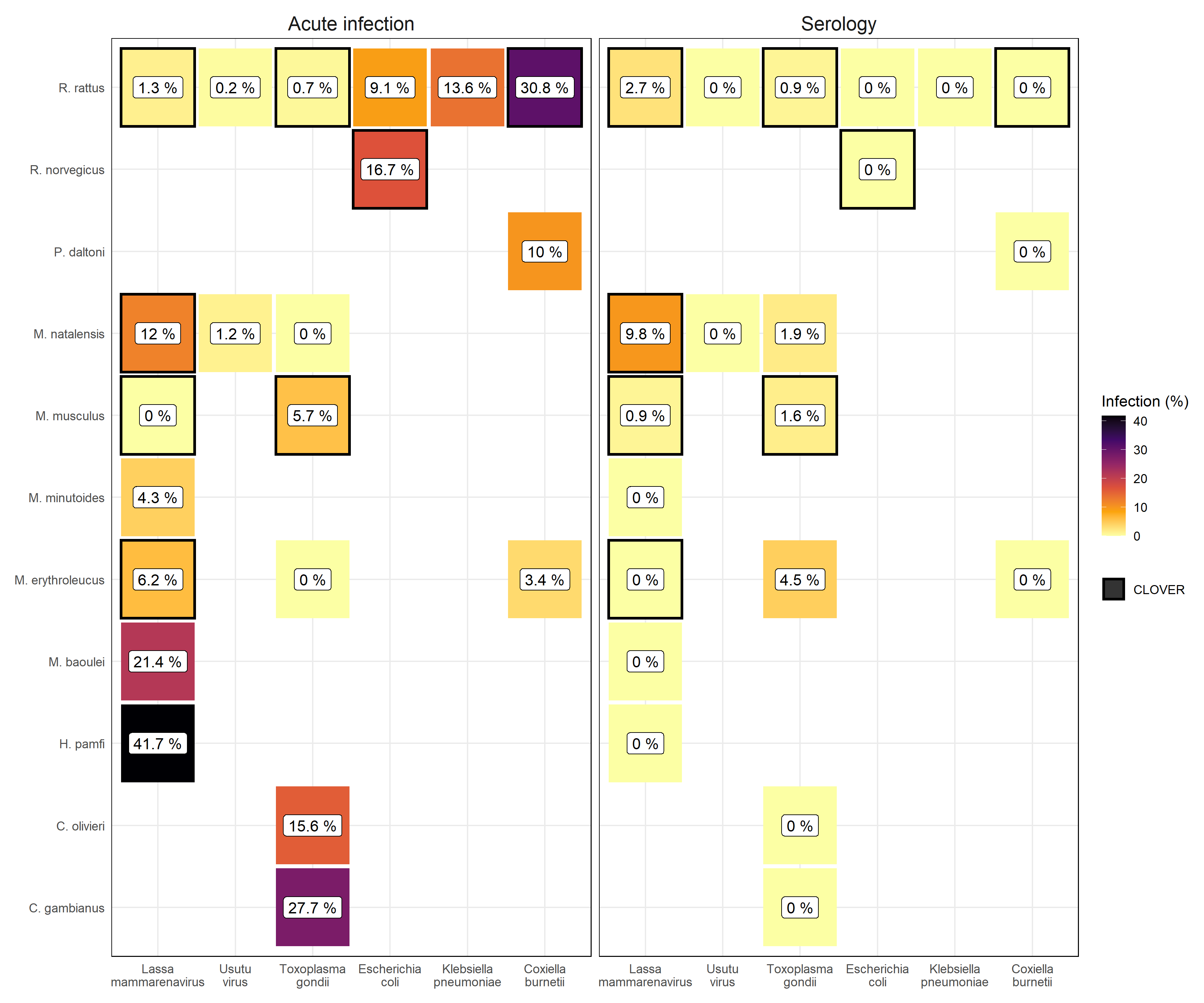


Figure 4. L) Identified species level host-pathogen associations through detection of acute infection (i.e. PCR, culture). Percentages and colour relate to the proportion of all assays that were positive. Associations with a black border are present in the CLOVER dataset. R) Identified species level host-pathogen associations through serological assays (i.e. ELISA). Percentages and colour relate to the proportion of all assays that were positive. Associations with a black border are present in the CLOVER dataset.

CLOVER included 399 host-pathogen associations we do not observe in rodent trapping studies among our included rodent species. The majority of these 329 (82%) pairs are from species with global distributions (*M. musculus*, *R. rattus* and *R. norvegicus*), or from those with wide ranging distributions in sub-Saharan Africa (31, 9%) (i.e., *A. niloticus*, *M. natalensis* and *Atelerix albiventris*).

For pathogens not identified to species level (i.e. family or higher taxa only) we identified 128 host-pathogen pairs among 32 rodent species and 25 pathogen families (Supplementary Figure 4.), with CLOVER containing 52 (41%) of these associations.

Rodent trapping studies identified rodent host species for six pathogens, *Toxoplasma gondii* (4), *Lassa mammarenavirus* (3), Usutu virus (2), *Coxiella burnetii* (2), *Escherichia coli* and *Klebsiella pneumoniae* (both 1), that were not present in this global host-pathogen association dataset.

## What is the spatial extent of pathogen testing within a hosts range?

The four most widely sampled pathogen species/families were Borreliaceae, *Lassa mammarenavirus*, Leptospiraceae and *Toxoplasma gondii* (Table 2.). Infection with species of Borreliaceae was assessed in 42 species, with evidence of infection in 17 rodent species. Among species with more than 500 samples the highest rates of infection were among *A. niloticus* (16%), *M. huberti* (11%) and *M. erythroleucus* (8%). The five most widely assayed species were sampled from a relatively small area of their species ranges (7.3-16%), however, there was good representation when compared to where rodent trapping studies have occurred (24-85%).

Infection with *Lassa mammarenavirus* was assessed in 28 species, with evidence of infection in 7 rodent species. Among species with more than 100 samples the highest rates of infection were among *M. natalensis* (22%), *M. erythroleucus* (6%) and *R. rattus* (4%). Species sampling occurred from limited areas within IUCN ranges (2-3%), however, sampling was more representative for rodent trapping studies (3-24%).

Infection with species of Leptospiraceae was assessed in 8 species, with evidence of infection in 5 rodent species. Among species with more than 100 samples *M. natalensis* (19%), *R. rattus* (11%) and *Crocidura olivieri* (10%) were most frequently infected. Species sampling occurred across less than 1% of these species IUCN ranges and for all except *R. norvegicus* for less than 1% of their detection range in rodnet trapping studies.

*Toxoplasma gondii* infection was assessed in 8 species, with evidence of infection in 6 rodent species. Among species with more than 100 samples *M. musculus* (7%), *M. erythroleucus* (4%) and *M. natalensis* (2%) were most commonly infected. Sampling occurred across less than 6% of their IUCN ranges, however, for *M. musculus*, *R. rattus* and *M. erythroleucus* sampling occurred across greater than 12% of their detection range.

**Table** : Table 2: Comparison of pathogen sampling ranges for the 4 most widely sampled pathogens and the 5 most sampled potential rodent host species. \* no IUCN range in West African

| Pathogen | Species | Administrative regions (n) | Tested (n) | Positive (n) | Area sampled  (1,000 km2) | IUCN area (%) | Trapped area (%) |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Borrelia sp. |  |  |  |  |  |  |  |
|  | *M. erythroleucus* | 65 | 1,563 | 140 | 273.1 | 7.3 | 50.8 |
|  | *A. niloticus* | 36 | 1,528 | 244 | 293.2 | 16 | 23.6 |
|  | *M. natalensis* | 42 | 731 | 54 | 250.5 | 7.7 | 42.8 |
|  | *M. huberti* | 14 | 718 | 81 | 58.6 | 10.1 | 84.5 |
|  | *P. daltoni* | 30 | 264 | 19 | 234.2 | 8.8 | 51.3 |
| Lassa mammarenavirus |  |  |  |  |  |  |  |
|  | *M. natalensis* | 45 | 3,113 | 713 | 106.9 | 3.3 | 18.3 |
|  | *M. musculus* | 2 | 141 | 0 | 6.2 | \* | 3.1 |
|  | *M. erythroleucus* | 7 | 139 | 9 | 55.9 | 1.5 | 10.4 |
|  | *R. rattus* | 12 | 88 | 2 | 34.5 | 3.4 | 8.8 |
|  | *H. pamfi* | 1 | 12 | 5 | 0.6 | 1.8 | 24.3 |
| Leptospira sp. |  |  |  |  |  |  |  |
|  | *R. rattus* | 54 | 626 | 65 | 3.3 | < 1 | < 1 |
|  | *A. niloticus* | 1 | 221 | 10 | 0.2 | < 1 | < 1 |
|  | *M. natalensis* | 34 | 126 | 24 | 1.6 | < 1 | < 1 |
|  | *C. olivieri* | 39 | 123 | 14 | 1.6 | < 1 | < 1 |
|  | *R. norvegicus* | 27 | 65 | 17 | 1.4 | \* | 17.9 |
| Toxoplasma gondii |  |  |  |  |  |  |  |
|  | *M. musculus* | 32 | 1,548 | 115 | 77.5 | \* | 38.1 |
|  | *R. rattus* | 18 | 428 | 8 | 61.7 | 6.1 | 15.7 |
|  | *M. erythroleucus* | 18 | 272 | 10 | 68.2 | 1.8 | 12.7 |
|  | *C. gambianus* | 3 | 47 | 13 | 2.4 | < 1 | 1.8 |
|  | *C. olivieri* | 2 | 32 | 5 | 0.5 | < 1 | < 1 |

# Discussion

We synthesised data from 126 rodent trapping studies containing information on more than 72,000 trapped rodents across 1,331 trapping sites producing an estimated 966,000 trap-nights. Trapping occurred across 14 West African countries, studies investigating known or potential zoonotic pathogens occurred within 19% of level-2 administrative regions across West Africa with important bias towards areas with high population density and human dominated landscapes. For several important rodent species, we identified discordance between IUCN species ranges, GBIF presence data and detections and non-detections from rodent trapping studies, particularly among non-native species (*R. rattus* and *M. musculus*). We compared host-pathogen associations from rodent trapping studies with a global dataset and identified missing associations for several important zoonotic infectious diseases including, Lassa fever, Toxoplasmosis and Q fever in commonly occurring rodent species. Finally, we assessed the spatial coverage of testing for important zoonotic pathogens and found low representativeness across their host species range.

Rodent trapping studies provide important information on the distribution of rodent species and their assemblages, we have identified important bias in the locations in which studies to data have been performed with large regions of countries including Nigeria, Guinea and Cote d’Ivoire being understudied. Trapping sites are clustered in areas with relatively high human population density and anthropogenic land use which can importantly bias our understanding of the distribution of rodent species and their pathogens across West Africa. Further effort is required to counteract this bias by sampling currently undersampled regions.

Global datasets of rodent host distribution (e.g., IUCN) and presence (e.g., GBIF) provide useful resources to model the hazard of zoonotic disease spillover and novel pathogen emergence. We show here that non-detection data from rodent trapping studies can provide additional information to describe the heterogeneity of rodent assemblages across diverse habitats in West Africa. Combining presence data from GBIF and detection/non-detection data from rodent trapping studies can substantially increase coverage across a rodent’s range, allowing improved estimates of rodent host prevalence for zoonotic infectious disease studies.

Host-pathogen association datasets are becoming increasing comprehensive alongside increased access to molecular discovery techniques for potential pathogens. We show that currently available data from rodent trapping studies can enrich these resources, particularly with prevalence data and geolocation to better understand the potential hosts and reservoirs of known zoonotic pathogens. Most of the host-pathogen associations from CLOVER not identified from rodent trapping studies occurred in species with ranges that go beyond our study area, suggesting that these pathogens do not exist in West Africa. Rodent trapping data can support analyses using these global datasets to predict novel pathogen emergence and to quantify the risk of known zoonotic disease spillover based on host distributions.

We have identified important limitations in the sampling of rodent zoonoses for known diseases across West Africa. For example, studies of *Lassa mammarenavirus* have taken place across 3% of *M. natalensis*’s range in West Africa. Lassa fever is known to be endemic in eight West African countries, although it is potentially more widely spread. Further rodent trapping studies are required to investigate this pathogen across a wider geographic range. Other important zoonotic diseases including Leptospirosis and Toxoplasmosis have been assessed over very limited regions of their hosts distribution.

Due to data sparsity, we were unable to account for temporal change over the six decades of rodent trapping studies. Land use change and population density have changed dramatically over this period in West Africa. We attempted to mitigate this by using the median year of trapping to understand the spatial biases in trapping activity, however, it is possible that land use and population density at trapping sites varied importantly between when the study was conducted and the situation in 2005. Despite this limitation, the finding that trapping is biased towards high density, human dominated landscapes is unlikely to importantly change.

We propose that rodent trapping studies can provide important data to supplement global datasets to quantify the hazard of zoonotic disease spillover and novel pathogen emergence. They can reduce some of the bias in global datasets however, important limitations remain. Further effort is required to survey rodent populations in non-human dominated landscapes and to assay pathogens across more of a host’s range.

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# Supplementary

## Supplementary Table 1

**Table** : Supplementary Table 1: Data extraction tool for studies meeting inclusion criteria

| Extraction tool | Variable | Description |
| --- | --- | --- |
| Study data |  |  |
|  | link | link to manuscript |
|  | year\_publication | year of publication |
|  | title | title of manuscript |
|  | journal\_name | journal |
|  | aim\_1 | stated aim of study |
|  | aim\_2 | stated aim of study |
|  | aim\_3 | stated aim of study |
|  | first\_author | first author of the study |
|  | reference\_uid | DOI/ISSN/ISBN of the publication |
|  | unique\_id | unique ID for the current study |
|  | metric | measurement of species presence abundance/presence |
|  | trap\_types | type of rodent traps used |
|  | trapping\_method | construction of the sampling grid |
|  | repeated\_visit | whether there were multiple study visits to the same sites |
|  | geolocation\_level | the level of geolocation reported |
|  | speciation | the level of speciation of trapped rodents |
|  | aim | aim of the study dichotomised to Ecology or Zoonotic risk |
|  | aim\_detail\_1 | categorisation of study aims |
|  | aim\_detail\_2 | whether a species accumulation curve to describe trapping effort is reported |
|  | species\_accumulation | whether there is a measure of rodent species diversity reported |
|  | diversity\_measurement | whether pathogens are assayed |
|  | trapping\_effort | completeness of reported trapping effort |
| Rodent data |  |  |
|  | unique\_id | unique ID for the current study |
|  | year\_trapping | year rodent trapping occurred (range) |
|  | month\_trapping | months trapping occurred (range) |
|  | country | country trapping occurred within |
|  | region | region trapping occurred within |
|  | town\_village | name of towns or villages trapping occurred within |
|  | latitude\_DMS\_N | latitude of trapping site in degrees minutes seconds (North) |
|  | longitude\_DMS\_W | longitude of trapping site in degrees minutes seconds (West) |
|  | latitude\_D\_N | latitude of trapping site in decimal degrees (North) |
|  | longitude\_D\_E | longitude of trapping site in decimal degrees (East) |
|  | UTM\_coordinates | location of trapping site in UTM coordinates |
|  | habitat | habitat type of trapping site |
|  | intensity\_use | the intensity of human disturbance in the trapping site |
|  | genus | reported genus of trapped rodent/small mammal species |
|  | species | reported species of trapped rodent/small mammal species |
|  | number | number of trapped individuals |
|  | trap\_nights | number of trap nights reported |
|  | capture\_rate | rate of capture if reported |
|  | trap\_night\_unit | the unit of trap night measurement |
|  | study\_nights | the number of study nights completed at the trap site |
| Pathogen data |  |  |
|  | unique\_id | unique ID for the current study |
|  | year\_trapping | year rodent trapping occurred (range) |
|  | month | months trapping occurred (range) |
|  | country | country trapping occurred within |
|  | region | region trapping occurred within |
|  | town\_village | name of towns or villages trapping occurred within |
|  | habitat | habitat type of trapping site |
|  | genus | reported genus of trapped rodent/small mammal species |
|  | species | reported species of trapped rodent/small mammal species |
|  | pathogen\_x | pathogens tested for, 1-7 possible columns |
|  | latitude\_DMS\_N | latitude of trapping site in degrees minutes seconds (North) |
|  | longitude\_DMS\_W | longitude of trapping site in degrees minutes seconds (West) |
|  | latitude\_D\_N | latitude of trapping site in decimal degrees (North) |
|  | longitude\_D\_E | longitude of trapping site in decimal degrees (East) |
|  | UTM\_coordinates | location of trapping site in UTM coordinates |
|  | path\_x\_tested | number of individuals assayed for the corresponding pathogen, 1-7 possible columns |
|  | pcr\_x\_positive | number of individuals PCR positive for the corresponding pathogen, 1-7 possible columns |
|  | ab\_ag\_x\_positive | number of individuals with positive serological assays for the corresponding pathogen, 1-7 possible columns |
|  | culture\_x\_positive | number of individuals culture positive for the corresponding pathogen, 1-7 possible columns |
|  | histo\_x\_positive | number of individuals histologically/histopathologically positive for the corresponding pathogen, 1-7 possible columns |

## Supplementary Table 2

**Table** : Supplementary Table 2: Included studies

| Publication link | Year | Author | Title | Journal | DOI/ISBN/ISSN | link |
| --- | --- | --- | --- | --- | --- | --- |
| [link](https%3A//doi.org/10.1515/mammalia-2020-0013) | 2021 | Mnqobi Mamba | Small mammals of a West African hotspot, the Ziama-Wonegizi-Wologizi transfrontier forest landscape | Mammalia | 10.1515/mammalia-2020-0013 | https://doi.org/10.1515/mammalia-2020-0013 |
| [link](https%3A//doi.org/10.3390/biology10010028) | 2021 | Umaru Bangura | Lassa virus circulation in small mammal populations in Bo district, Sierra Leone | Biology | 10.3390/biology10010028 | https://doi.org/10.3390/biology10010028 |
| [link](https%3A//doi.org/10.17420/ap6602.262) | 2020 | Adama Zida | Mastomys natalensis, Cricetomys gambianus and Taterillus sp. were found PCR positive for Leishmania major in Burkina Faso, West Africa | Annals of Parasitology | 10.17420/ap6602.262 | https://doi.org/10.17420/ap6602.262 |
| [link](https%3A//doi.org/10.25225/jvb.20009) | 2020 | Violaine Nicolas | Small mammal inventory in the Lama forest reserve (south Benin), with new cytogenetical data | Journal of Vertebrate Biology | 10.25225/jvb.20009 | https://doi.org/10.25225/jvb.20009 |
| [link](https%3A//doi.org/10.1080/22221751.2020.1766381) | 2020 | Joachim Marien | Households as hotspots of Lassa fever? Assessing the spatial distribution of Lassa virus-infected rodents in rural villages of Guinea | Emerging Microbes and Infections | 10.1080/22221751.2020.1766381 | https://doi.org/10.1080/22221751.2020.1766381 |
| [link](https%3A//doi.org/10.1007/s10530-020-02304-7) | 2020 | Christophe Diagne | Association between temporal patterns in helminth assemblages and successful range expansion of exotic Mus musculus domesticus in Senegal | Biological Invasions | 10.1007/s10530-020-02304-7 | https://doi.org/10.1007/s10530-020-02304-7 |
| [link](https%3A//doi.org/10.3390/pathogens9030202) | 2020 | Handi Dahmana | Rodents as hosts of pathogens and related zoonotic disease risk | Pathogens | 10.3390/pathogens9030202 | https://doi.org/10.3390/pathogens9030202 |
| [link](https%3A//doi.org/10.3201/eid2606.200107) | 2020 | Stefano Catalano | Multihost transmission of Schistosoma mansoni in Senegal, 2015-2018 | Emerging Infectious Diseases | 10.3201/eid2606.200107 | https://doi.org/10.3201/eid2606.200107 |
| [link](https%3A//dx.doi.org/10.24189/ncr.2020.005) | 2020 | Laurent Ahissa | Species composition and community structure of terrestrial small mammals in Tanoé-Ehy Swamp Forest (South-East Ivory Coast): implication for conservation | Nature Conservation Research | 10.24189/ncr.2020.005 | https://dx.doi.org/10.24189/ncr.2020.005 |
| [link](https%3A//doi.org/10.24072/pci.ecology.100044) | 2020 | Claire Stragier | Interplay between historical and current features of the cityscape in shaping the genetic structure of the house mouse ( Mus musculus domesticus) in Dakar (Senegal, West Africa) | Peer Community in Ecology | 10.1101/557066 | https://doi.org/10.24072/pci.ecology.100044 |
| [link](https%3A//doi.org/10.3897/BDJ.7.e34754) | 2019 | Natalie Weber | New records of bats and terrestrial small mammals from the Seli River in Sierra Leone before the construction of a hydroelectric dam | Biodiversity Data Journal | 10.3897/BDJ.7.e34754 | https://doi.org/10.3897/BDJ.7.e34754 |
| [link](https%3A//doi.org/10.1080/22221751.2019.1605846) | 2019 | Joachim Marien | Evaluation of rodent control to fight Lassa fever based on field data and mathematical modelling | Emerging Microbes and Infections | 10.1080/22221751.2019.1605846 | https://doi.org/10.1080/22221751.2019.1605846 |
| [link](https%3A//doi.org/10.3390/d11120238) | 2019 | Karmidine Hima | Native and invasive small mammals in urban habitats along the commercial axis connecting Benin and Niger, West Africa | Diversity | 10.3390/d11120238 | https://doi.org/10.3390/d11120238 |
| [link](https%3A//doi.org/10.3390/v11020181) | 2019 | Moussa Diagne | Usutu virus isolated from rodents in Senegal | Viruses | 10.3390/v11020181 | https://doi.org/10.3390/v11020181 |
| [link](https%3A//doi.org/10.1016/j.ijppaw.2019.02.003) | 2019 | Stefano Catalano | Plagiorchis sp. in small mammals of Senegal and the potential emergence of a zoonotic trematodiasis | IJP: Parasites and Wildlife | 10.1016/j.ijppaw.2019.02.003 | https://doi.org/10.1016/j.ijppaw.2019.02.003 |
| [link](https%3A//doi.org/10.1101/616466) | 2019 | L Karan | Lassa Virus in the Host Rodent Mastomys Natalensis within Urban Areas of N’zerekore, Guinea | bioRxiv | 10.1101/616466 | https://doi.org/10.1101/616466 |
| [link](https%3A//doi.org/10.3201/eid2510.180523) | 2019 | Agnes Yadouleton | Lassa Virus in Pygmy Mice, Benin, 2016–2017 | Emerging Infectious Diseases | 10.3201/eid2510.180523 | https://doi.org/10.3201/eid2510.180523 |
| [link](https%3A//doi.org/10.2478/foecol-2019-0001) | 2019 | Safianu Rabiu | Demographic response of the Gambian gerbil to seasonal changes in savannah fallow fields | Folio Oecologica | 10.2478/foecol-2019-0001 | https://doi.org/10.2478/foecol-2019-0001 |
| [link](https%3A//doi.org/10.11648/j.eeb.20190404.11) | 2019 | Karmidine Hima | Population Dynamics and Genetics of Gerbillus nigeriae in Central Sahel: Implications for Rodent Pest Control | Ecology and Evolutionary Biology | 10.11648/j.eeb.20190404.11 | https://doi.org/10.11648/j.eeb.20190404.11 |
| [link](https%3A//doi.org/10.3390/urbansci3030099) | 2019 | Gualbert Houemenou | Pathogenic Leptospira in Commensal Small Mammals from the Extensively Urbanized Coastal Benin | Urban Science | 10.3390/urbansci3030099 | https://doi.org/10.3390/urbansci3030099 |
| [link](https%3A//doi.org/10.3126/ijasbt.v7i4.25581) | 2019 | Kouame Akpatou | Assessment of Terrestrial Small Mammals in an Agro-industrial Company Concession, Western Liberia | International Journal of Applied Sciences and Biotechnology | 10.3126/ijasbt.v7i4.25581 | https://doi.org/10.3126/ijasbt.v7i4.25581 |
| [link](https%3A//doi.org/10.1016/j.ijpara.2018.11.004) | 2018 | Lokman Galal | Diversity of Toxoplasma gondii strains shaped by commensal communities of small mammals | International Journal for Parasitology | 10.1016/j.ijpara.2018.11.004 | https://doi.org/10.1016/j.ijpara.2018.11.004 |
| [link](https%3A//doi.org/10.1017/S0031182018001427) | 2018 | Stefano Catalano | Rodents of Senegal and their role as intermediate hosts of Hydatigera spp. (Cestoda: Taeniidae) | Parasitology | 10.1017/S0031182018001427 | https://doi.org/10.1017/S0031182018001427 |
| [link](https%3A//doi.org/10.3389/fmicb.2018.00150) | 2018 | Katharina Schaufler | Clinically relevant ESBL-producing K. pneumoniae ST307 and E. coli ST38 in an urban West African rat population | Frontiers in Microbiology | 10.3389/fmicb.2018.00150 | https://doi.org/10.3389/fmicb.2018.00150 |
| [link](https%3A//doi.org/10.1186/s13071-018-2991-5) | 2018 | Ayodeji Olayemi | Widespread arenavirus occurrence and seroprevalence in small mammals, Nigeria | Parasites and Vectors | 10.1186/s13071-018-2991-5 | https://doi.org/10.1186/s13071-018-2991-5 |
| [link](https%3A//doi.org/10.1051/parasite/2018036) | 2018 | Carine Brouat | Seroprevalence of Toxoplasma gondii in commensal rodents sampled across Senegal, West Africa | Parasite | 10.1051/parasite/2018036 | https://doi.org/10.1051/parasite/2018036 |
| [link](https%3A//doi.org/10.1007/s10661-018-6858-1) | 2018 | Benjamin Ofori | Urban green area provides refuge for native small mammal biodiversity in a rapidly expanding city in Ghana | Environmental Monitoring and Assessment | 10.1007/s10661-018-6858-1 | https://doi.org/10.1007/s10661-018-6858-1 |
| [link](https%3A//doi.org/10.1016/j.actatropica.2018.07.028) | 2018 | Joshua Kamani | Prevalence of Hepatozoon and Sarcocystis spp. in rodents and their ectoparasites in Nigeria | Acta Tropica | 10.1016/j.actatropica.2018.07.028 | https://doi.org/10.1016/j.actatropica.2018.07.028 |
| [link](http%3A//ncr-journal.bear-land.org/article/173) | 2018 | Kouame Akpatou | Terrestrial small mammal diversity and abundance in Taï National Park, Côte d'Ivoire | Nature Conservation Research | 10.24189/ncr.2018.067 | http://ncr-journal.bear-land.org/article/173 |
| [link](https%3A//doi.org/10.3347/kjp.2018.56.1.93) | 2018 | Isaac Clement | Endoparasites of Small Mammals in Edo State, Nigeria | The Korean Journal of Parasitology | 10.3347/kjp.2018.56.1.93 | https://doi.org/10.3347/kjp.2018.56.1.93 |
| [link](https%3A//doi.org/10.1007/s00436-017-5404-3) | 2017 | Alexis Ribas | Whipworm diversity in West African rodents: a molecular approach and the description of Trichuris duplantieri n. sp. (Nematoda: Trichuridae) | Parasitological Research | 10.1007/s00436-017-5404-3 | https://doi.org/10.1007/s00436-017-5404-3 |
| [link](https%3A//doi.org/10.1038/hdy.2017.18) | 2017 | C Lippens | Genetic structure and invasion history of the house mouse (Mus musculus domesticus) in Senegal, West Africa: a legacy of colonial and contemporary times. | Heredity | 10.1038/hdy.2017.18 | https://doi.org/10.1038/hdy.2017.18 |
| [link](https%3A//doi.org/10.1038/s41598-017-14880-1) | 2017 | Christophe Diagne | Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities | Scientific Reports | 10.1038/s41598-017-14880-1 | https://doi.org/10.1038/s41598-017-14880-1 |
| [link](https%3A//doi.org/10.1089/vbz.2017.2135) | 2017 | Christophe Diagne | Serological survey of zoonotic viruses in invasive and native commensal rodents in Senegal, West Africa | Vector-Borne and Zoonotic Diseases | 10.1089/vbz.2017.2135 | https://doi.org/10.1089/vbz.2017.2135 |
| [link](http%3A//link.springer.com/10.1007/s10661-017-5960-0) | 2017 | Daniel Attuquayefio | Impact of mining and forest regeneration on small mammal biodiversity in the Western Region of Ghana | Environmental Monitoring and Assessment | 10.1007/s10661-017-5960-0 | http://link.springer.com/10.1007/s10661-017-5960-0 |
| [link](https%3A//doi.org/10.3201/eid2104.141469) | 2015 | Thomasz Leski | Sequence Variability and Geographic Distribution of Lassa Virus, Sierra Leone | Emerging Infectious Diseases | 10.3201/eid2104.141469 | https://doi.org/10.3201/eid2104.141469 |
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## Supplementary Table 3

**Table** : Supplementary Table 3.1: GAM model Trap night density ~ Tweedie(coordinates)

| **Component** | **Term** | **Estimate** | **Std Error** | **t-value** | **p-value** |
| --- | --- | --- | --- | --- | --- |
| A. parametric coefficients | (Intercept) | -2.075 | 0.127 | -16.367 | \*\*\* |
| **Component** | **Term** | **edf** | **Ref. df** | **F-value** | **p-value** |
| B. smooth terms | s(x,y) | 23.615 | 29.000 | 9.284 | \*\*\* |
| Signif. codes: 0 <= '\*\*\*' < 0.001 < '\*\*' < 0.01 < '\*' < 0.05 < '.' < 0.1 < '' < 1 | | | | | |
|  | | | | | |
| Adjusted R-squared: 0.0343, Deviance explained 0.340 | | | | | |
| fREML : 4264.082, Scale est: 12.139, N: 1450 | | | | | |

**Table** : Supplementary Table 3.2: GAM model Trap night density ~ Tweedie(log(population density) + coordinates)

| **Component** | **Term** | **Estimate** | **Std Error** | **t-value** | **p-value** |
| --- | --- | --- | --- | --- | --- |
| A. parametric coefficients | (Intercept) | -4.423 | 0.188 | -23.520 | \*\*\* |
| **Component** | **Term** | **edf** | **Ref. df** | **F-value** | **p-value** |
| B. smooth terms | s(log(pop\_2005)) | 1.001 | 1.001 | 9.983 | \*\* |
| s(x,y) | 71.399 | 103.273 | 2.177 | \*\*\* |
| Signif. codes: 0 <= '\*\*\*' < 0.001 < '\*\*' < 0.01 < '\*' < 0.05 < '.' < 0.1 < '' < 1 | | | | | |
|  | | | | | |
| Adjusted R-squared: 0.260, Deviance explained 0.601 | | | | | |
| -REML : 553.599, Scale est: 6.788, N: 1450 | | | | | |

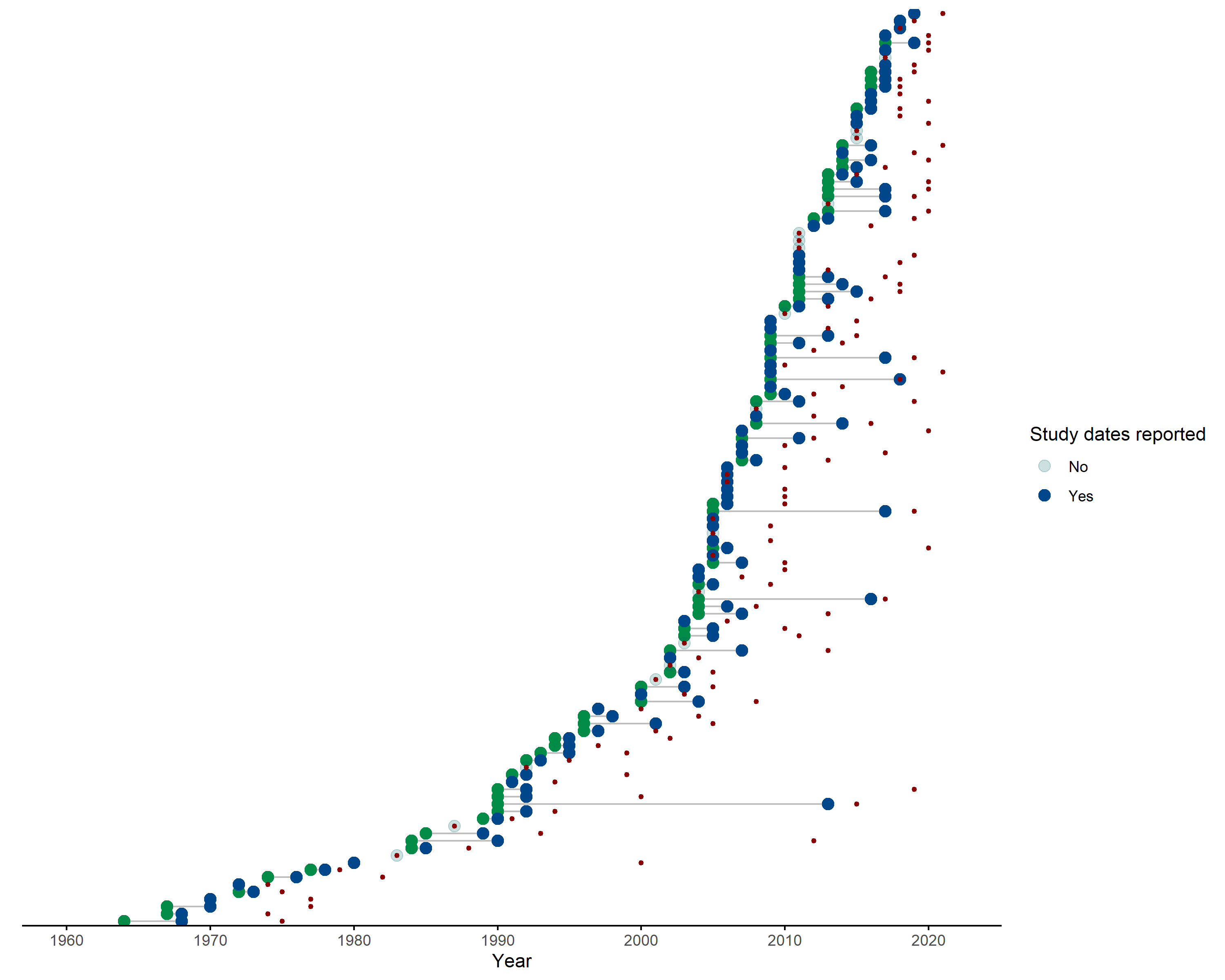
**Table** : Supplementary Table 3.3: GAM model Trap night density ~ Tweedie(proportion cropland + proportion shrubland + proportion tree cover + proportion urban + coordinates)

| **Component** | **Term** | **Estimate** | **Std Error** | **t-value** | **p-value** |
| --- | --- | --- | --- | --- | --- |
| A. parametric coefficients | (Intercept) | -4.415 | 0.183 | -24.141 | \*\*\* |
| **Component** | **Term** | **edf** | **Ref. df** | **F-value** | **p-value** |
| B. smooth terms | s(cropland) | 1.000 | 1.000 | 1.907 |  |
| s(shrubland) | 1.000 | 1.001 | 0.157 |  |
| s(tree\_cover) | 1.001 | 1.002 | 0.951 |  |
| s(urban) | 7.537 | 8.435 | 5.644 | \*\*\* |
| s(x,y) | 58.892 | 85.513 | 2.173 | \*\*\* |
| Signif. codes: 0 <= '\*\*\*' < 0.001 < '\*\*' < 0.01 < '\*' < 0.05 < '.' < 0.1 < '' < 1 | | | | | |
|  | | | | | |
| Adjusted R-squared: 0.472, Deviance explained 0.601 | | | | | |
| -REML : 551.305, Scale est: 6.758, N: 1450 | | | | | |

**Table** : Supplementary Table 3.4: Final GAM model Trap night density ~ Tweedie(proportion tree cover + proportion urban + coordinates)

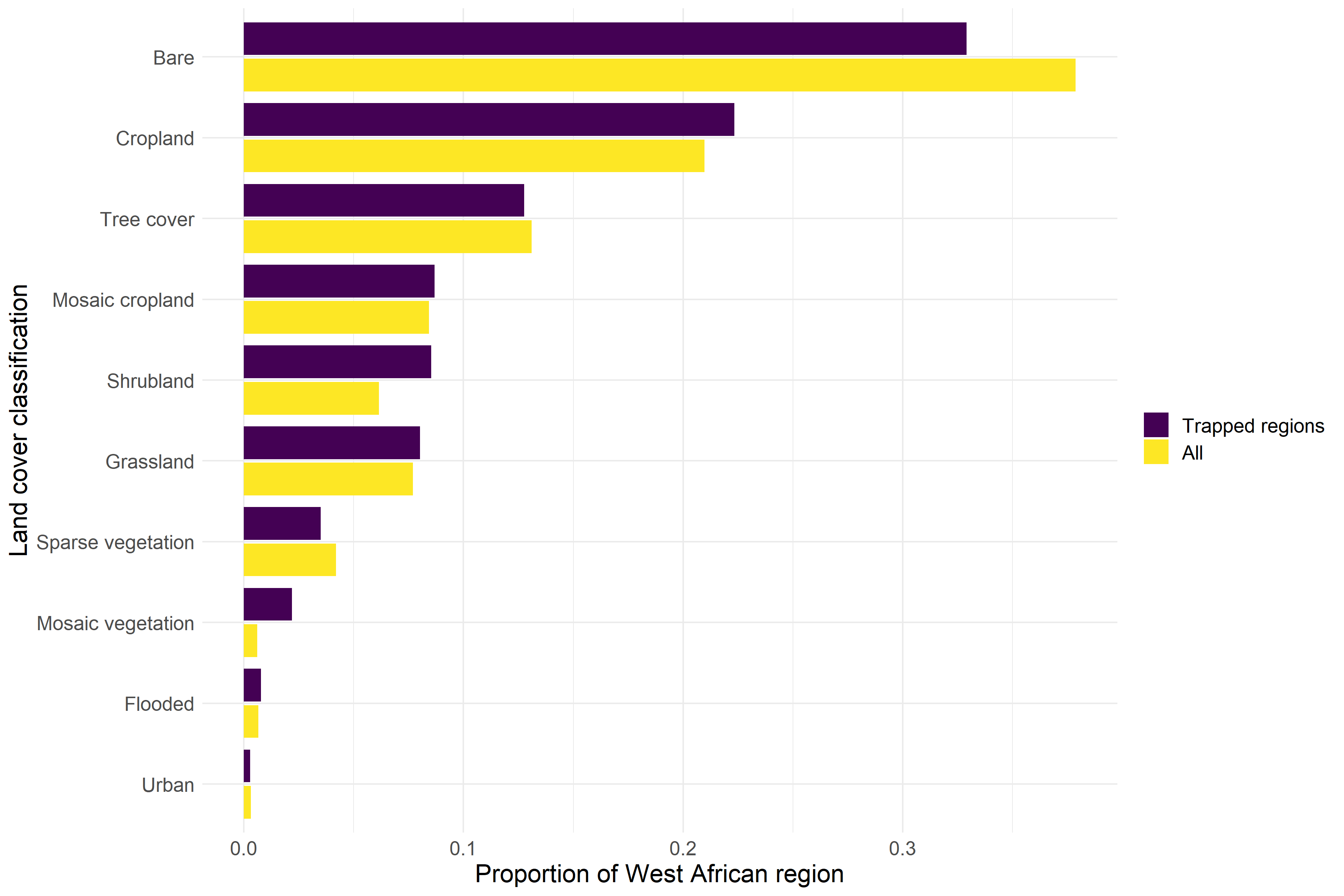
| **Component** | **Term** | **Estimate** | **Std Error** | **t-value** | **p-value** |
| --- | --- | --- | --- | --- | --- |
| A. parametric coefficients | (Intercept) | -4.449 | 0.183 | -24.312 | \*\*\* |
| **Component** | **Term** | **edf** | **Ref. df** | **F-value** | **p-value** |
| B. smooth terms | s(tree\_cover) | 1.003 | 1.006 | 0.016 |  |
| s(urban) | 7.553 | 8.446 | 5.363 | \*\*\* |
| s(x,y) | 62.366 | 90.388 | 2.113 | \*\*\* |
| Signif. codes: 0 <= '\*\*\*' < 0.001 < '\*\*' < 0.01 < '\*' < 0.05 < '.' < 0.1 < '' < 1 | | | | | |
|  | | | | | |
| Adjusted R-squared: 0.523, Deviance explained 0.610 | | | | | |
| -REML : 551.460, Scale est: 6.535, N: 1450 | | | | | |

## Supplementary Figure 1



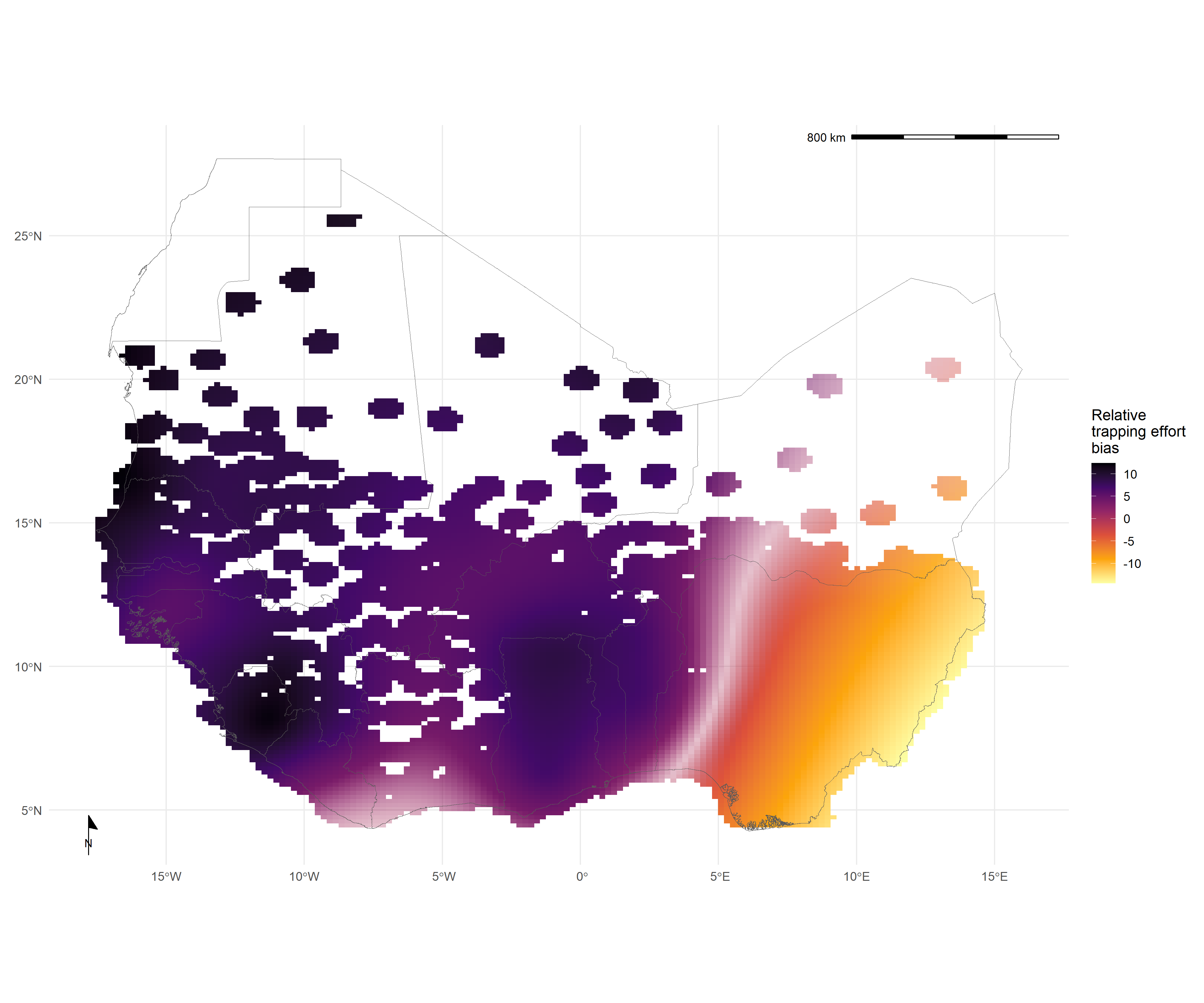
Supplementary Figure 1. Green points represent the start date of rodent trapping studies, blue points representing the final trapping activity. Red points indicate the publication of studies. Increasing numbers of studies have been published since 2000 with more studies being conducted over repeated visits.

## Supplementary Figure 2



Supplementary Figure 2. Comparison between proportion of land use between regions trapped and all land use in West Africa. Cropland, Shrubland and Grassland were trapped at than representative rates while Bare habitats, Forested regions and Urban landscapes were trapped at lower than representative rates.

## Supplementary Figure 3



Supplementary Figure 3. Relative trapping effort bias across West Africa from the subset of included studies reporting trapping effort adjusted for proportion urban land cover and proportion tree cover. Predictions are limited to areas around trap sites (coloured areas), uncertainty in the estimate of bias is represented by colour transparency/pallor. Purple regions represent areas with higher than expected trapping effort, yellow regions represent areas lower than expected trapping effort

## Supplementary Figure 4



Supplementary Figure 4. L) Identified host-pathogen associations at pathogen family level through detection of acute infection (i.e. PCR, culture). Percentages and colour relate to the proportion of all assays that were positive. Associations with a black border are present in the CLOVER dataset. R) Identified host-pathogen associations at pathogen family level through serological assays (i.e. ELISA). Percentages and colour relate to the proportion of all assays that were positive. Associations with a black border are present in the CLOVER dataset.