sampbias, a method for quantifying geographic sampling biases in species distribution data

Alexander Zizka[1,2], Alexandre Antonelli[3,4,5], Daniele Silvestro[3,4,6]

1. German Centre for Integrative Biodiversity Research Halle-Jena-Leipzig (iDiv), University of Leipzig, Deutscher Platz 5e, 04103 Leipzig, Germany

2. Naturalis Biodiversity Center, Leiden University, Leiden, Darwinweg 2, 2333 CR Leiden The Netherlands

3. Gothenburg Global Biodiversity Centre, University of Gothenburg, Box 461, 405 30 Gothenburg, Sweden

4. Department for Biological and Environmental Sciences, University of Gothenburg, Box 461, 405 30 Gothenburg, Sweden

5. Royal Botanic Gardens Kew, TW9 3AE, Richmond, Surrey, United Kingdom

6. Department of Biology, University of Fribourg, Ch. du Musée 10, 1700 Fribourg, Switzerland

Abstract

Geo-referenced species occurrences from public databases have become essential to biodiversity research and conservation. However, geographical biases are widely recognized as a factor limiting the usefulness of such data for understanding species diversity and distribution. In particular, differences in sampling intensity across a landscape due to differences in human accessibility are ubiquitous but may differ in strength among taxonomic groups and datasets. Although several factors have been described to influence human access (such as presence of roads, rivers, airports and cities), quantifying their specific and combined effects on recorded occurrence data remains challenging. Here we present *sampbias*, an algorithm and software for quantifying the effect of accessibility biases in species occurrence datasets. *Sampbias* uses a Bayesian approach to estimate how sampling rates vary as a function of proximity to one or multiple bias factors. The results are comparable among bias factors and datasets. We demonstrate the use of *sampbias* on a dataset of mammal occurrences from the island of Borneo, showing a high biasing effect of cities and a moderate effect of roads and airports. *Sampbias* is implemented as a well-documented, open-access and user-friendly R package that we hope will become a standard tool for anyone working with species occurrences in ecology, evolution, conservation and related fields.

Keywords

Background

Publicly available datasets of geo-referenced species occurrences, such as provided by the Global Biodiversity Information Facility (www.gbif.org) have become a fundamental resource in biological sciences, especially in biogeography, conservation, and macroecology. However, these datasets are typically not collected systematically and rarely include information on collection effort. Instead, they are often compiled from a variety of sources (e.g., scientific expeditions, census counts, genetic barcoding studies and citizen-science observations). Species occurrences are therefore often subject to multiple sampling biases (Meyer et al. 2016).

Sampling biases that may affect the recording of species occurrences (presence, absence and abundance, Isaac and Pocock 2015, Boakes et al. 2010) include the under-sampling of specific taxa ("taxonomic bias", e.g., birds *vs.* nematodes), specific geographic regions ("geographic bias", e.g., easily accessible *vs.* remote areas), and specific temporal periods ("temporal bias", e.g., wet *vs.* dry season). In particular geographic sampling bias—the fact that sampling effort is spatially biased, rather than equally distributed over the study area—is likely to be widespread in all non-systematically collected datasets of species distributions.

Many aspects can lead to sampling biases, including socio-economic factors (e.g., national research spending, history of scientific research; Zizka et al. 2020, Meyer et al. 2015, Daru et al. 2018), political factors (e.g., armed conflict, democratic rights; Rydén et al. 2020), and physical accessibility (e.g., distance to a road or river, terrain conditions, slope; Yang et al. 2014, Botts et al. 2011). Especially physical accessibility by people is omnipresent as a bias factor (e.g., Lin et al. 2015, Kadmon et al. 2004, Engemann et al. 2015), across spatial scales, as the commonly used term "roadside bias" testifies. In practice, this means that most

57 species observations are made in or near cities, along roads, paths, rivers and near human
58 settlements. Relatively fewer observations are expected to be available from inaccessible areas
59 in e.g., a tropical rainforest or a mountain top. Since the recording of different taxonomic
60 groups poses different challenges, geographic sampling bias and the effect of accessibility may
61 differ among taxonomic groups (Vale and Jenkins 2012).

62 The implications of not considering geographic sampling biases in biodiversity research are
63 likely substantial (Barbosa et al. 2013, Meyer et al. 2016, Yang et al. 2013). The presence of
64 geographic sampling biases is broadly recognized (e.g., Kadmon et al. 2004), and approaches
65 exist to account for it in some analyses—such as species-richness estimates (Engemann et
66 al. 2015), occupancy models (Kery and Royle 2016), and abundance estimates (Shimadzu
67 and Darnell 2015). In the case of species distribution modelling—the statistical estimation of
68 species geographic distributions based on known occurrences and environmental conditions—
69 geographically biased sampling is problematic because it often causes environmentally biased
70 sampling which decreases model performance (Kadmon et al. 2004, Bystriakova et al. 2012,
71 Varela et al. 2014, Lobo and Tognelli 2011, Kramer-Schadt et al. 2013). Many approaches
72 exist to remedy the effect of biased sampling on species distribution models (Fourcade et al.
73 2014), including rarefaction to reduce clumped sampling in geographic (Beck et al. 2014,
74 Aiello-Lammens et al. 2015, Boria et al. 2014) or environmental space (Varela et al. 2014),
75 collecting background points for presence-only models to reflect the same sampling bias as
76 the presence records (Phillips et al. 2009), and explicitly modelling sampling bias (Fithian et
77 al. 2015, Stolar and Nielsen 2015, Komori et al. 2020). In contrast, few attempts have been
78 made to compare the geographic sampling bias among datasets (Fernández and Nakamura

79 2015, Ruete 2015, Monsarrat et al. 2019) and to our knowledge, no tools exist to quantify

80 the effect size of specific bias factors and compare it among them. We define as *bias factors*

81 any anthropogenic or natural features that facilitate human access and sampling, such as

82 roads, rivers, airports, and cities.

83 It is unrealistic to expect that accessibility bias in biodiversity data will disappear even

84 after more automated observation technologies are developed. It is therefore crucial that

85 researchers realise the intrinsic biases associated with the data they deal with, especially in

86 cross-taxonomic studies, since occurrence datasets from different taxa are likely differently

87 affected by sampling biases due to differences in specimen collection and transportation. This

88 is the first step towards estimating to which extent these biases may affect their analyses,

89 results and conclusions. Any study dealing with species occurrence data should arguably

90 assess the strength of accessibility biases in the underlying data. Such a quantification can

91 also help researchers to target further sampling efforts.

92 Here, we present *sampbias* v1.0.4, a probabilistic method to quantify accessibility bias in

93 datasets of species occurrences. *Sampbias* is implemented as a user-friendly R-package and

94 uses a Bayesian approach to address three questions:

95 1) How strong is the accessibility bias in a given dataset?

96 2) How strong is the effect of different bias factors in causing the overall accessibility bias?

97 3) How is accessibility bias distributed in space?

98 *Sampbias* is implemented in R (R Core Team 2019), based on commonly used packages for

99 data handling (`ggplot`, Wickham 2009, `forcats`, 2019, `tidyr`, Wickham and Henry 2019,

100 `dplyr`, Wickham et al. 2019, `magrittr`, Bache and Wickham 2014, `viridis`, Garnier 2018),

101 handling geographic information and geo-computation (`raster`, Hijmans 2019, `sp`, Pebesma

102 and Bivand 2005, Bivand et al. 2013) and statistical modelling (`stats`, R Core Team 2019).

103 *Sampbias* offers an easy and largely automated means for biodiversity scientists and non-

104 specialists alike to explore bias in species occurrence data, in a way that is comparable across

105 datasets. The results may be used to identify priorities for further collection or digitalization

106 efforts and to assess the reliability of scientific results based on publicly available species

107 distribution data.

Methods and Features

General concept

110 Under the assumption that organisms occur across the entire area of interest, we can expect

111 the number of sampled occurrences in a restricted area, such as a single biome, to be

112 distributed uniformly in space (even though, of course, the density of individuals and the

113 species diversity may be heterogeneous). With *sampbias* we assess to which extent variation

114 in sampling rates can be explained by distance from bias factors.

115 *Sampbias* works at a user-defined spatial scale, and any dataset of multi-species occurrence

116 records can be tested against any geographic gazetteer. Reliability increases with increasing

117 dataset size. Default global gazetteers for airports, cities, rivers and roads are provided

118 with *sampbias*, and user-defined gazetteers can be added easily. Species occurrence data as

119 downloaded from the data portal of GBIF can be directly used as input data for *sampbias*.

The output of the package includes measures of the sampling rates across space, which are comparable between different gazetteers (e.g., comparing the biasing effect of roads and rivers), different taxa (e.g., birds *vs.* flowering plants) and different data sets (e.g., specimens *vs.* human observations).

Distance calculation

Sampbias uses gazetteers of the geographic location of bias factors (hereafter indicated with B) to generate a regular grid across the study area. By default the study area is defined by the geographic extent of the study dataset, but it can also be customized via user-defined polygons, for instance to limit the analyses to an environmentally homogeneous region (e.g., a rainforest) or an area of special interest (e.g., a national park). In this case all occurrence records outside the user-defined area will be disregarded for the analysis.. For each grid cell i, we then compute a vector $X_i(j)$ of minimum distances (straight aerial distance, "as the crow flies") to each bias factor $j \in B$. The resolution of the grid defines the precision of the distance estimates, for instance a 1×1 degree raster will yield approximately a 110 km precision at the equator. Due to the assumption of homogeneous sampling and a computational trade-off between the resolution of the regular grid and the extent of the study area (for instance, a 1 second resolution for a global dataset would become computationally prohibitive in most practical cases), *sampbias* is best suited for local or regional datasets at high resolution (c. 100 – 10,000 m). Since the differences in grid cell size are negligible on the local and regional scale, sampbias uses a latitude/longitude grid by default, but a custom grid in any projection and coordinate reference system—for instance an equal area grid, which is often more suitable for

141 large spatial analyses—may be provided by the user.

Quantifying accessibility bias using a Bayesian framework

143 We describe the observed number of sampled occurrences S_i within each cell i as the result of

144 a Poisson sampling process with rate λ_i. We model the rate λ_i as a function of a parameter

145 q, which represents the expected number of occurrences per cell in the absence of biases,

146 i.e. when $\sum_{j=1}^{B} X_i(j) = 0$. Additionally, we model λ_i to decrease exponentially as a function

147 of distance from bias factors, such that increasing distances will result in a lower sampling

148 rate. For a single bias factor the rate of cell i with distance X_i from a bias is:

$$\lambda_i = q \times \exp\left(-wX_i\right)$$

149 where $w \in \mathbb{R}^+$ defines the steepness of the Poisson rate decline, such that $w \approx 0$ results in a

150 null model of uniform sampling rate q across cells. In the presence of multiple bias factors

151 (e.g., roads and rivers), the sampling rate decrease is a function of the cumulative effects of

152 each bias and its distance from the cell:

$$\lambda_i = q \times \exp\left(-\sum_{j=1}^{B} w_j X_i(j)\right) \quad (1)$$

153 where a vector $\mathbf{w} = [w_1, ..., w_B]$ describes the amount of bias attributed to each specific factor.

154 To quantify the amount of bias associated with each factor, we jointly estimate the parameters

155 q and $\mathbf{w}$ in a Bayesian framework. We use Markov Chain Monte Carlo (MCMC) to sample

156 these parameters from their posterior distribution:

$$P(q, \mathbf{w}|\mathbf{S}) \propto \prod_{i=1}^{N} Poi(S_i|\lambda_i) \times P(q)P(\mathbf{w}) \quad (2)$$

157 where the likelihood of sampled occurrences S_i within each cell $Poi(S_i|\lambda_i)$ is the probability

158 mass function of a Poisson distribution with rate per cell defined as in Eqn. (1). The likelihood

159 is then multiplied across the N cells considered. We use exponential priors on the parameters

160 q and $\mathbf{w}$, $P(q) \sim \Gamma(1, 0.01)$ and $P(\mathbf{w}) \sim \Gamma(1, 1)$, respectively. We chose exponential priors

161 because they represent the standard choice for rate parameters such as q and the weights

162 $\mathbf{w}$, all of which must be positive and have support $[0, +\text{inf}]$. We designed the priors to be

163 informative (i.e. not allowing negative values) and yet vague enough to encompass a much

164 wider range of parameter space than the range of values observed in empirical tests. Custom

165 priors, within the flexible family of gamma distributions, which include the exponential priors

166 used here, are possible via the `prior_q` and `prior_w` arguments of the `calculate_bias`

167 function. Additionally, since the null expectation in the absence of biases is that the weights

168 are close to 0, we implement a hierarchical model, in which the rate parameter of the gamma

169 prior can be itself estimated from the data. Thus, we set $P(\mathbf{w}) \sim \Gamma(a = 1, b)$ and assign a

170 vague hyper-prior on the rate $P(b) \sim \Gamma(\alpha_0 = 1, \beta_0 = 0.001)$. The choice of conjugate gamma

171 distribution allows us to sample the rate directly from its posterior distribution:

$$b \sim \Gamma(\alpha_0 + aB, \ \beta_0 \sum_{j=1}^{B} w_j) \quad (3)$$

172 The use of a hyper-prior has the advantage of making the prior on the weights more flexible

173 and able to adapt to different datasets reducing the need for user-defined arbitrary choices.

174 Additionally, it works as a regularization technique reducing the risks of over-parametrization,

175 by shrinking the weights around small values when there is no evidence in the data indicating

176 a bias.

177 We summarize the parameters by computing the mean of the posterior samples and their

178 standard deviation. We interpret the magnitude of the elements in **w** as a function of the

179 importance of the individual biases. We note, however, that this test is not explicitly intended

180 to assess the significance of each bias factor. Because several bias factors might be correlated

181 (e.g. cities and airports), simply summing their effect from independent analyses would

182 result in an overestimation of the total bias. It is therefore important to jointly estimate the

183 effects of correlated factors, as this is based on the likelihood of the data given the combined

184 effects of all biasing factors. A Bayesian variable selection method could be used to quantify

185 the expected amount of bias in the data predicted by single or a particular combination of

186 predictors, but falls beyond the scope of the current study.

187 We summarize the results by mapping the estimated 'textcolor{blue}{(the relative deviation

188 of sampling rate from the maximum sampling rate (or on user choice the estimated sampling

189 rates}, λ_i) across space. These rates represent the expected number of sampled occurrences

190 for each grid cell and provide a graphical representation of the spatial variation of sampling

191 rates. Provided that the cells are of equal size, the estimated rates will be comparable across

192 data sets, regions, and taxonomic groups. Analysing different regions, biomes, or taxa in

193 separate analyses allows to account for differences in sampling rates, which are not linked

194 with bias factors. For instance, the unbiased sampling rate q is expected to differ between a

highly sampled clade like birds and under-sampled groups of invertebrates, but their sampling biases (**w**) might be similar across the two groups.

Example and empirical validation

A default *sampbias* analysis can be run with few lines of code in R. The main function calculate_bias creates an object of the class "sampbias", for which the package provides a plotting and summary method. Based on a data.frame including species identity and geographic coordinates. Additional options exist to provide custom gazetteers, study area, spatial grid and grain size of the analysis, as well as some operators for the calculation of the bias distances, including priors for q and **w**. A tutorial on how to use *sampbias* is available with the package and in the electronic supplement of this publication (Appendix S1).

To exemplify the use of *sampbias*, we downloaded the occurrence records of all mammals available from the island of Borneo (n = 6,262, GBIF.org 2016) and ran *sampbias* using the default gazetteers as shown in the example code below, to test the biasing effect of the main airports, cities and roads in the dataset. The example dataset is provided with *sampbias*.

We found a strong effect of cities on sampling intensity, a moderate effect of roads and airports and a negligible effect of rivers (Fig. 1). All models predict a low number of collection records in the centre of Borneo (Fig.), which reflects the original data, and where accessibility means are low (Figure S1 in Appendix S2). The empirical example illustrates the use of *sampbias*, for detailed analyses or a smaller geographic scale, higher resolution gazetteers, including smaller roads and rivers and a higher spatial resolution would be desirable. Results might change with increasing resolution, since roads and rivers might have a stronger effect on

216 higher resolutions (facilitating most the access to their immediate vicinity), whereas cities

217 and airports might have a stronger effect on the larger scale (facilitating access to a larger

218 area).

```r
library(sampbias)


# a data table with species identity, longitude, and latitude

example.in <- read.csv(system.file("extdata",

                                   "mammals_borneo.csv",

                                   package="sampbias"),

                       sep = "\t")


# running sampbias

## 'res' defines the resolution of the spatial grid

## for distance calculation in degrees latitude and longitude

## 'buffer' defines the buffer around the study area to account for biasing

## structure adjacent to the study area, in degrees latitude and longitude

## All other options at default, see ?calculate_bias for a description

example.out <- calculate_bias(x = example.in,

                             res = 0.05,

                             buffer = 0.5)


# summary
```

```
summary(example.out)

plot(example.out)


# projecting the bias effect in space

proj <- project_bias(example.out)

map_bias(proj)
```

We ran simulation experiment to assess whether the estimated bias weights differ significantly from a null expectation of random sampling. To do so, we first created ten replicates of an unbiased data by generating 6262 random occurrences across Borneo (the same number as in the empirical dataset) and then ran a *sampbias* with the same settings as for the empirical dataset on each of these replicates. We found that the estimated bias range were significantly different (credible intervals non-overlapping) than in the null model for cities, roads and airports (Figure S2 in Appendix S1).

Sampbias is designed to work with sparsely sampled datasets, and to estimate bias effects from datasets with low coverage. To test the performance of *sampbias* on small datasets we ran an additional simulation experiment. We ran the analyses with the same settings as for the empirical dataset on a set of rarified datasets, sub-sampling the initial dataset to 3,131, 626, 62 records respectively (three replicates each), and then compared the estimated bias weights for all bias factors to the estimates for the empirical dataset. The results showed that parameter estimates and the projection of the bias effect in space were robust to decreases in data, although uncertainty increased (Figs. S3 and S4, in Appendix S1). The results show that *sampbias* reliably rejected a biasing effect even for small datasets (Figs. S4 and S5, in

Appendix S2). In general, the more records, the more precise the parameter estimates will be.

Data accessibility

Sampbias is available under a GNU General Public license v3 from https://github.com/azizka/sampbias, and includes the example dataset as well as a tutorial (Appendix S1) and a summary of possible warnings produced by the package (Appendix S3).
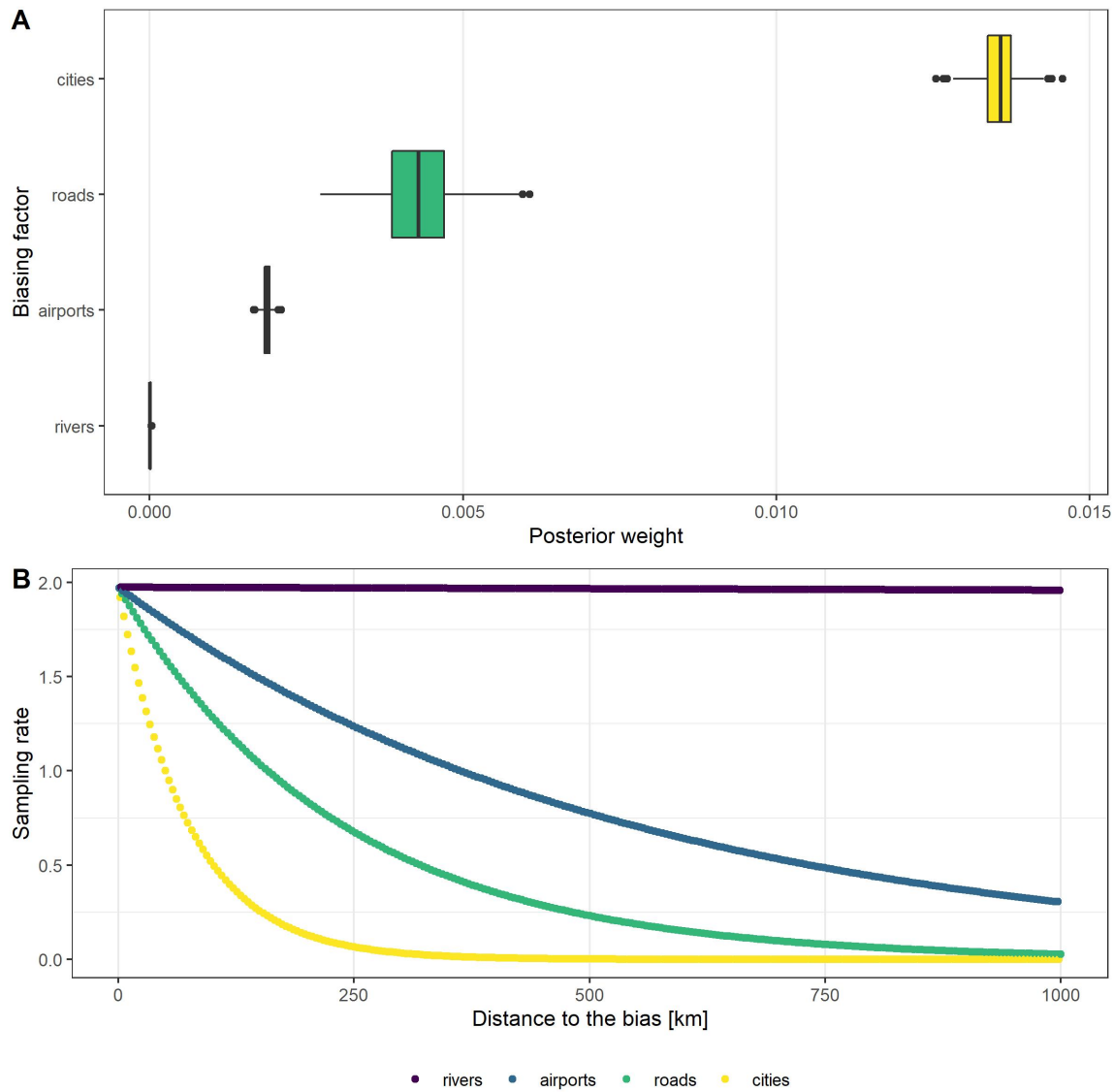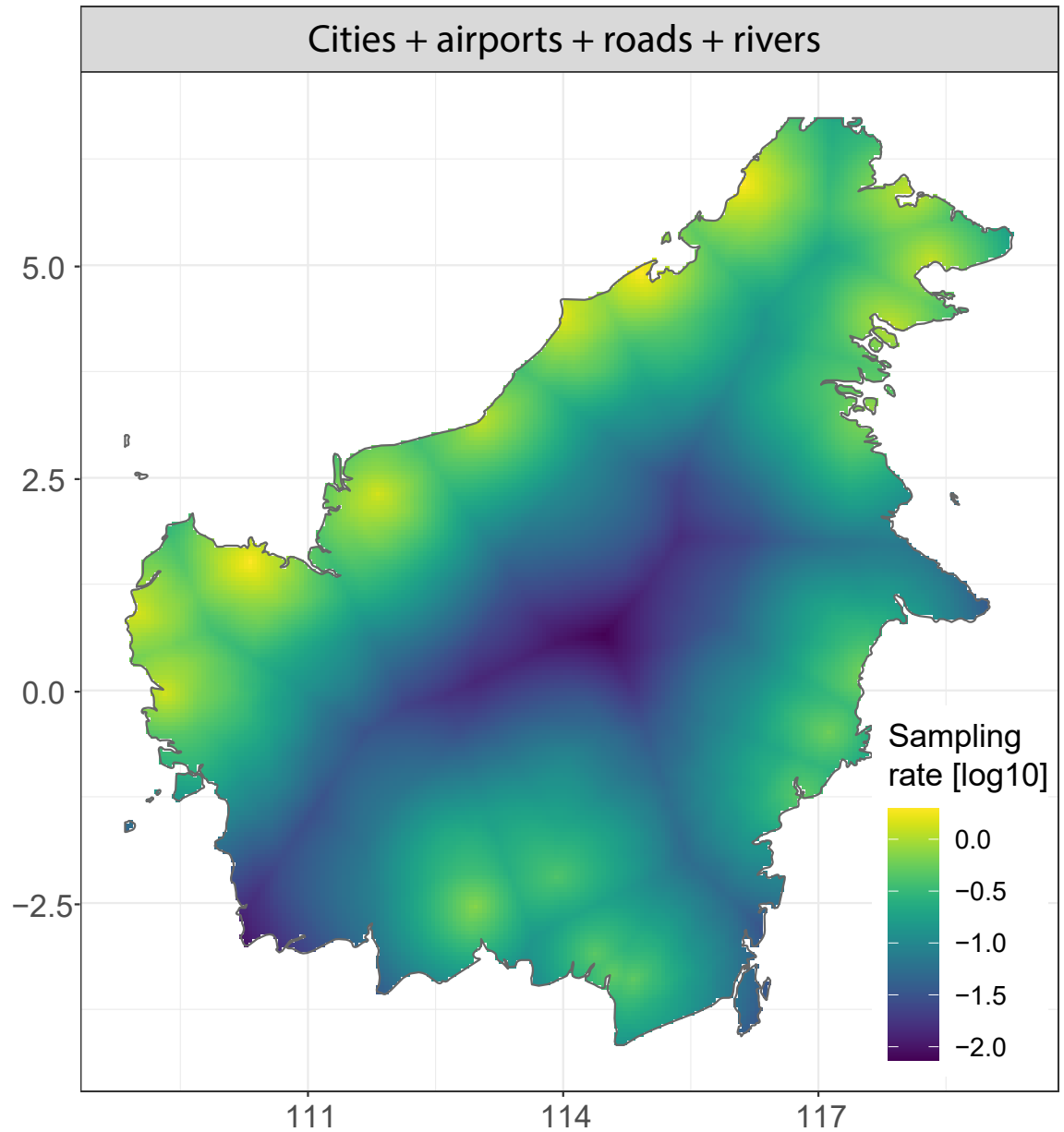
Figures

Figure 1: Results of the empirical validation analysis, estimating the accessibility bias in mammal occurrences from Borneo. A) bias weights (w) defining the effects of each bias factor, B) sampling rate as function of distance to the closest instance of each bias factor (the expected number of occurrences) given the inferred *sampbias* model. At the study scale of 0.05 degrees (c. 5x5km) *sampbias* finds the strongest biasing effect for the proximity of cities and roads.

Cities + airports + roads + rivers

\begin{figure}

\caption{Spatial projection of the sampling bias in an empirical example dataset of mammal

occurrences on the Indonesian island of Borneo (downloaded from www.gbif.org. GBIF.org,

2016). The colours show the projection of the The colours show the projection of the

log10-transformed sampling rates (i.e. expected number of occurrences per cell) given the

inferred *sampbias* model. The highest undersampling is in the centre of the island. DIfferent

visualizations, including among others the untransformed sampling rate are also implemented

249   in sampbias. \end{figure}

Supplementary material

Appendix S1 - Tutorial running *sampbias* in R

Appendix S2 - Supplementary Figures

Appendix S3 - Possible warnings and their solutions

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