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Large regional variation in global impacts of agriculture on terrestrial insects and other arthropods

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ABSTRACT

Many insects and other arthropods are reported to be in rapid decline worldwide, mainly driven by changes in land use and climate. At the same time, arthropods provide many important services that benefit agriculture, and thus their losses may pose risks to food security. Although biodiversity responses vary between global realms, this spatial heterogeneity is not well-understood and is rarely addressed in global analyses. To understand the geographical variation of biodiversity change better, we investigated the responses of arthropod diversity to agricultural land use and intensity for six geopolitical regions, using a global dataset of biodiversity records. We show that agricultural intensification generally leads to average biodiversity declines, but we find large variation in responses per region. Notably, responses in Europe are minimal or even significantly positive. Further investigation suggests that responses in Europe may be attributable to a combination of a primary vegetation baseline that is subject to comparatively high levels of disturbance and fragmentation, and significant compositional changes that have favoured widespread generalists and non-native species. Conversely, narrow-ranging habitat specialists, particularly of forests, are associated with significant declines. These findings have important consequences for global biodiversity assessments and associated predictions of ecosystem service delivery, which are likely underestimating land use impacts on biodiversity by relying on statistical model coefficients that are heavily biased towards Europe and may fail to report important compositional changes by focussing analyses solely on species richness and total abundance.

1 Introduction

Insects and other arthropods are reported to be in rapid decline worldwide, driven principally by the expansion and intensification of agriculture (Raven and Wagner, 2021; Wagner et al., 2021). While there is ongoing speculation as to whether insects are in decline globally, given considerable variation in trends between species, orders and regions, and a significant monitoring bias towards the northern hemisphere (Dirzo et al., 2014; Klink et al., 2020; Outhwaite et al., 2020), the data that is available suggests that terrestrial insect abundance is decreasing globally at ca. 10% per decade, while freshwater insect abundance is increasing at approximately the same rate (Klink et al., 2020). It is, moreover, estimated that 5-10% of insect species may have gone extinct since the start of the industrial era, numbering between 250,000 and 500,000 species (Cardoso et al., 2020). Many arthropod species provide valuable ecosystem services for agricultural systems, such as crop pollination and pest regulation (Costanza et al., 1997; Dainese et al., 2019; Potts et al., 2016b; Yang and Gratton, 2014), and thus declines in arthropod abundance and diversity may pose substantial risks to food production and human well-being (Millard et al., 2023; Pereira et al., 2024; Potts et al., 2016a), particularly in regions that rely heavily on animal pollination and natural pest control.

While biodiversity is changing worldwide, the magnitude and direction of change has been shown to vary widely between biogeographic realms (Almond et al., 2022; Olson et al., 2001), with the strongest declines observed in the neotropics. Although large-scale analyses have highlighted stark differences in biodiversity responses to land use between the tropical and temperate zones (Millard et al., 2021; Newbold et al., 2020; Outhwaite et al., 2022), it remains common to report on global statistics, which, in turn, are frequently used in combination with land-use projections of integrated assessment models (IAMs) to estimate future impacts on biodiversity and ecosystem service delivery (e.g., Kim et al., 2018; Kozicka et al., 2023; Leclère et al., 2020; Pereira et al., 2024; Schipper et al., 2020). Such approaches may be missing important regional context (Bevan et al., 2025), and since global ecological data availability tends to be highly biased towards Europe and North America (Proença et al., 2017; Trimble and Aarde, 2012), where contemporary biodiversity change appears to be less pronounced (Almond et al., 2022), global statistics are likely underestimating impacts on biodiversity for large parts of the planet.

In order to estimate the impacts of land use on biodiversity better across the globe, an improved understanding of the regional heterogeneity of responses is needed. In this study, we investigated differences in the responses of arthropod diversity to agricultural land use and land-use intensity across six world regions, with a particular focus on Europe, where preliminary results show changes in diversity from primary vegetation to be either minimal or even significantly positive (Fig. 1). Although this is not an entirely unexpected result, as it is known that impacts of land use on biodiversity are less pronounced in temperate regions (Newbold et al., 2020), it is important to understand better what drives these responses in Europe, particularly since biodiversity data collection tends to be highly biased towards the European continent. Indeed, the fact that Europe is a data-rich region means that further investigation is statistically feasible.

Impacts of anthropogenic stressors such as agricultural expansion and intensification on species assemblages can be estimated by comparing biodiversity in anthropogenic land-use types against an undisturbed baseline that is assumed to represent species assemblages in their natural state, typically termed 'primary vegetation' (Hudson et al., 2017). However, it is difficult to determine a 'virgin' state of nature, and it is known that anthropogenic stressors in Europe have been high (and accelerating) since the 18th and 19th centuries, long before widespread biodiversity monitoring has taken place (Mihoub et al., 2017), impacting biodiversity within the natural habitats that are used as baseline condition. Among these stressors, deforestation to clear land for pasture and cropland has likely been the most influential (Darby, 1955), rapidly transforming the mixed deciduous and boreal forests that had come to dominate Europe following the end of the last glacial period (Williams, 2003). This deforestation has been persistent, and reconstructions suggest that by 1850, deforestation had reached 60-70% in central Europe and in excess of 90% in Britain (Kaplan et al., 2017). Although the industrial revolution helped to alleviate pressure on European forests, and helped intensify agriculture to put aside space for nature, the associated reliance on agro-chemicals has come to be identified as one of the main contemporary drivers of insect declines in Europe (Benton et al., 2002; Fox, 2013). As a result of these persistent pressures on the natural environment and the domination of landscapes by anthropogenic habitats, the baseline condition of the remainder of natural habitat in Europe has thus likely been gradually degraded (Soga and Gaston, 2018). The result of using natural habitat of this contemporary nature as a baseline in statistical models of the impact of land use on biodiversity is that impacts are likely to be less negative than if they had been compared against truly undisturbed primary vegetation.

In terms of species compositions, this long history of land-use change on the European subcontinent has likely produced both winners and losers (Newbold et al., 2018), as forest clearings and the loss of primary vegetation would have benefited open-habitat generalists at the expense of closed-canopy, forest specialists. Additionally, winners of land-use change tend to be non-native and invasive (Chytrý et al., 2008; Liu et al., 2023; Pyšek et al., 2020), which may mask declines in native biodiversity (Van Kleunen et al., 2015). This appears to be particularly relevant in Europe, North America and Australasia, where the number of introductions of non-native species dominate compared to other regions (Seebens et al., 2025). The baseline natural habitat in regions like Europe may thus be relatively more dominated by non-native, widespread and generalist species than in regions without a long history of human impact on the environment. Depending on the extent of change in species compositions within natural habitat, differences in arthropod (alpha) diversity between primary vegetation and agricultural land use may thus be considerably less pronounced in Europe than in other regions.

We explore three main hypotheses that may explain differences in biodiversity–land-use responses of arthropods between Europe and other regions: We hypothesise that as a result of Europe's long history of land-use change (1) structurally, natural habitat in Europe is more fragmented, and thus less surrounded by other natural habitat, than in other regions, with the result that many of the species that would have been present within large tracts of natural habitat will have disappeared; (2) homogenization in European ecosystems over time has led to compositional similarities between natural vegetation and agricultural sites, and thus species turnover between natural habitat and agricultural sites is lower than in other regions; and (3) winners, i.e. species that respond positively in agricultural land use, tend to be widespread habitat generalists and non-native species, which have had more opportunity to establish themselves in Europe than in other regions, with the result that overall responses in Europe are less negative than in other regions. In testing the third hypothesis we compare the effect of range extent, habitat specificity and non-nativeness on arthropod diversity and specifically compare Europe against North America. These regions span a similar latitudinal range and are thus subject to similar climatic conditions, and are comparable in terms of economic development and agricultural land use. Crucially, ecosystems in Europe and North America have been subject to different land-use histories and we thus expect to see differences in the degree to which widespread generalists and non-native species mask declines of native specialists.

2 Methods

2.1 Biodiversity data

The arthropod records used in this study stem from the PREDICTS database, which contains worldwide, site-level species occurrence and abundance records sourced from published studies that sampled from land-use types along a gradient of intensity (Hudson et al., 2017). These data are nested at four levels: 'source' (a unique publication), 'study' (a collection of data within a source that has a consistent sampling methodology), 'block' (a collection of sites in a distinct spatial cluster) and 'site' (a geographic location at which records were sampled). We used the updated version of the PREDICTS database (Hudson et al., 2023, version 1.1), and an additional data release (Contu et al., 2022), to obtain 1,079,780 records of 10,200 arthropod species, across 7978 sites worldwide (Table 1 and Fig. 1). The sampled species belong to the orders Coleoptera (26.1% of records), Hymenoptera (17.8%), Lepidoptera (17.7%), Sarcoptiformes (13.6%), Mesostigmata (7.6%), Araneae (4.5%), Hemiptera (4.4%), Diptera (2.7%), Entomobryomorpha (2.0%) , Poduromorpha (1.4%) and other orders (5.3%), with slight variation between regions (Table S2). We investigated biodiversity responses for agricultural sites (cropland, pasture and tree plantation) at three use-intensities (minimal, light and intense) and compared these against responses in primary vegetation (native vegetation not known or inferred to have ever been completely destroyed) and secondary vegetation (vegetation that is in various stages of recovery after the original primary vegetation was completely destroyed, e.g., for a period of agricultural use). In the latter category, we did not include 'young' (early successional stage) secondary vegetation, which may be very similar to disturbed agricultural land. Exact definitions of these land-use types and their use-intensities, as used in the PREDICTS database, can be found in the supplementary information A (Table S1).

We compared the responses of arthropod diversity to land use across six world regions: North America, Europe, South and Southeast Asia, South and Central America, sub-Saharan Africa and Australasia (Australia and New Zealand), largely similarly to Almond et al. (2022). Although these regions broadly mirror the world's biogeographic realms (Olson et al., 2001), they were selected primarily as geopolitical regions with largely shared land-use histories. Although Europe and East Asia share the same biogeographic realm (the Palearctic) their land-use histories differ in important ways, which we expect to have led to differences in the contemporary responses of biodiversity to land use and land-use change. These regions were, furthermore, selected on the basis of data availability, which meant that Oceania, North Africa, Central Asia and East Asia were omitted from the analysis. Following a preliminary sensitivity analysis (see supplementary information A; Section B.7) in which we found a disproportionately strong influence of a single study from the Azores islands on European biodiversity responses, we decided to remove the Azores islands from the dataset, given its geographical isolation from the rest of Europe. As such, records from Europe are restricted to continental Europe, Great Britain and Ireland. For consistency, we removed records from similarly sized island groups from other regions, which led to the removal of Comoros from sub-Saharan Africa and Puerto Rico from South and Central America (as a result this region does not contain data from the Caribbean).

For the majority of this regional analysis, we modelled arthropod diversity responses to an aggregate agricultural land-use category (combining cropland, pasture and plantations), but for Europe we further investigated responses to individual land-use types (where sample sizes were sufficient) and compared these against global responses. In order to determine whether the diversity responses of arthropods are indicative of a general European pattern, we also modelled biodiversity responses for vertebrate species (in Europe and globally). Preprocessed and filtered to natural and agricultural land use, vertebrate records in PREDICTS totalled 559,074 globally (5032 species), distributed across 7842 sites and 224 studies. Europe comprised 51,665 records (183 species), 1157 sites and 15 studies. The majority of vertebrate records stemmed from bird species, with Passeriformes (song birds) as the largest order (46.2% of global records). Vertebrate records in Europe consisted entirely of bird species, with Passeriformes comprising 60.3% of records.

For the further comparative analysis between Europe and North America, we extracted species data on range extent, habitat specificity and non-native status from additional data sources (see Sections 2.5, 2.6 and 2.7). To maximise the number of species for which we could extract these data, we manually checked species' Latin binomial names in the PREDICTS database (for Europe and North America) for errors such as abbreviations and spelling mistakes or inconsistencies, and compared names with the Global Biodiversity Information Facility (GBIF) taxonomic backbone to ensure that, where possible, synonyms were harmonised to a single species.

Table 1: Counts of unique species, studies, sites and total records for arthropods in the PREDICTS database, filtered for natural vegetation and agricultural land-use types. Europe comprises the most data-rich region in the database.

Region	Unique species	Studies	Sites	Total records	Records %
North America	2141	43	988	141,634	14.5
Europe	4098	118	3412	396,728	40.5
South and Southeast Asia	898	30	525	77,555	7.9
South and Central America	1494	85	1125	79,986	8.2
Sub-Saharan Africa	659	21	426	44,263	4.5
Australasia	708	26	712	238,825	24.4
Tropical Zone	2732	122	1858	192,389	19.7
Temperate Zone	7127	202	5330	786,602	80.3
Total	9800	323	7188	978,991	100.0

2.2 Main modelling framework

As biodiversity metrics, we primarily modelled species richness, total abundance and Simpson's diversity index, which is a measure of evenness (Simpson, 1949). Rather than modelling Simpson's diversity index directly, we modelled its inverse to convert the index to a diversity measure that reflects the effective number of species, allowing responses to be comparable with species richness (Jost, 2006). We modelled these three metrics with mixed effects models using R Statistical Software (R Core Team, 2024, version 4.5.1) with the Bayesian modelling package `brms` (Bürkner, 2021, version 2.22.0). We modelled species richness with a zero-inflated negative binomial distribution, in order to account for overdispersion and zero-inflation. Total abundance and Simpson's diversity index were modelled with a log-normal distribution, which we found fit the data well. In cases where sampling effort varied between sites within a study, we corrected abundance measurements by dividing by relative sampling effort (relative to the maximum sampling effort in the study), assuming that recorded abundance scales linearly with sampling effort (Newbold et al., 2015). This applied to 9.1% of studies in our dataset and 17.6% of abundance measurements. Due to these corrections, total abundance was not modelled as a count variable but rather as a continuous variable with a log-normal distribution (Newbold et al., 2015).

We did not rescale abundance relative to the maximum recorded abundance within studies, as in De Palma et al. (2021), for the reason that model diagnostics of log-transformed total abundance indicated better model fit than either models of log-transformed rescaled abundance or models of rescaled abundance using a zero-and-one-inflated beta distribution (see Section E of Supplementary Information B). We suspect that the model diagnostics of log-transformed total abundance showed better fit because we modelled diversity records within a single phylum (Arthropoda), which means that problematic between-study sampling and reporting differences that abundance rescaling is meant to address are possibly less pronounced than in the case of modelling records across various phyla and kingdoms (De Palma et al., 2021). We did investigate differences in modelled abundance responses to land use between these models, including a zero-inflated negative binomial model of total abundance, and note that while there is some variation between models and the significance of certain responses (predominantly in data-scarce regions), model choice does not meaningfully change general regional patterns and conclusions drawn from these in this study (Fig. S20).

For all three diversity metrics, we estimated regional differences in biodiversity responses to land use by modelling land use and region as interactive fixed effects, using study-level random intercepts to account for differences in sampling methods and study-design as well as block-level random intercepts to account for any spatial structuring in the sites sampled within each study (Eq. 1). We present model predictions as the median and 95% credible interval from a sample of 1,000 posterior draws of the expected response conditional on the fixed effects. Where predictions are presented as changes from primary vegetation, we divided the posterior response samples of all land-use types by primary vegetation and computed the median and 95% credible intervals from these relative responses.

$$\text{Diversity} \sim \text{Land use} \times \text{Region} + (1|\text{Study/Block}) \tag{1}$$

2.3 Natural habitat

In order to investigate the landscape composition of natural habitat surrounding PREDICTS sites, we computed the percentage of natural habitat within a 5km radius of the PREDICTS sites (square buffer). We used the land-use layers from Matej et al. (2025), which have a 30 arcsecond resolution (approximately 1km^2 at the equator) and span the years 1992–2020. These land-use classes are derived from the land cover product of the European Space Agency Climate Change Initiative (ESA CCI LC) and use statistics from the Food and Agriculture Organization (FAO) to discern land cover into 32 land-use classes. From these classes, we aggregated the wilderness and forestry classes, as well as grazing land characterized by open wooded lands, to constitute natural habitat.

We also used the dataset's land-use intensity layers to investigate differences in the use-intensity of natural habitat between regions. Land-use intensity is estimated as human appropriation of net primary production (HANPP), which is an indicator that quantifies the effects of human-induced changes in productivity and harvest on ecological biomass flows (Haberl et al., 2014). The total HANPP of the natural habitat in a buffer is comprised of the HANPP due to land use change ($\mathrm{HANPP}_{\mathrm{luc}}$, which equals the difference between the actual NPP of the habitat and the potential NPP in the hypothetical absence of land use) and the HANPP due to harvest ($\mathrm{HANPP}_{\mathrm{harv}}$, which equals the difference between the actual NPP and the NPP remaining in ecosystems after harvest, $\mathrm{NPP}_{\mathrm{eco}}$). By definition, the HANPP of wilderness areas, and the $\mathrm{HANPP}_{\mathrm{luc}}$ of forestry areas, are zero. We converted HANPP to a percentage of potential NPP ($\mathrm{NPP}_{\mathrm{pot}} = \mathrm{NPP}_{\mathrm{eco}} + \mathrm{HANPP}_{\mathrm{harv}} + \mathrm{HANPP}_{\mathrm{luc}}$) to obtain a metric that is comparable across regions and land use types (%HANPP) (Erb et al., 2013). We computed %HANPP and the percentage of natural habitat area within the buffers surrounding sites from the year in which the midpoint of the sampling duration of the site occurred (i.e., the date half-way between the first and last sampling dates) and for each site computed their mean values in the buffer. Finally, we estimated the connectivity of the natural habitat surrounding PREDICTS sites within a larger buffer with 10km radius with three metrics – mean patch size, patch density and the aggregation index (He et al., 2000) – using the R package `landscapemetrics` (Hesselbarth et al., 2019, version 2.2.1). To achieve this, the layers of fractional natural habitat were converted into binary layers using three different natural habitat (NH) thresholds: NH$\geq$0.3, NH$\geq$0.5 and NH$\geq$0.7.

2.4 Compositional dissimilarity

We compared compositional dissimilarity between species in natural vegetation (primary and secondary vegetation) and in agricultural land use with Sørensen's index (Mueller-Dombois, 1974). Sørensen's dissimilarity $S = \frac{b+c}{2a+b+c} \in [0, 1]$ is a popular dissimilarity measure in the study of ecological communities (McCune and Grace, 2002), where a designates the number of species observed in both sites, and b and c designate the number of unique species sampled in each site individually. We further partitioned Sørensen's index into nestedness and turnover (Baselga, 2010), using the `betapart` R package (Baselga and Orme, 2012, version 1.6.1), to determine the extent to which dissimilarity is the result of species replacement (turnover) or species loss (nestedness; i.e., the extent to which composition in one land use is a subset of the other). We only compared sites within the same study and computed dissimilarity exclusively for site combinations in the off-diagonal of the pairwise dissimilarity matrix to avoid problems of non-independence from using all possible pairwise comparisons (Longacre et al., 2005).

Species compositions in agricultural sites were compared against primary and secondary vegetation, rather than just primary vegetation, because within-study comparisons between primary vegetation and agriculture were found to be scarce in the PREDICTS database, limiting the land-use coefficients that we were able to estimate. This was found to be particularly the case for light- and intense-use agriculture in Europe, where within-study comparisons with secondary vegetation are much more abundant than with primary vegetation. In addition, dissimilarity between secondary vegetation and primary vegetation was not found to be significantly different from dissimilarity between primary vegetation and other primary vegetation in any region (Fig. S8), which suggests that the comparison of dissimilarity between agricultural sites and all natural vegetation sites may be sufficiently representative of a comparison with just primary vegetation. We used Sørensen's index, which is an occurrence-based index, rather than indices that incorporate individual species abundances, to further maximise the number of possible land-use comparisons by being able to make use of both occurrence and abundance records (which were coerced into presence/absence).

We estimated compositional dissimilarity for each region and between each land use and natural vegetation pair (including natural vegetation with other natural vegetation sites) using a generalised linear mixed effects model (Eq. 2). Differently to our models of diversity, we modelled dissimilarity with a zero-and-one-inflated beta distribution as the variable is bounded by zero and one and was found to be inflated at these boundaries. Since between-study differences in sampling methods and taxa studied may lead to different levels of zero- and one-inflation, we modelled the zero- and one-inflation parameters of the model with study-level random intercepts (Equation 2). Furthermore, we included the geographical distance between site pairs as an explanatory variable to account for the fact that nearby assemblages are expected to share more species than distant assemblages. Similarly to Newbold et al. (2016), we randomised the order of pairwise comparisons of sites 100 times, which obtained 100 instantiations of our dataset, and thus 100 individual model fits. For each model, we sampled 100 predictions from the posterior distribution, keeping geographical distance fixed at the mean. Median values and

95% credible intervals were then computed over the full range of the 10,000 (100 models × 100 posterior samples) predictions.

$$
\begin{aligned}
\text{Dissimilarity} &\sim \text{Land use pair} \times \text{Region} + \text{GeoDistance} + (1|\text{Study}) \\
\text{beta(zero inflation)} &\sim (1|\text{Study}) \\
\text{beta(one inflation)} &\sim (1|\text{Study})
\end{aligned}
\tag{2}
$$

2.5 Range extent

We computed range extent estimates for arthropods in Europe and North America from observation data from the Global Biodiversity Information Facility (GBIF, 2024a,b), which we filtered to include only presences and exclude fossil and living specimens (e.g., from zoos). This was done by computing a convex hull around the observation points using the R package `concaveman` (Gombin et al., 2020, version 1.1.0), and then summing the total area of the hull using `terra` (Hijmans, 2024, version 1.8.60). Range extent examples for four selected species are provided in Fig. S16. We obtained range extents for 3579 out of 4098 arthropods from the PREDICTS database for Europe (297,672 records), and 1859 out of 2141 arthropods for North America (93,644 records). We divided these data into two categories, based on the percentiles within each region: Narrow range (percentiles 0–50%; 1790 species and 124,953 records in Europe; 930 species and 46,139 records in North America) and wide range (percentiles 50–100%; 1789 species and 172,719 records in Europe; 929 species and 47,505 records in North America). Diversity metrics (richness, abundance and Simpson's index) were then modelled for each region individually with linear mixed effects models of land use and range extent as interactive fixed effects (Eq. 3).

$$
\text{Diversity} \sim \text{Land use} \times \text{Range extent} + (1|\text{Study/Block}) \tag{3}
$$

2.6 Habitat specificity

We obtained data on habitat specificity for European arthropods from the European habitat assessments of the International Union for Conservation of Nature (IUCN) Red List of Threatened Species (IUCN (International Union for Conservation of Nature), 2024). Habitat requirements are unknown for the majority of arthropod species, even in well-studied regions like Europe and

Table 2: Weighting table used to estimate habitat specificity from IUCN habitat types. The habitat specificity score HSS is computed as the sum of all weights of habitat types. A high score implies low habitat specificity, and vice versa.

Suitability	Major importance	Weight
Suitable	Yes	1.0
Suitable	No, Unknown or NA	0.5
Marginal or Unknown	-	0.3

North America, which meant that we were able to obtain habitat assessments for only 744 out of 4098 arthropods from the PREDICTS database for Europe (82,696 records). Analogously to Sykes et al. (2020), we then computed a habitat specificity score HSS as a weighted sum of the number of habitat types recorded as being used by a species (Table 2). Due to a scarcity of UICN habitat assessments for North America, we obtained North American assessments from the NatureServe database instead (NatureServe, 2024). This resulted in assessments for 377 out of 2141 arthropods (14,024 records). In this case, we computed HSS by attributing unit weight to each habitat type as the NatureServe assessments do not include measures of 'suitability' or 'major importance'. We divided habitat specificity into two categories: High specificity (HSS percentiles 0–50%) and low specificity (HSS percentiles 50–100%). Although percentiles for Europe and North America are computed from different data sources, we observe high similarity between HSS density plots (Fig. S18) and thus expect a comparison of distributional percentiles to be sensible. Finally, diversity metrics were modelled for each region individually with linear mixed models of land use and habitat specificity as interactive fixed effects (Eq. 4).

$$\text{Diversity} \sim \text{Land use} \times \text{Habitat specificity} + (1|\text{Study/Block}) \tag{4}$$

2.7 Non-native species

Data on non-native species in Europe were obtained from the European Alien Species Information Network (EASIN; European Commission - Joint Research Centre, 2024), which includes all species that are non-native to Europe as determined by the European Commission. These species are not necessarily invasive (i.e., causing harm by outcompeting native species, altering habitats, or spreading disease in a new environment), but can become invasive and thus detrimental to local ecosystems once established. In total, 3389 arthropods species were extracted from the database. Following the extraction from EASIN, we cross-referenced the species names with GBIF to obtain a list of known synonyms for each species. Comparing the full list of species names and synonyms with species records in the PREDICTS database for Europe, we then determined which species in the database are non-native to Europe. In this way, 209 out of the 4098 European arthropods in our subset of the PREDICTS database were identified as non-native (14,000 records). We note that some of the species sampled in PREDICTS and not identified as non-native may actually be non-native, but not recorded in EASIN. Moreover, since the EASIN classifications treat species as either native or non-native to Europe as a whole, we were not able to address cases where species are native in some parts of Europe but non-native in other parts.

For North America, data on non-native species were obtained from the Global Register of Introduced and Invasive Species (GRIIS; Pagad et al., 2018). Extracting data from the contiguous United States (Simpson et al., 2023b), Alaska (Simpson et al., 2023a) and Canada (Pagad, 2022) obtained 3902 arthropod species. After cross-referencing with GBIF and obtaining synonyms, 73 out of the 2141 North American arthropods our subset of the PREDICTS database were identified as non-native (4659 records).

We computed the proportion of non-native species in a site 1) as the proportion of non-native species to the total number of species and 2) as the proportion of the total abundance of non-native species to total abundance of all species in a site. We modelled these variables as a function of land use using a generalised linear mixed effects model with a zero-and-one-inflated beta distribution (Eq. 5). Similarly to our model of compositional similarity, we modelled the zero- and one-inflation parameters of the model with study-level random intercepts.

$$\begin{gathered}\text{Proportion} \sim \text{Land use} + (1|\text{Study/Block}) \\ \text{beta(zero inflation)} \sim (1|\text{Study}) \\ \text{beta(one inflation)} \sim (1|\text{Study})\end{gathered} \tag{5}$$

2.8 Model testing

We inspected model fit by generating observed versus fitted plots and posterior predictive checks, and used Moran's I test to check for residual spatial autocorrelation. We ensured the converge of `brms` models by inspecting R-hat values and visually ensuring that Markov chains were well-mixed. Additionally, we inspected the empirical cumulative distribution function (ECDF) of probability integral transform (PIT) values, which can be interpreted as the Bayesian counterpart to the QQ-plot, to check whether predictive distributions were well-calibrated (deviations from the diagonal can indicate misfit, bias and over- or underdispersion). Information on goodness of fit are summarised for all main models in Table S2 of Supplementary Information A, while individual model diagnostic plots and estimated parameters are available in Supplementary Information B for complete transparency.

3 Results

3.1 Regional responses to land use

Changes in arthropod diversity from primary to secondary vegetation and agricultural land use are significantly negative globally and for most individual regions, with the notable exception of Europe, where diversity responses are not significantly different from primary vegetation, or even significantly positive in the case total abundance change in minimal-use agriculture (Fig. 1). Although diversity in Europe decreases marginally with increasing agricultural use-intensity, changes remain statistically indistinguishable from the primary vegetation baseline (zero) and are substantially elevated over global responses. The fact that a large number of PREDICTS sites stem from agricultural sites in Europe (Fig. 1; samples size), while the samples size for primary vegetation in Europe is comparable to that of other regions (Tables S3 to S5), lends confidence to the accuracy of these responses.

We observe the most consistently negative responses of diversity with agricultural use-intensity for North America, South and Central America, sub-Saharan Africa and South and Southeast Asia. Responses of species richness and total abundance are especially negative in intense-use agriculture in sub-Saharan Africa. Moreover, responses in sub-Saharan Africa are significantly more negative than global responses, which implies that estimating land use impacts of agriculture on biodiversity in the region with global PREDICTS responses would severely underestimate impacts. In North America, declines in evenness (Simpson's diversity index) tend to be more extreme than declines in species richness, which suggests that in addition to substantial changes in species numbers, assemblages in agriculture are disproportionately dominated by few species. To a lesser extent, the same can be observed for Europe. For all other regions, declines in Simpson's diversity tend to be less extreme than declines in species richness. Diversity declines with agricultural use-intensity are less consistent in Australasia,

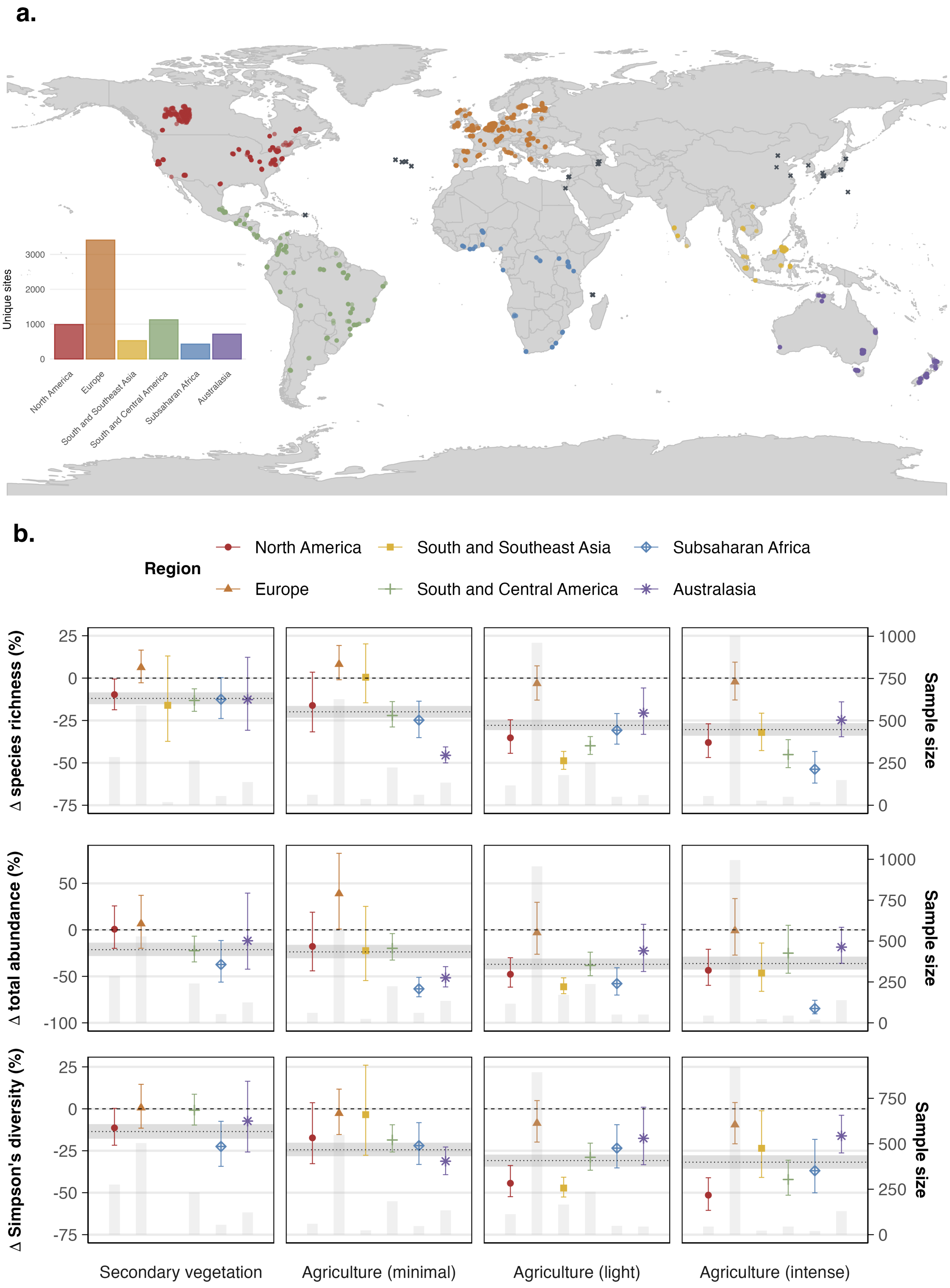

Figure 1: (a) Sites with arthropod records from the PREDICTS database used in this study. Sites discarded from the regional analysis (stemming from regions that lacked enough data and from small islands that were removed following a sensitivity analysis) are displayed as crosses. (b) Responses of species richness, total abundance and Simpson's diversity index per land use and region, relative to primary vegetation. Points indicate median modelled responses and error bars represent 95% credible intervals. Dotted lines indicate global responses, which include sites discarded from the regional analysis (a), with 95% credible intervals shaded. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown.

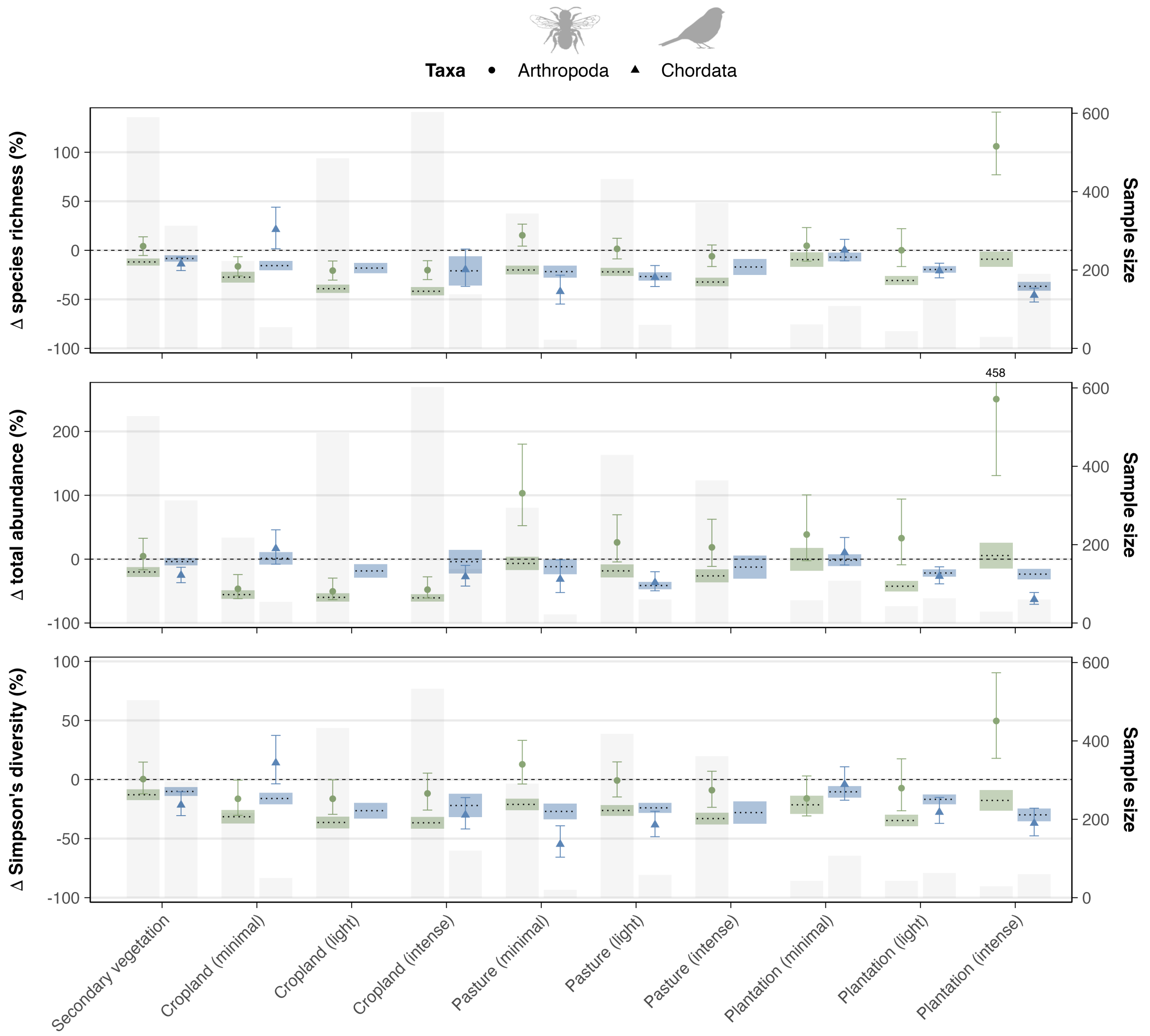

Figure 2: Responses of species richness, total abundance and Simpson's diversity index, relative to primary vegetation, per agricultural land-use type & intensity in Europe, for arthropods (circles), vertebrates (triangles) and plants (squares). Dotted lines indicate global responses, with 95% credible intervals shaded. Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown.

where declines in species richness are significantly negative but changes in total abundance tend to be marginal and non-significant (with the exception of minimal-use agriculture).

Although biodiversity responses to agricultural intensification in Europe show little overall change from primary vegetation (Fig. 1), species richness and total abundance are nevertheless significantly reduced in European cropland (Fig. 2). Positive responses in Europe are, instead, limited to minimal-use pasture and intense-use tree plantations. Nevertheless, responses in all individual agricultural land use types (cropland, pasture and tree plantation) and intensities are consistently elevated over global responses (Fig. 2). Interestingly, responses of arthropod diversity in Europe are not mirrored by vertebrates (phylum Chordata; Fig. 2). In fact, responses of vertebrates in Europe tend to match global responses very closely (with the notable exception of minimal-use cropland).

3.2 Natural habitat availability

The availability of natural habitat surrounding PREDICTS primary vegetation sites in Europe is substantially lower compared to South and Southeast Asia and South and Central America, but is comparable to North America, sub-Saharan Africa and Australasia (Fig. 3b). Natural habitat availability tends to decrease with increasing agricultural use-intensity in all regions. At the same time, the %HANPP of the natural habitat surrounding primary vegetation sites is notably higher in Europe than in most other regions except sub-Saharan Africa. In fact, the %HANPP of natural habitat surrounding European primary vegetation is comparable to that of secondary vegetation and agricultural sites. Furthermore, natural habitat tends to be less aggregated (more fragmented) in Europe (Fig. 3c). Habitat fragmentation is particularly evident when computed for higher natural habitat thresholds, which suggests that it is particularly dense patches of natural vegetation (high coverage of natural habitat) that are fragmented. Results for other habitat connectivity metrics such as mean patch size and patch density are similar although differences between Europe and other regions are smaller (Fig. S4).

It is clear, however, that the sampling of primary vegetation sites in PREDICTS is subject to considerable bias (Fig. 3a). While primary vegetation sites in Europe and the Americas are sampled relatively representatively across the region, South and Southeast Asia and sub-Saharan Africa lack samples from important biodiversity hotspots such as New Guinea and the Congo Basin, and large tracts of wilderness in central (outback) Australia are data-deficient (Fig. S5). Compared to regional averages, natural habitat surrounding PREDICTS primary vegetation sites tends to considerably under-represent wilderness areas while over-representing forestry areas (Fig. S6). In Europe, it is particularly evident that the proportion of wilderness making up natural habitat in the region is lower than in other regions (restricted primarily to patches in the Alps, Iceland and northern Scandinavia; Fig. S5), and that PREDICTS primary vegetation sites severely undersample this wilderness (0.11% of natural habitat surrounding primary vegetation sites within a 5km radius is wilderness versus a regional average of 8.36%; Fig. S6).

Regional averages of the %HANPP of natural habitat are highest in Europe and South and Southeast Asia, but whereas the %HANPP of natural habitat surrounding PREDICTS primary

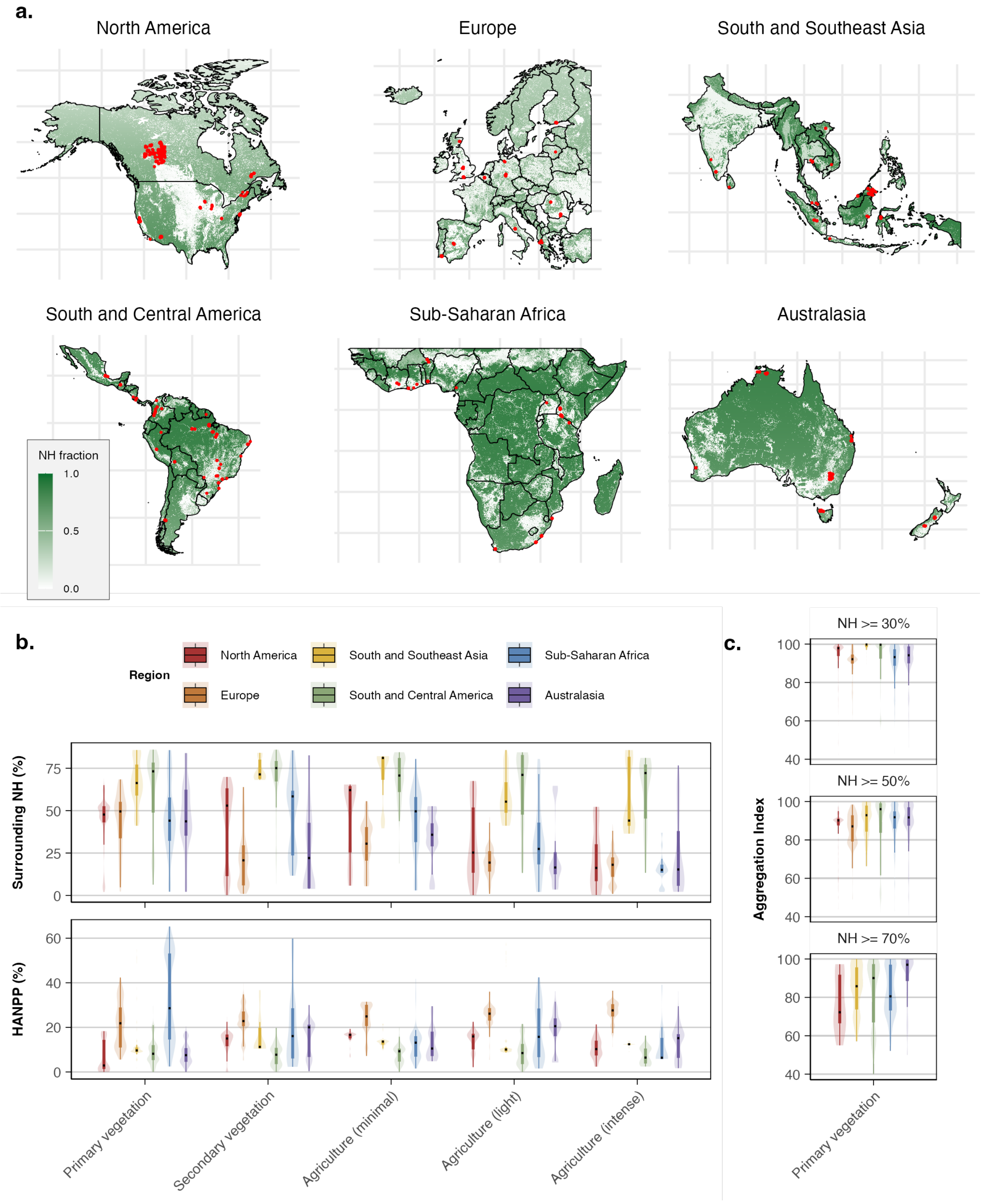

Figure 3: (a): Natural habitat (wilderness, forestry areas and open woodland grazing land) availability in each region, from Matej et al. (2025) for the year 2005, with the primary vegetation sites from PREDICTS that were used in this study plotted as red points. (b): The percentage of surrounding natural habitat and HANPP as a percentage of the potential NPP of natural habitat, within a 5km-radius of PREDICTS sites, separated by land use in each region. (c): Degree of connectivity of natural habitat surrounding primary vegetation sites within a larger 10km-radius buffer, estimated with the aggregation index (He et al., 2000) and shown for three different thresholds of natural habitat. Europe is missing from the 70% threshold as there were no PREDICTS primary vegetation sites in Europe with natural habitat exceeding 70% anywhere within a 5-km buffer. (b) and (c) show violin plots of the data distributions, overlaid on box and whisker plots with the median values plotted as black lines.

vegetation sites in Europe is considerably elevated above the regional average, the opposite is true in South and Southeast Asia (Fig. S7), suggesting that PREDICTS primary vegetation sites are biased towards higher use-intensity in Europe and towards lower use-intensity in South and Southeast Asia. Moreover, we observe a strong bias of PREDICTS primary vegetation sites in sub-Saharan Africa towards higher %HANPP and thus use-intensity (particularly for forestry), such that %HANPP surrounding primary vegetation sites is comparable with Europe, although regional averages are considerably lower. These sampling biases help explain why the average %HANPP surrounding a site tends to be higher in primary vegetation sites in sub-Saharan Africa than in Europe (Fig. 3b). In the Americas, %HANPP values of natural habitat surrounding PREDICTS primary vegetation samples mirrors regional averages fairly well, but wilderness areas are nevertheless undersampled and forestry areas oversampled (Fig. S6).

3.3 Species Composition

In Europe, compositional dissimilarity between minimal-use agriculture and natural vegetation (primary and secondary vegetation) is 41.9% (95% credible interval: [29.8, 55.7]) higher than the baseline dissimilarity between natural vegetation and other natural vegetation sites (Fig. 4). This dissimilarity is overwhelmingly the result of species turnover, which suggests that arthropod assemblages in minimal-use agriculture tend to consist of novel, possibly more disturbance-tolerant species not found in natural vegetation. Fitting the models against individual land-use types in Europe shows that this turnover stems predominantly from cropland and pasture sites, while higher compositional similarity is observed between natural vegetation and tree plantations (Fig. S10). At increasing agricultural use-intensities in Europe, we observe more homogeneity between agriculture and natural vegetation as total dissimilarity and turnover drop to comparable levels as the natural vegetation baseline. However, sample sizes of dissimilarity between natural vegetation and intense-use agriculture tend to be very small (in all regions), which means that these responses are uncertain and unlikely to be representative.

In comparison, increasing agricultural intensification in North America is not associated with significant differences in overall compositional dissimilarity (although this may partly reflect limited sample sizes). Nevertheless, median nestedness in both light- and intense-use agriculture is considerably elevated above the baseline, indicating that compositional differences primarily reflect species loss rather than turnover. This mirrors significant declines in richness observed with agricultural intensification (Fig. 1) and thus suggests that assemblages

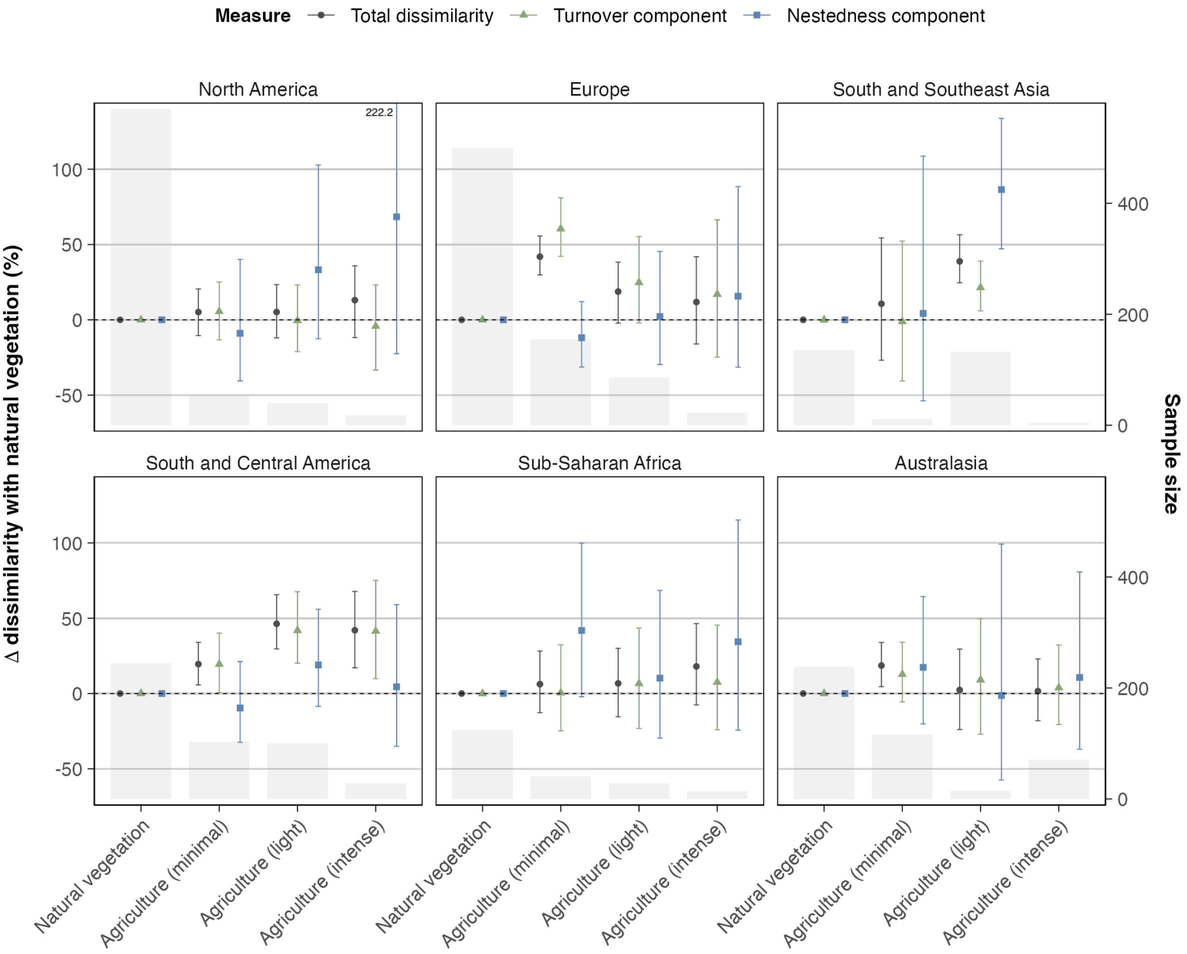

Figure 4: Compositional dissimilarity (Sørensen's Index) of each land use with natural vegetation (primary and secondary vegetation) per region, shown relative to the dissimilarity of natural vegetation with other natural vegetation sites (%). A more positive relative response of turnover indicates that dissimilarity is driven more by species replacement, whereas a more positive relative response of nestedness indicates that dissimilarity is driven more by species loss (i.e., the extent to which composition in one land use is a subset of the other). Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown.

in light- and intense-use agriculture tend to represent species-poor subsets of those found in natural vegetation. Increased compositional dissimilarity comparable to that found in European minimal-use agriculture can also be observed in South and Southeast Asia (light-use agriculture) and in South and Central America (light- and intense-use agriculture), each coinciding with substantial biodiversity declines (Fig. 1). The dominant components of this dissimilarity differ, however: in South and Southeast Asia, dissimilarity is driven primarily by nestedness, whereas in South and Central America it is dominated by turnover. Nevertheless, where sample sizes are larger, relative responses of species richness and total abundance to agricultural land use tend to be positively associated with relative responses of species turnover and negatively with nestedness (Fig. S11 and Fig. S12).

3.4 Effects of range extent, habitat specificity and non-native species

In Europe, we observe highly significant differences between the responses of species richness and total abundance of narrow-and wide-ranging species, and species with high- and low habitat specificity (Fig. 5): Wide-ranging species and habitat generalists (low habitat specificity) are associated with substantial increases in agricultural sites relative to primary vegetation, while narrow-ranging species and habitat specialists (high habitat specificity) are associated with considerable declines. In North America, on the other hand, differences in responses between these groups of species is negligible: Both narrow- and wide-ranging species, and both habitat generalists and specialists are associated with declines in species richness and total abundance in agriculture. Further analysis per individual land-use types in Europe, which were estimable for cropland and pasture, highlights that differences in responses tend to be considerably larger in cropland than in pasture (Fig. S14), which suggests that it is particularly in cropland that wide-ranging species and habitat generalists are able to outcompete narrow-ranging species and habitat specialists.

In both regions, the proportion of non-native species as a fraction of species richness is slightly elevated in light- and intense-use agriculture over primary vegetation, but this is only significant in North America (Fig. 5, right and top). Slight increases over primary vegetation can also be observed for non-native proportions as a fraction of total abundance, but these are not significant in either region (Fig. 5, right and bottom). Indeed, for North America, it should be noted that sample sizes are small and thus 95% credible intervals can be large. In absolute terms, however, the proportion of non-native species is consistently higher in Europe than in

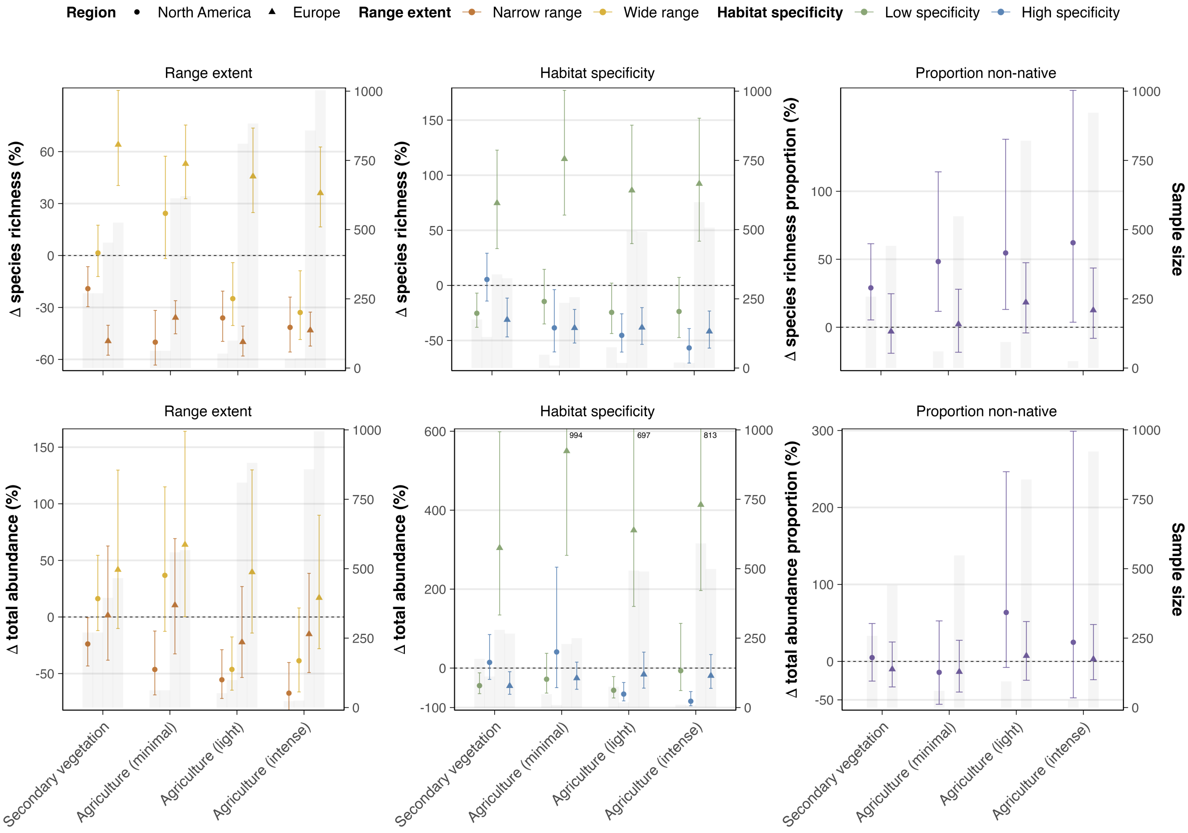

Figure 5: Comparison of European and North American arthropod diversity responses (species richness and total abundance) to agricultural land use, relative to primary vegetation. Shown are the responses of species with narrow and wide range extents (left; range extents below or above the median, respectively), species with low or high habitat specificity (centre; habitat specificity scores above or below the median, respectively), and the relative proportion of non-native species in a given site, either as a fraction of species richness (top) or of total abundance (bottom). Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites). Only model coefficients computed from at least 10 sites are shown.

North America, particularly in primary vegetation, although credible intervals largely overlap (Fig. S13).

4 Discussion

This analysis has revealed important differences in the biodiversity responses of arthropods to agricultural land use between large world regions. Our results show that in Europe, overall arthropod diversity in agricultural sites is comparable to primary vegetation, and tends to be higher in minimal-use agriculture, while other regions, and global averages, tend to show significant declines (Fig. 1). However, while responses in Europe are consistently more positive than global averages, non-negative responses in Europe are limited to pasture and plantation sites, while richness and abundance are nevertheless significantly reduced in cropland (Fig. 2). Similar variation between land use types is likely to exist in other regions, but a lack of data currently prohibits such comparisons. These results mirror previous findings of land-use impacts on insects in Germany, where changes in biomass and richness were found to be most negative in arable fields, followed by meadow and forest, and, overall, agricultural landscapes were found to be higher in biomass (although not richness) than semi-natural ones (Uhler et al., 2021). Thus, our finding of biodiversity gains in minimal-use agriculture in Europe is not entirely unexpected. Indeed, it has long been understood that low-intensity environmental disturbance can benefit ecological diversity, as stipulated by the intermediate disturbance hypothesis (Connell, 1978). In fact, mixed natural and agricultural landscapes typically boast a higher diversity of habitats than the original vegetation – habitat diversity being one of strongest predictors of ecological diversity (Thomas, 2013).

Our regional analysis of natural habitat and %HANPP suggest that the representativeness of primary vegetation sites sampled for arthropods in the PREDICTS database is relatively poor in all investigated regions, showing bias towards low proportions of wilderness and high %HANPP (use-intensity). This selection bias is likely the result of accessibility issues, given that intact primary vegetation in wilderness areas are neither easy to sample, nor in close proximity to other land-use types of interest (e.g., agricultural or urban areas). This suggests that, in addition to real shifts in baseline biodiversity that may reduce differences in biodiversity between natural and anthropogenic land use types, the compounding effect of sampling bias towards more accessible, and thus often more degraded, primary vegetation suggests that biodiversity estimates in primary vegetation are likely to be underestimates. This implies that estimates of biodiversity change between primary vegetation and agricultural sites are, too, likely to be underestimates (the only exception to this is South and Southeast Asia, where %HANPP of natural habitat surrounding PREDICTS primary vegetation sites is considerably lower than the regional average, and thus biodiversity in primary vegetation may be overestimated for the region). This underestimation of biodiversity change for most of the world's regions is concerning, given that our estimates of richness and abundance change between primary vegetation and intense-use agriculture are already high (e.g., median reductions of 53.5% in species richness and 84.6% in total abundance in sub-Saharan Africa; Fig. 1). This may have important implications for previous studies of land use impacts on biodiversity using the PREDICTS database, which are typically measured relative to primary vegetation sites (e.g., Millard et al., 2021; Newbold et al., 2015; Outhwaite et al., 2022).

Our analysis of compositional dissimilarity showed that biodiversity gains in minimal-use agriculture in Europe coincide with significant species turnover compared with natural vegetation, whereas dissimilarity between natural habitat and light- or intense-use agriculture is comparable to that among natural habitats, suggesting that increasing agricultural use-intensity is not necessarily associated with greater compositional divergence.(Fig. 4). This demonstrates the limitations of commonly used diversity metrics such as species richness and total abundance, which may show little overall change despite important compositional changes (Fletcher Jr. et al., 2025), but it also highlights that on average, assemblages found in natural vegetation in Europe are no more compositionally dissimilar than intensively farmed agricultural land is to natural vegetation, which suggests that baseline diversity in primary vegetation in Europe may be considerably degraded. Indeed, in comparison with North America, primary vegetation in Europe is more fragmented and subject to considerably higher %HANPP (Fig. 3). Furthermore, proportions of non-native species, which tend to establish more easily in disturbed habitats (Liu et al., 2023), are considerably higher in primary vegetation in Europe than in North America (Fig. S13). The investigation into European arthropod characteristics showed that biodiversity gains in agriculture are predominantly associated with wide-ranging habitat-generalists, while narrow-ranged species and habitat specialists are marked by significant declines (Fig. 5). Taken together, this paints a picture of winners and losers, and widespread ecosystem transformation, despite little overall change in biodiversity metrics such as richness, abundance and evenness between primary vegetation and agricultural sites (Fig. 1). Indeed, as a result of widespread ecosystem transformation, primary vegetation may cease to function as an ecologically informative baseline, and important declines in the diversity of native habitat specialists may become masked by increases of (possibly non-native) widespread habitat generalists.

We may compare these findings with North America, where we observe large declines in arthropod diversity in light- and intense-use agriculture (Fig. 1), no evidence of turnover between natural vegetation and agricultural sites (Fig. 4), and only a marginal effect of range extent and habitat specificity (Fig. 5). This suggests that North American ecosystems, natural or anthropogenic, have possibly undergone less transformation, perhaps as a result of a more recent history of land-use change. Interestingly, we did find significant increases in the proportion of non-native species with increasing agricultural land-use intensity, which may drive changes in species composition in the future. We do note, however, that the PREDICTS data for North America contained records for only a very small number of the total number of non-native arthropod species obtained for North America from the GRIIS database (73 out of 3902 species), which means that absolute model predictions of non-native proportions are almost certainly underestimates. Similarly, we were only able to obtain data on habitat specificity for very few species in North America, and these data were heavily biased towards Hymenopteran species in both regions, which suggests that the presented biodiversity responses may not be representative estimates for other arthropod orders (Fig. S19). Range extents were obtained for a larger group of species, whose distributions of taxonomic orders better reflect the complete distributions for each region (Fig. S2 and Fig. S17). It should also be noted that within-study comparisons between natural vegetation and agricultural sites, from which compositional dissimilarity was estimated, were scarce in all regions (Fig. 4). This is particularly evident for Europe, where agricultural sites are otherwise very well sampled (Fig. 1). This highlights an important data deficiency, which will need to be addressed by future studies in order to allow for more reliable estimates of compositional change between natural vegetation and anthropogenic land-use types.

The positive biodiversity responses of arthropods in intense-use tree plantations in Europe (Fig. 2) appear to stand at odds with the finding that forest species respond particularly negatively to agricultural intensification (Fig. **??**). It should be noted, however, that the European arthropod data from intense-use plantation stems from a single study, which is a study on micro-arthropods sampled from soil cores in the Netherlands, which suggests it is unlikely to be representative. It is notable, however, that almost half (42.3%) of PREDICTS data on arthropods in Europe was sampled from soil cores, but none of these data were sampled in primary vegetation, which may draw into question the extent to which responses between primary vegetation and other land-use types can be reliably compared. We thus refitted our models on PREDICTS data from without soil core samples, but found that this did not meaningfully change biodiversity–land use responses (Fig. S23 and Fig. S24).

Finally, it is interesting that European biodiversity responses of vertebrates differ substantially from those of arthropods (Fig. 2). We did not investigate the responses of vertebrates further in this work, and thus can only speculate on possible reasons for this disparity, but possible explanations may be linked to the ability of arthropods to successfully exploit microhabitats in agricultural landscapes (García-Tejero and Taboada, 2016) or to characteristically short lifespans and rapid reproduction rates, which allow populations to rebound quickly after declines.

5 Conclusion

In this study, we have found considerable differences in the responses of arthropod diversity to agricultural land use and intensity between major world regions, which emphasise that Europe exhibits minimal declines with agricultural intensification. As the best-sampled region in our dataset with major influence over global biodiversity statistics, which go on to be used in integrated assessments to estimate the impacts of land-use change on biodiversity and ecosystem provisions, it is important to understand these findings better. We have found evidence consistent with the hypothesis that a long history of land-use change in Europe and associated deforestation of wild forests has resulted in natural vegetation that is composed of very little true wilderness, and is more fragmented and subject to higher use-intensity than in other regions. Our results support the hypothesis that this history of land-use change and agricultural expansion has primarily benefited wide-ranging habitat generalists and non-native species, while specialists of the forested natural habitat that was once widely available on the landmass have been largely filtered out. At the same time, we have found that primary vegetation sites sampled for arthropod records in the PREDICTS database tend to be biased towards natural habitat that is subject to considerably higher use-intensity than regional averages and is composed of disproportionately low proportions of wilderness area. With the exception of South and Southeast Asia, these biases suggest that biodiversity estimates in primary vegetation are likely to be underestimates, and thus changes in biodiversity relative to primary vegetation are also likely to be underestimates. Despite suspected shift in baselines and sampling biases, our results do highlight the possible value that minimal-use agriculture in Europe, such as organic, regenerative and mixed-cropping systems may hold to arthropod diversity, where large species turnover compared with natural vegetation points to distinct assemblages that may have adapted well to low-intensity disturbance.

Our results underscore the complexity and nuance of modelling and estimating threats to local biodiversity. Moreover, the heterogeneity in responses apparent between regions and species groups echoes the findings of mixed biodiversity trends worldwide (Johnson et al., 2024; Klink et al., 2020; Martins et al., 2022) and reinforce the picture that environmental and ecosystem change in the Anthropocene can boost local biodiversity (Thomas, 2013), at the same time as species are globally being lost at an unprecedented rate (Dirzo et al., 2014; Wagner et al., 2021). In Europe, changes in species composition appear to have resulted in novel arthropod assemblages that may prove to be resilient to low-intensity agricultural disturbance and well-adapted to open and mixed-use landscapes. For global analyses of impacts of land use on insect or arthropod diversity, which tend to be biased towards the European continent, this implies, however, that global estimates of biodiversity change likely underestimate land-use driven declines in most of the world's major regions, while overestimating declines for the European continent. As such, region-specific analyses appear necessary to avoid masking important regional variations in ecological responses. This aim is conditional, however, on a considerable increase in systematic biodiversity sampling in many of the world's regions, since most are currently severely undersampled, hindering robust statistical analysis.

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Supplementary Information A

Contents

A Tables

A.1 PREDICTS definitions of land use types and intensities

Table S1: Definitions of land use types and levels of intensity used by PREDICTS database (Hudson et al., 2017).

Land use	Definition	Minimal use	Light use	Intense use
Primary vegetation	PRIMARY vegetation (forest or non-forest) is native vegetation that is not known or inferred to have ever been completely destroyed, before the year in which the biodiversity was sampled, by human actions or by extreme natural events that do not normally play a role in ecosystem dynamics. Sites where primary vegetation has been destroyed by natural events that are part of the normal ecosystem dynamic (e.g. fire in Mediterranean ecosystems) remain as primary vegetation provided that colonization from adjacent habitat and regeneration is possible. Sites in urban and suburban settings where the vegetation has never been completely destroyed should also be classed as primary vegetation. Synonyms include “ancient woodland”, “old-growth forest” and “natural grassland” (unless any indication is given of a previous land use class). Primary vegetation can be used by people (e.g., fruit harvesting, selective logging). Primary vegetation includes sites where people have tried to restore degraded habitat, so long as the native vegetation has never been destroyed. Sites where the original vegetation is known to have been completely destroyed should not be classed as primary vegetation.	Any disturbances identified are very minor (e.g., a trail or path) or very limited in the scope of their effect (e.g., hunting of a particular species of limited ecological importance).	One or more disturbances of moderate intensity (e.g., selective logging) or breadth of impact (e.g., bushmeat extraction), which are not severe enough to markedly change the nature of the ecosystem. Primary sites in suburban settings are at least Light use.	One or more disturbances that is severe enough to markedly change the nature of the ecosystem; this includes clear-felling of part of the site too recently for much recovery to have occurred. Primary sites in fully urban settings should be classed as Intense use.

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Land use	Definition	Minimal use	Light use	Intense use
Secondary vegetation	SECONDARY vegetation is where the original primary vegetation was completely destroyed. This could be by human actions (including fire), and includes where sites are recovering to a natural state following a period of human-dominated land use (cropland, plantation forest, pasture or urban). Also counted as secondary are places where natural events (fires, storms etc.) have destroyed the vegetation, but not where the vegetation is naturally maintained by fire (such as climatically Mediterranean systems), which would be primary. Secondary vegetation includes areas where humans have made an active attempt (through planting etc.) to return an area where the natural vegetation was previously destroyed to a more natural state. Synonyms include “old-field”, “abandoned” and “fallow”. Although not managed as intensively as the human-dominated classes, such sites can be used by people in much the same way as primary vegetation sites.	As for Primary Vegetation-Minimal use	As for Primary Vegetation-Light use	As for Primary Vegetation-Intense use
Cropland	CROPLAND is land that people have planted with herbaceous crops, even if these crops will be fed to livestock once harvested. Sites described as “fields”, “arable”, “ploughed” or “tilled” all qualify as cropland. If cropland is abandoned, including temporary abandonment (i.e. fallow), it becomes Secondary vegetation.	Low-intensity farms, typically with small fields, mixed crops, crop rotation, little or no inorganic fertiliser use, little or no pesticide use, little or no ploughing, little or no irrigation, little or no mechanisation.	Medium intensity farming, typically showing some but not many of the following: large fields, annual ploughing, inorganic fertiliser application, pesticide application, irrigation, no crop rotation, mechanisation, monoculture crop. Organic farms in developed countries often fall within this category, as may high-intensity farming in developing countries.	High-intensity monoculture farming, typically showing many of the following features: large fields, annual ploughing, inorganic fertiliser application, pesticide application, irrigation, mechanisation, no crop rotation.

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Land use	Definition	Minimal use	Light use	Intense use
Pasture	PASTURE is land where livestock is known to be grazed regularly or permanently. The plant species may be predominantly native (as in rangelands) or strongly associated with humans (as in European-style pastures). Land that is planted with a crop for harvesting and subsequently feeding to livestock is Cropland, not Pasture. However, if vegetation is planted and livestock are grazed directly on this vegetation, then this does count as pasture.	Pasture with minimal input of fertiliser and pesticide, and with low stock density (not high enough to cause significant disturbance or to stop regeneration of vegetation).	Pasture either with significant input of fertiliser or pesticide, or with high stock density (high enough to cause significant disturbance or to stop regeneration of vegetation).	Pasture with significant input of fertiliser or pesticide, and with high stock density (high enough to cause significant disturbance or to stop regeneration of vegetation).
Plantation forest	PLANTATION FOREST applies to previously cleared areas that people have planted with crop trees or crop shrubs for commercial or subsistence harvesting of wood and/or fruit. The species planted may or may not be native. Planting an area with native woody plants for habitat restoration rather than for goods does not constitute plantation forest; rather this would be secondary vegetation with the stage dependent on the architectural complexity (see definitions under secondary vegetation). Likewise, natural regrowth is not a plantation forest, even if the regrowth will be harvested. If plantation forest is abandoned, it becomes Secondary vegetation – and may have a greater architectural complexity than the time since abandonment might suggest.	Extensively managed or mixed timber, fruit/coffee, oil-palm or rubber plantations in which native understorey and/or other native tree species are tolerated, which are not treated with pesticide or fertiliser, and which have not been recently (¡ 20 years) clear-felled.	Monoculture fruit/coffee/rubber plantations with limited pesticide input, or mixed species plantations with significant inputs. Monoculture timber plantations of mixed age with no recent (¡ 20 years) clear-felling. Monoculture oil-palm plantations with no recent (¡ 20 years) clear-felling.	Monoculture fruit/coffee/rubber plantations with significant pesticide input. Monoculture timber plantations with similarly aged trees or timber/oil-palm plantations with extensive recent (¡ 20 years) clear-felling.

A.2 Model diagnostic summaries

Table S2: Summaries of model fit (R^2) and convergence (R-hat values) for the main models fitted in this study.

Model	Distribution family	Model equation	Conditional R^2	Marginal R^2	R-hats	nSites
Global model of species richness	zero_inflated_negbinomial	Species_richness ~ UI2 + (1 | SS/SSB), zi ~ 1	0.905 (95% CI [0.893, 0.912])	0.005 (95% CI [0.003, 0.007])	1.00-1.01	7604
Regional model of species richness	zero_inflated_negbinomial	Species_richness ~ UI2 * Region + (1 | SS/SSB), zi ~ 1	0.918 (95% CI [0.908, 0.925])	0.025 (95% CI [0.006, 0.059])	1	7188
Global model of total abundance	gaussian	LogAbund ~ UI2 + (1 | SS/SSB)	0.905 (95% CI [0.903, 0.907])	0.005 (95% CI [0.003, 0.006])	1.00-1.01	7122
Regional model of total abundance	gaussian	LogAbund ~ UI2 * Region + (1 | SS/SSB)	0.910 (95% CI [0.908, 0.912])	0.053 (95% CI [0.023, 0.086])	1.00-1.01	6751
Global model of Simpson's diversity	gaussian	LogSimp ~ UI2 + (1 | SS/SSB)	0.694 (95% CI [0.685, 0.702])	0.035 (95% CI [0.027, 0.043])	1	6726
Regional model of Simpson's diversity	gaussian	LogSimp ~ UI2 * Region + (1 | SS/SSB)	0.707 (95% CI [0.699, 0.716])	0.056 (95% CI [0.036, 0.084])	1	6355
Global model of species richness (individual land use types, phylum: Arthropoda)	zero_inflated_negbinomial	Species_richness ~ LU + (1 | SS/SSB), zi ~ 1	0.903 (95% CI [0.892, 0.911])	0.008 (95% CI [0.005, 0.011])	1	7604
Europe model of species richness (individual land use types, phylum: Arthropoda)	zero_inflated_negbinomial	Species_richness ~ LU + (1 | SS/SSB), zi ~ 1	0.917 (95% CI [0.908, 0.924])	0.007 (95% CI [0.003, 0.012])	1	3412
Global model of total abundance (individual land use types, phylum: Arthropoda)	gaussian	LogAbund ~ LU + (1 | SS/SSB)	0.907 (95% CI [0.905, 0.909])	0.018 (95% CI [0.014, 0.022])	1.00-1.01	7122
Europe model of total abundance (individual land use types, phylum: Arthropoda)	gaussian	LogAbund ~ LU + (1 | SS/SSB)	0.938 (95% CI [0.937, 0.940])	0.025 (95% CI [0.019, 0.032])	1.00-1.01	3211
Global model of Simpson's diversity (individual land use types, phylum: Arthropoda)	gaussian	LogSimp ~ LU + (1 | SS/SSB)	0.694 (95% CI [0.686, 0.702])	0.044 (95% CI [0.034, 0.055])	1.00-1.01	6726
Europe model of Simpson's diversity (individual land use types, phylum: Arthropoda)	gaussian	LogSimp ~ LU + (1 | SS/SSB)	0.690 (95% CI [0.677, 0.703])	0.020 (95% CI [0.010, 0.032])	1	3032
Global model of species richness (individual land use types, phylum: Chordata)	zero_inflated_negbinomial	Species_richness ~ LU + (1 | SS/SSB), zi ~ 1	0.855 (95% CI [0.848, 0.862])	0.011 (95% CI [0.007, 0.015])	1	7842
Europe model of species richness (individual land use types, phylum: Chordata)	zero_inflated_negbinomial	Species_richness ~ LU + (1 | SS/SSB), zi ~ 1	0.850 (95% CI [0.837, 0.861])	0.084 (95% CI [0.031, 0.160])	1	1157
Global model of total abundance (individual land use types, phylum: Chordata)	gaussian	LogAbund ~ LU + (1 | SS/SSB)	0.838 (95% CI [0.834, 0.841])	0.008 (95% CI [0.006, 0.010])	1.00-1.01	7007
Europe model of total abundance (individual land use types, phylum: Chordata)	gaussian	LogAbund ~ LU + (1 | SS/SSB)	0.790 (95% CI [0.778, 0.801])	0.052 (95% CI [0.035, 0.070])	1	966
Global model of Simpson's diversity (individual land use types, phylum: Chordata)	gaussian	LogSimp ~ LU + (1 | SS/SSB)	0.749 (95% CI [0.743, 0.755])	0.019 (95% CI [0.014, 0.024])	1	6708
Europe model of Simpson's diversity (individual land use types, phylum: Chordata)	gaussian	LogSimp ~ LU + (1 | SS/SSB)	0.769 (95% CI [0.756, 0.782])	0.057 (95% CI [0.036, 0.082])	1	923

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Model	Distribution family	Model equation	Conditional R^2	Marginal R^2	R-hats	nSites
Regional model of total dissimilarity	zero_one_inflated_beta	Dissimilarity ~ LU * Region + Dist_geo + (1 | SS), zoi ~ (1 | SS), coi ~ (1 | SS)	0.434 (95% CI [0.412, 0.457])	0.102 (95% CI [0.071, 0.136])	1	2858
Regional model of turnover	zero_one_inflated_beta	Turnover ~ LU * Region + Dist_geo + (1 | SS), zoi ~ (1 | SS), coi ~ (1 | SS)	0.368 (95% CI [0.344, 0.391])	0.074 (95% CI [0.049, 0.104])	1	2858
Regional model of nestedness	zero_one_inflated_beta	Nestedness ~ LU * Region + Dist_geo + (1 | SS), zoi ~ (1 | SS), coi ~ (1 | SS)	0.155 (95% CI [0.134, 0.177])	0.036 (95% CI [0.019, 0.061])	1	2858
Europe model of species richness and range extent	zero_inflated_negbinomial	Species_richness ~ UI2 * Quants + (1 | SS/SSB), zi ~ 1	0.800 (95% CI [0.780, 0.820])	0.037 (95% CI [0.021, 0.056])	1.00-1.01	6114
North America model of species richness and range extent	zero_inflated_negbinomial	Species_richness ~ UI2 * Quants + (1 | SS/SSB), zi ~ 1	0.848 (95% CI [0.831, 0.861])	0.005 (95% CI [0.001, 0.012])	1	1697
Europe model of total abundance and range extent	gaussian	LogAbund ~ UI2 * Quants + (1 | SS/SSB)	0.825 (95% CI [0.820, 0.830])	0.030 (95% CI [0.026, 0.034])	1	5741
North America model of total abundance and range extent	gaussian	LogAbund ~ UI2 * Quants + (1 | SS/SSB)	0.581 (95% CI [0.559, 0.600])	0.023 (95% CI [0.011, 0.037])	1	1677
Europe model of species richness and habitat specificity	zero_inflated_negbinomial	Species_richness ~ UI2 * Quants + (1 | SS/SSB), zi ~ 1	0.757 (95% CI [0.747, 0.767])	0.044 (95% CI [0.023, 0.073])	1	3389
North America model of species richness and habitat specificity	zero_inflated_negbinomial	Species_richness ~ UI2 * Quants + (1 | SS/SSB), zi ~ 1	0.646 (95% CI [0.610, 0.677])	0.040 (95% CI [0.007, 0.102])	1	605
Europe model of total abundance and habitat specificity	gaussian	LogAbund ~ UI2 * Quants + (1 | SS/SSB)	0.693 (95% CI [0.683, 0.704])	0.126 (95% CI [0.114, 0.138])	1	3233
North America model of total abundance and habitat specificity	gaussian	LogAbund ~ UI2 * Quants + (1 | SS/SSB)	0.630 (95% CI [0.595, 0.663])	0.061 (95% CI [0.032, 0.101])	1	585
Europe model of non-native proportions of richness	zero_one_inflated_beta	SiteSpeciesProps ~ UI2 + (1 | SS/SSB), zoi ~ (1 | SS), coi ~ (1 | SS)	0.353 (95% CI [0.309, 0.402])	0.003 (95% CI [2.961e-04, 0.008])	1	2837
North America model of non-native proportions of richness	zero_one_inflated_beta	SiteSpeciesProps ~ UI2 + (1 | SS/SSB), zoi ~ (1 | SS), coi ~ (1 | SS)	0.658 (95% CI [0.552, 0.715])	0.002 (95% CI [7.614e-08, 0.012])	1	832
Europe model of non-native proportions of abundance	zero_one_inflated_beta	SiteTotAbunProps ~ UI2 + (1 | SS/SSB), zoi ~ (1 | SS), coi ~ (1 | SS)	0.364 (95% CI [0.313, 0.412])	0.004 (95% CI [1.334e-04, 0.010])	1	2837
North America model of non-native proportions of abundance	zero_one_inflated_beta	SiteTotAbunProps ~ UI2 + (1 | SS/SSB), zoi ~ (1 | SS), coi ~ (1 | SS)	0.576 (95% CI [0.440, 0.648])	0.003 (95% CI [2.082e-06, 0.027])	1	832

A.3 Regional responses

Table S3: Regional responses of species richness to land use, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Global	Primary vegetation	0.0	NA	NA	166	1908
Global	Secondary vegetation	-12.0	-15.7	-8.3	174	1488
Global	Agriculture (minimal)	-19.9	-23.2	-16.1	108	1201
Global	Agriculture (light)	-27.8	-31.0	-24.9	145	1691
Global	Agriculture (intense)	-30.4	-33.8	-26.7	94	1316
Europe	Primary vegetation	0.0	NA	NA	22	230
Europe	Secondary vegetation	5.5	-3.4	14.6	61	590
Europe	Agriculture (minimal)	7.3	-1.5	17.0	40	628
Europe	Agriculture (light)	-4.0	-12.4	5.8	51	961
Europe	Agriculture (intense)	-3.2	-12.5	7.2	46	1003
North America	Primary vegetation	0.0	NA	NA	23	469
North America	Secondary vegetation	-9.9	-18.7	0.3	19	285
North America	Agriculture (minimal)	-16.3	-33.3	4.2	6	62
North America	Agriculture (light)	-35.1	-45.1	-23.7	16	117
North America	Agriculture (intense)	-37.9	-47.8	-26.6	13	55
South and Southeast Asia	Primary vegetation	0.0	NA	NA	30	264
South and Southeast Asia	Secondary vegetation	-16.1	-35.5	11.1	7	18
South and Southeast Asia	Agriculture (minimal)	0.5	-15.0	18.9	8	36
South and Southeast Asia	Agriculture (light)	-48.9	-54.2	-43.3	12	179
South and Southeast Asia	Agriculture (intense)	-32.1	-42.5	-20.0	6	28
South and Central America	Primary vegetation	0.0	NA	NA	56	335
South and Central America	Secondary vegetation	-13.0	-19.9	-6.5	57	265
South and Central America	Agriculture (minimal)	-22.1	-28.6	-14.3	32	223
South and Central America	Agriculture (light)	-39.7	-44.8	-34.0	40	252
South and Central America	Agriculture (intense)	-45.1	-52.9	-36.2	11	50
Subsaharan Africa	Primary vegetation	0.0	NA	NA	17	241
Subsaharan Africa	Secondary vegetation	-11.6	-23.2	1.2	8	54
Subsaharan Africa	Agriculture (minimal)	-24.8	-34.8	-14.5	11	62
Subsaharan Africa	Agriculture (light)	-30.2	-38.1	-21.3	9	50
Subsaharan Africa	Agriculture (intense)	-53.5	-61.9	-43.0	6	19

Continued on next page

Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Australasia	Primary vegetation	0.0	NA	NA	10	232
Australasia	Secondary vegetation	-13.0	-31.7	12.2	10	136
Australasia	Agriculture (minimal)	-45.4	-50.0	-41.0	5	134
Australasia	Agriculture (light)	-20.1	-32.2	-5.8	10	61
Australasia	Agriculture (intense)	-24.7	-34.9	-14.0	11	149

Table S4: Regional responses of total abundance to land use, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Global	Primary vegetation	0.0	NA	NA	146	1711
Global	Secondary vegetation	-21.3	-28.1	-13.8	162	1363
Global	Agriculture (minimal)	-23.7	-30.6	-16.1	103	1131
Global	Agriculture (light)	-37.1	-42.5	-30.9	136	1640
Global	Agriculture (intense)	-36.2	-42.7	-28.8	88	1277
Europe	Primary vegetation	0.0	NA	NA	19	161
Europe	Secondary vegetation	6.6	-19.9	37.1	56	528
Europe	Agriculture (minimal)	39.0	0.9	82.3	37	570
Europe	Agriculture (light)	-3.0	-26.2	29.6	49	957
Europe	Agriculture (intense)	-0.8	-27.2	33.6	45	995
North America	Primary vegetation	0.0	NA	NA	22	443
North America	Secondary vegetation	0.7	-19.9	25.7	19	285
North America	Agriculture (minimal)	-17.8	-44.1	19.0	6	62
North America	Agriculture (light)	-47.8	-61.6	-30.0	16	117
North America	Agriculture (intense)	-43.5	-59.7	-20.9	12	45
South and Southeast Asia	Primary vegetation	0.0	NA	NA	22	230
South and Southeast Asia	Secondary vegetation	-39.6	-73.8	34.3	5	5
South and Southeast Asia	Agriculture (minimal)	-22.4	-54.5	25.2	6	24
South and Southeast Asia	Agriculture (light)	-61.2	-68.6	-51.6	10	171
South and Southeast Asia	Agriculture (intense)	-46.5	-66.1	-14.2	4	23
South and Central America	Primary vegetation	0.0	NA	NA	52	308
South and Central America	Secondary vegetation	-22.4	-34.5	-6.8	55	241
South and Central America	Agriculture (minimal)	-19.8	-32.5	-4.0	32	223
South and Central America	Agriculture (light)	-38.2	-49.3	-24.0	37	238

Continued on next page

Region	Land use	Median	2.5%	97.5%	nStudies	nSites
South and Central America	Agriculture (intense)	-25.0	-46.7	4.9	10	44
Subsaharan Africa	Primary vegetation	0.0	NA	NA	16	235
Subsaharan Africa	Secondary vegetation	-37.3	-56.2	-11.5	8	54
Subsaharan Africa	Agriculture (minimal)	-63.5	-72.0	-51.1	11	62
Subsaharan Africa	Agriculture (light)	-57.8	-70.1	-40.7	9	50
Subsaharan Africa	Agriculture (intense)	-84.6	-90.3	-75.8	6	19
Australasia	Primary vegetation	0.0	NA	NA	8	212
Australasia	Secondary vegetation	-11.7	-42.3	39.5	8	125
Australasia	Agriculture (minimal)	-51.6	-61.4	-39.6	5	134
Australasia	Agriculture (light)	-22.6	-44.8	5.9	9	51
Australasia	Agriculture (intense)	-18.6	-36.0	2.7	10	139

Table S5: Regional responses of Simpson's diversity index to land use, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Global	Primary vegetation	0.0	NA	NA	146	1597
Global	Secondary vegetation	-13.6	-17.8	-9.1	161	1320
Global	Agriculture (minimal)	-24.4	-28.2	-20.2	101	1056
Global	Agriculture (light)	-30.9	-34.5	-27.3	136	1558
Global	Agriculture (intense)	-31.8	-35.7	-27.7	88	1195
Europe	Primary vegetation	0.0	NA	NA	19	161
Europe	Secondary vegetation	0.6	-11.5	14.6	56	504
Europe	Agriculture (minimal)	-2.7	-15.3	11.7	37	550
Europe	Agriculture (light)	-8.5	-19.8	4.9	49	894
Europe	Agriculture (intense)	-9.5	-20.8	3.8	45	923
North America	Primary vegetation	0.0	NA	NA	22	436
North America	Secondary vegetation	-11.3	-21.7	0.3	19	276
North America	Agriculture (minimal)	-17.3	-32.7	3.6	5	60
North America	Agriculture (light)	-44.4	-52.4	-33.8	16	113
North America	Agriculture (intense)	-51.5	-60.5	-41.1	12	45
South and Southeast Asia	Primary vegetation	0.0	NA	NA	22	230
South and Southeast Asia	Secondary vegetation	-13.7	-44.8	35.7	5	5
South and Southeast Asia	Agriculture (minimal)	-3.5	-27.7	26.0	6	24

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Region	Land use	Median	2.5%	97.5%	nStudies	nSites
South and Southeast Asia	Agriculture (light)	-47.2	-52.6	-40.8	10	166
South and Southeast Asia	Agriculture (intense)	-23.5	-40.9	-1.1	4	23
South and Central America	Primary vegetation	0.0	NA	NA	52	286
South and Central America	Secondary vegetation	-0.8	-9.7	8.7	54	233
South and Central America	Agriculture (minimal)	-18.6	-25.7	-9.5	32	184
South and Central America	Agriculture (light)	-28.9	-36.6	-20.5	37	236
South and Central America	Agriculture (intense)	-42.1	-51.5	-30.6	10	44
Subsaharan Africa	Primary vegetation	0.0	NA	NA	16	154
Subsaharan Africa	Secondary vegetation	-22.4	-34.3	-7.4	8	54
Subsaharan Africa	Agriculture (minimal)	-21.9	-33.2	-8.2	10	48
Subsaharan Africa	Agriculture (light)	-23.4	-35.2	-9.5	9	49
Subsaharan Africa	Agriculture (intense)	-36.9	-50.1	-18.2	6	19
Australasia	Primary vegetation	0.0	NA	NA	8	208
Australasia	Secondary vegetation	-7.3	-25.7	16.4	8	123
Australasia	Agriculture (minimal)	-31.2	-39.2	-22.8	5	134
Australasia	Agriculture (light)	-17.6	-33.3	0.9	9	44
Australasia	Agriculture (intense)	-16.1	-26.3	-3.8	10	129

A.4 Regional responses per land use type and intensity

Table S6: Global and European responses of species richness to land use for arthropods and vertebrates, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Arthropoda	Global	Primary vegetation	0.0	NA	NA	166	1908
Arthropoda	Global	Secondary vegetation	-11.9	-15.6	-8.2	174	1488
Arthropoda	Global	Cropland (minimal)	-27.4	-32.8	-21.8	43	364
Arthropoda	Global	Cropland (light)	-39.1	-43.3	-34.7	58	697
Arthropoda	Global	Cropland (intense)	-41.8	-45.9	-37.5	52	716
Arthropoda	Global	Pasture (minimal)	-20.0	-24.4	-15.3	44	664
Arthropoda	Global	Pasture (light)	-22.0	-25.9	-17.8	63	641
Arthropoda	Global	Pasture (intense)	-32.3	-36.6	-27.8	29	461
Arthropoda	Global	Plantation (minimal)	-9.5	-16.9	-2.2	43	173
Arthropoda	Global	Plantation (light)	-30.8	-35.2	-26.1	45	353
Arthropoda	Global	Plantation (intense)	-9.1	-16.6	-1.2	22	139
Arthropoda	Europe	Primary vegetation	0.0	NA	NA	22	230
Arthropoda	Europe	Secondary vegetation	4.2	-5.3	13.8	61	590
Arthropoda	Europe	Cropland (minimal)	-16.4	-26.2	-6.5	23	223
Arthropoda	Europe	Cropland (light)	-20.7	-30.4	-10.9	26	485
Arthropoda	Europe	Cropland (intense)	-20.2	-29.9	-10.6	33	603
Arthropoda	Europe	Pasture (minimal)	15.3	4.3	26.7	21	344
Arthropoda	Europe	Pasture (light)	1.5	-8.7	12.3	25	432
Arthropoda	Europe	Pasture (intense)	-6.1	-16.5	5.4	18	371
Arthropoda	Europe	Plantation (minimal)	4.6	-11.1	23.2	11	61
Arthropoda	Europe	Plantation (light)	0.1	-16.5	22.0	8	44
Arthropoda	Europe	Plantation (intense)	106.0	77.0	141.0	1	29
Chordata	Global	Primary vegetation	0.0	NA	NA	173	3473
Chordata	Global	Secondary vegetation	-8.4	-11.6	-5.1	91	1348
Chordata	Global	Cropland (minimal)	-15.6	-19.9	-10.5	20	319
Chordata	Global	Cropland (light)	-18.1	-23.4	-12.9	17	135
Chordata	Global	Cropland (intense)	-20.9	-34.5	-4.7	5	146
Chordata	Global	Pasture (minimal)	-21.7	-27.6	-15.3	19	142
Chordata	Global	Pasture (light)	-26.7	-31.0	-22.4	24	308
Chordata	Global	Pasture (intense)	-17.0	-24.9	-8.7	10	109

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Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Chordata	Global	Plantation (minimal)	-6.9	-11.2	-2.2	33	490
Chordata	Global	Plantation (light)	-19.6	-23.1	-16.2	46	985
Chordata	Global	Plantation (intense)	-36.8	-41.2	-32.1	22	387
Chordata	Europe	Primary vegetation	0.0	NA	NA	7	147
Chordata	Europe	Secondary vegetation	-13.9	-20.6	-7.0	6	313
Chordata	Europe	Cropland (minimal)	21.3	1.5	44.0	1	54
Chordata	Europe	Cropland (intense)	-19.7	-36.7	1.3	1	138
Chordata	Europe	Pasture (minimal)	-42.0	-54.8	-25.3	2	22
Chordata	Europe	Pasture (light)	-27.5	-36.9	-15.5	4	60
Chordata	Europe	Pasture (intense)	0.7	-45.5	69.4	1	1
Chordata	Europe	Plantation (minimal)	0.3	-10.8	11.2	4	108
Chordata	Europe	Plantation (light)	-20.9	-28.1	-13.2	6	124
Chordata	Europe	Plantation (intense)	-45.8	-52.7	-38.6	5	190

Table S7: Global and European responses of total abundance to land use for arthropods and vertebrates, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Arthropoda	Global	Primary vegetation	0.0	NA	NA	146	1711
Arthropoda	Global	Secondary vegetation	-20.1	-27.2	-11.6	162	1363
Arthropoda	Global	Cropland (minimal)	-55.5	-61.7	-48.4	41	358
Arthropoda	Global	Cropland (light)	-59.8	-65.6	-52.6	58	697
Arthropoda	Global	Cropland (intense)	-60.6	-66.4	-55.1	50	705
Arthropoda	Global	Pasture (minimal)	-6.7	-17.2	3.8	41	614
Arthropoda	Global	Pasture (light)	-18.3	-27.8	-7.1	58	624
Arthropoda	Global	Pasture (intense)	-26.2	-36.2	-15.9	27	448
Arthropoda	Global	Plantation (minimal)	-0.3	-17.5	18.6	41	159
Arthropoda	Global	Plantation (light)	-42.3	-49.5	-33.1	40	319
Arthropoda	Global	Plantation (intense)	5.6	-13.0	27.6	19	124
Arthropoda	Europe	Primary vegetation	0.0	NA	NA	19	161
Arthropoda	Europe	Secondary vegetation	4.7	-16.6	32.7	56	528
Arthropoda	Europe	Cropland (minimal)	-46.5	-61.9	-24.1	22	218
Arthropoda	Europe	Cropland (light)	-50.4	-63.4	-29.7	26	485
Arthropoda	Europe	Cropland (intense)	-47.7	-60.9	-27.6	32	602

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Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Arthropoda	Europe	Pasture (minimal)	103.2	52.4	180.1	18	294
Arthropoda	Europe	Pasture (light)	26.2	-4.4	69.5	23	429
Arthropoda	Europe	Pasture (intense)	18.5	-11.4	62.5	17	364
Arthropoda	Europe	Plantation (minimal)	38.6	-2.4	100.6	10	58
Arthropoda	Europe	Plantation (light)	32.9	-8.8	94.2	7	43
Arthropoda	Europe	Plantation (intense)	250.6	130.9	458.1	1	29
Chordata	Global	Primary vegetation	0.0	NA	NA	156	3045
Chordata	Global	Secondary vegetation	-3.8	-9.5	2.2	81	1209
Chordata	Global	Cropland (minimal)	1.3	-8.1	11.6	20	319
Chordata	Global	Cropland (light)	-18.4	-28.2	-6.9	14	131
Chordata	Global	Cropland (intense)	-3.9	-21.1	16.2	5	146
Chordata	Global	Pasture (minimal)	-11.8	-22.8	0.6	18	139
Chordata	Global	Pasture (light)	-41.3	-46.8	-35.2	24	308
Chordata	Global	Pasture (intense)	-12.4	-27.2	8.8	10	109
Chordata	Global	Plantation (minimal)	-1.7	-10.3	8.0	30	477
Chordata	Global	Plantation (light)	-21.7	-27.7	-15.8	38	875
Chordata	Global	Plantation (intense)	-23.4	-31.2	-14.5	19	249
Chordata	Europe	Primary vegetation	0.0	NA	NA	7	147
Chordata	Europe	Secondary vegetation	-25.1	-36.8	-12.6	6	313
Chordata	Europe	Cropland (minimal)	16.6	-7.9	46.0	1	54
Chordata	Europe	Cropland (intense)	-27.4	-42.1	-9.8	1	138
Chordata	Europe	Pasture (minimal)	-31.3	-52.3	-1.0	2	22
Chordata	Europe	Pasture (light)	-36.5	-49.5	-19.7	4	60
Chordata	Europe	Pasture (intense)	6.7	-65.3	228.9	1	1
Chordata	Europe	Plantation (minimal)	10.2	-9.2	33.9	4	108
Chordata	Europe	Plantation (light)	-26.8	-38.6	-12.0	5	63
Chordata	Europe	Plantation (intense)	-63.0	-70.7	-52.2	4	60

Table S8: Global and European responses of Simpson's diversity index to land use for arthropods and vertebrates, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient.

Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Arthropoda	Global	Primary vegetation	0.0	NA	NA	146	1597
Arthropoda	Global	Secondary vegetation	-12.9	-17.4	-8.2	161	1320

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Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Arthropoda	Global	Cropland (minimal)	-31.5	-37.0	-25.5	38	331
Arthropoda	Global	Cropland (light)	-36.3	-41.3	-31.2	58	645
Arthropoda	Global	Cropland (intense)	-36.6	-41.3	-31.2	50	634
Arthropoda	Global	Pasture (minimal)	-21.1	-26.0	-16.1	41	584
Arthropoda	Global	Pasture (light)	-26.2	-30.6	-21.6	57	605
Arthropoda	Global	Pasture (intense)	-33.1	-37.8	-27.7	27	442
Arthropoda	Global	Plantation (minimal)	-21.4	-28.2	-12.7	40	141
Arthropoda	Global	Plantation (light)	-34.7	-39.5	-29.7	40	308
Arthropoda	Global	Plantation (intense)	-17.7	-26.8	-9.2	19	119
Arthropoda	Europe	Primary vegetation	0.0	NA	NA	19	161
Arthropoda	Europe	Secondary vegetation	0.4	-12.1	14.8	56	504
Arthropoda	Europe	Cropland (minimal)	-16.3	-30.3	-0.5	21	216
Arthropoda	Europe	Cropland (light)	-16.3	-29.5	-0.2	26	433
Arthropoda	Europe	Cropland (intense)	-11.8	-25.9	5.4	32	533
Arthropoda	Europe	Pasture (minimal)	12.8	-3.8	33.1	18	291
Arthropoda	Europe	Pasture (light)	-0.8	-14.8	14.9	23	418
Arthropoda	Europe	Pasture (intense)	-9.0	-23.5	7.0	17	361
Arthropoda	Europe	Plantation (minimal)	-16.0	-30.8	3.0	9	43
Arthropoda	Europe	Plantation (light)	-7.3	-26.4	17.5	7	43
Arthropoda	Europe	Plantation (intense)	49.6	17.9	90.4	1	29
Chordata	Global	Primary vegetation	0.0	NA	NA	156	2953
Chordata	Global	Secondary vegetation	-10.1	-13.9	-6.4	81	1093
Chordata	Global	Cropland (minimal)	-16.1	-20.9	-11.0	20	313
Chordata	Global	Cropland (light)	-26.4	-32.6	-19.1	14	131
Chordata	Global	Cropland (intense)	-22.0	-31.1	-11.2	5	128
Chordata	Global	Pasture (minimal)	-27.0	-33.6	-20.3	18	134
Chordata	Global	Pasture (light)	-24.0	-28.1	-19.6	24	299
Chordata	Global	Pasture (intense)	-28.0	-37.2	-18.2	10	109
Chordata	Global	Plantation (minimal)	-10.4	-15.3	-5.4	30	476
Chordata	Global	Plantation (light)	-16.8	-20.8	-12.3	38	833
Chordata	Global	Plantation (intense)	-29.9	-34.8	-24.0	18	239
Chordata	Europe	Primary vegetation	0.0	NA	NA	7	147
Chordata	Europe	Secondary vegetation	-21.6	-30.5	-10.4	6	297
Chordata	Europe	Cropland (minimal)	14.2	-3.6	37.3	1	50
Chordata	Europe	Cropland (intense)	-30.0	-41.8	-15.3	1	120

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Taxa	Region	Land use	Median	2.5%	97.5%	nStudies	nSites
Chordata	Europe	Pasture (minimal)	-54.8	-65.7	-39.2	2	20
Chordata	Europe	Pasture (light)	-38.3	-48.4	-26.9	4	58
Chordata	Europe	Pasture (intense)	-29.9	-70.1	67.0	1	1
Chordata	Europe	Plantation (minimal)	-4.1	-17.5	10.8	4	107
Chordata	Europe	Plantation (light)	-27.7	-37.1	-15.2	5	63
Chordata	Europe	Plantation (intense)	-36.9	-47.7	-24.3	4	60

A.5 Compositional dissimilarity

Table S9: Compositional dissimilarity (total, turnover and nestedness) for each region and land use compared with natural vegetation, relative to the dissimilarity between natural vegetation and other natural vegetation sites within the same region (median, 2.5% and 97.5% percentiles of model responses), and number of sites per coefficient.

Measure	Region	Land use	median	lower	upper	nSites
Total dissimilarity	Europe	Natural vegetation	0.0	0.0	0.0	500
Total dissimilarity	Europe	Agriculture (minimal)	41.9	29.8	55.7	155
Total dissimilarity	Europe	Agriculture (light)	18.8	-2.2	38.3	86
Total dissimilarity	Europe	Agriculture (intense)	11.8	-16.0	41.9	23
Total dissimilarity	North America	Natural vegetation	0.0	0.0	0.0	570
Total dissimilarity	North America	Agriculture (minimal)	5.2	-10.5	20.5	54
Total dissimilarity	North America	Agriculture (light)	5.2	-11.9	23.3	40
Total dissimilarity	North America	Agriculture (intense)	13.1	-11.8	35.8	18
Total dissimilarity	South and Southeast Asia	Natural vegetation	0.0	0.0	0.0	136
Total dissimilarity	South and Southeast Asia	Agriculture (minimal)	10.6	-26.8	54.4	11
Total dissimilarity	South and Southeast Asia	Agriculture (light)	38.8	24.7	56.5	132
Total dissimilarity	South and Southeast Asia	Agriculture (intense)	NA	NA	NA	5
Total dissimilarity	South and Central America	Natural vegetation	0.0	0.0	0.0	245
Total dissimilarity	South and Central America	Agriculture (minimal)	19.5	5.7	33.9	103
Total dissimilarity	South and Central America	Agriculture (light)	46.3	29.6	65.6	100
Total dissimilarity	South and Central America	Agriculture (intense)	42.0	17.1	67.8	28
Total dissimilarity	Sub-Saharan Africa	Natural vegetation	0.0	0.0	0.0	124
Total dissimilarity	Sub-Saharan Africa	Agriculture (minimal)	6.2	-12.7	28.2	41
Total dissimilarity	Sub-Saharan Africa	Agriculture (light)	6.7	-15.4	30.0	28
Total dissimilarity	Sub-Saharan Africa	Agriculture (intense)	18.0	-7.6	46.4	14
Total dissimilarity	Australasia	Natural vegetation	0.0	0.0	0.0	238
Total dissimilarity	Australasia	Agriculture (minimal)	18.6	4.5	33.9	116
Total dissimilarity	Australasia	Agriculture (light)	2.3	-23.9	29.5	15
Total dissimilarity	Australasia	Agriculture (intense)	1.6	-18.1	23.0	70
Nestedness component	Europe	Natural vegetation	0.0	0.0	0.0	500
Nestedness component	Europe	Agriculture (minimal)	-11.9	-31.3	12.0	155
Nestedness component	Europe	Agriculture (light)	2.2	-29.6	45.4	86
Nestedness component	Europe	Agriculture (intense)	15.7	-31.4	88.4	23
Nestedness component	North America	Natural vegetation	0.0	0.0	0.0	570

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Measure	Region	Land use	median	lower	upper	nSites
Nestedness component	North America	Agriculture (minimal)	-9.0	-40.5	40.1	54
Nestedness component	North America	Agriculture (light)	33.3	-12.5	102.7	40
Nestedness component	North America	Agriculture (intense)	68.4	-22.5	222.2	18
Nestedness component	South and Southeast Asia	Natural vegetation	0.0	0.0	0.0	136
Nestedness component	South and Southeast Asia	Agriculture (minimal)	4.2	-53.8	108.7	11
Nestedness component	South and Southeast Asia	Agriculture (light)	86.5	47.2	133.7	132
Nestedness component	South and Southeast Asia	Agriculture (intense)	NA	NA	NA	5
Nestedness component	South and Central America	Natural vegetation	0.0	0.0	0.0	245
Nestedness component	South and Central America	Agriculture (minimal)	-9.6	-32.4	21.2	103
Nestedness component	South and Central America	Agriculture (light)	18.9	-8.5	56.0	100
Nestedness component	South and Central America	Agriculture (intense)	4.4	-35.0	59.0	28
Nestedness component	Sub-Saharan Africa	Natural vegetation	0.0	0.0	0.0	124
Nestedness component	Sub-Saharan Africa	Agriculture (minimal)	41.8	-2.1	99.8	41
Nestedness component	Sub-Saharan Africa	Agriculture (light)	10.2	-29.6	68.4	28
Nestedness component	Sub-Saharan Africa	Agriculture (intense)	34.3	-24.4	115.2	14
Nestedness component	Australasia	Natural vegetation	0.0	0.0	0.0	238
Nestedness component	Australasia	Agriculture (minimal)	17.4	-20.2	64.4	116
Nestedness component	Australasia	Agriculture (light)	-1.3	-57.3	99.2	15
Nestedness component	Australasia	Agriculture (intense)	10.6	-37.0	80.7	70
Turnover component	Europe	Natural vegetation	0.0	0.0	0.0	500
Turnover component	Europe	Agriculture (minimal)	60.4	42.1	81.0	155
Turnover component	Europe	Agriculture (light)	24.8	-2.0	55.3	86
Turnover component	Europe	Agriculture (intense)	17.0	-24.9	66.4	23
Turnover component	North America	Natural vegetation	0.0	0.0	0.0	570
Turnover component	North America	Agriculture (minimal)	5.6	-13.3	25.1	54
Turnover component	North America	Agriculture (light)	-0.4	-21.1	23.2	40
Turnover component	North America	Agriculture (intense)	-4.2	-33.4	23.2	18
Turnover component	South and Southeast Asia	Natural vegetation	0.0	0.0	0.0	136
Turnover component	South and Southeast Asia	Agriculture (minimal)	-1.1	-40.7	52.2	11
Turnover component	South and Southeast Asia	Agriculture (light)	21.4	5.9	39.0	132
Turnover component	South and Southeast Asia	Agriculture (intense)	NA	NA	NA	5
Turnover component	South and Central America	Natural vegetation	0.0	0.0	0.0	245
Turnover component	South and Central America	Agriculture (minimal)	19.5	0.6	40.0	103
Turnover component	South and Central America	Agriculture (light)	41.9	20.1	67.7	100
Turnover component	South and Central America	Agriculture (intense)	41.5	9.8	75.2	28

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Measure	Region	Land use	median	lower	upper	nSites
Turnover component	Sub-Saharan Africa	Natural vegetation	0.0	0.0	0.0	124
Turnover component	Sub-Saharan Africa	Agriculture (minimal)	0.5	-24.8	32.3	41
Turnover component	Sub-Saharan Africa	Agriculture (light)	6.6	-23.1	43.4	28
Turnover component	Sub-Saharan Africa	Agriculture (intense)	7.6	-23.9	45.4	14
Turnover component	Australasia	Natural vegetation	0.0	0.0	0.0	238
Turnover component	Australasia	Agriculture (minimal)	12.8	-5.6	34.1	116
Turnover component	Australasia	Agriculture (light)	9.1	-26.9	49.6	15
Turnover component	Australasia	Agriculture (intense)	3.9	-20.6	32.2	70

A.6 Effects of range extent, habitat specificity and non-native proportions

Table S10: Responses of species richness to land use for Europe and North America, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient. Prop. non-native: The proportion of non-native species as a fraction of species richness at a site.

Region	Category	Land use	Median	2.5%	97.5%	nStudies	nSites
Europe	Narrow range	Primary vegetation	0.0	NA	NA	16	174
Europe	Narrow range	Secondary vegetation	-49.4	-57.6	-40.3	42	453
Europe	Narrow range	Agriculture (minimal)	-35.9	-45.2	-26.1	37	613
Europe	Narrow range	Agriculture (light)	-49.9	-58.1	-40.8	37	810
Europe	Narrow range	Agriculture (intense)	-43.2	-52.3	-32.7	38	858
Europe	Wide range	Primary vegetation	0.0	NA	NA	16	174
Europe	Wide range	Secondary vegetation	64.0	40.4	95.4	49	525
Europe	Wide range	Agriculture (minimal)	53.0	32.8	75.4	38	621
Europe	Wide range	Agriculture (light)	45.7	24.8	73.6	43	883
Europe	Wide range	Agriculture (intense)	36.1	16.5	62.7	46	1003
Europe	High specificity	Primary vegetation	0.0	NA	NA	7	77
Europe	High specificity	Secondary vegetation	-31.2	-46.7	-11.5	20	324
Europe	High specificity	Agriculture (minimal)	-38.6	-52.3	-21.8	18	256
Europe	High specificity	Agriculture (light)	-38.2	-53.5	-20.2	26	492
Europe	High specificity	Agriculture (intense)	-41.7	-56.9	-23.3	28	507
Europe	Low specificity	Primary vegetation	0.0	NA	NA	6	66
Europe	Low specificity	Secondary vegetation	74.7	33.4	122.7	21	338
Europe	Low specificity	Agriculture (minimal)	114.8	63.8	177.0	16	235
Europe	Low specificity	Agriculture (light)	86.3	37.9	145.4	26	495
Europe	Low specificity	Agriculture (intense)	92.3	40.1	151.7	29	599
Europe	Prop. non-native	Primary vegetation	0.0	NA	NA	13	105
Europe	Prop. non-native	Secondary vegetation	-3.1	-19.1	24.6	46	441
Europe	Prop. non-native	Agriculture (minimal)	2.3	-18.4	28.0	36	548
Europe	Prop. non-native	Agriculture (light)	18.3	-4.2	47.5	42	821
Europe	Prop. non-native	Agriculture (intense)	12.5	-8.2	43.6	45	922
N. America	Narrow range	Primary vegetation	0.0	NA	NA	19	405
N. America	Narrow range	Secondary vegetation	-19.1	-29.6	-6.5	18	270
N. America	Narrow range	Agriculture (minimal)	-50.1	-63.3	-31.7	6	62

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Region	Category	Land use	Median	2.5%	97.5%	nStudies	nSites
N. America	Narrow range	Agriculture (light)	-36.1	-49.6	-20.6	10	52
N. America	Narrow range	Agriculture (intense)	-41.5	-55.7	-24.0	8	33
N. America	Wide range	Primary vegetation	0.0	NA	NA	20	409
N. America	Wide range	Secondary vegetation	1.5	-12.1	17.5	18	270
N. America	Wide range	Agriculture (minimal)	24.4	-1.8	57.4	6	62
N. America	Wide range	Agriculture (light)	-24.9	-40.4	-4.1	13	99
N. America	Wide range	Agriculture (intense)	-32.9	-48.5	-8.8	9	35
N. America	High specificity	Primary vegetation	0.0	NA	NA	7	57
N. America	High specificity	Secondary vegetation	5.4	-14.2	29.2	7	112
N. America	High specificity	Agriculture (minimal)	-38.5	-60.4	-3.9	1	9
N. America	High specificity	Agriculture (light)	-45.3	-60.5	-25.8	4	18
N. America	High specificity	Agriculture (intense)	-56.7	-70.5	-39.2	3	18
N. America	Low specificity	Primary vegetation	0.0	NA	NA	8	73
N. America	Low specificity	Secondary vegetation	-25.3	-38.0	-7.0	8	175
N. America	Low specificity	Agriculture (minimal)	-14.6	-35.0	14.6	2	48
N. America	Low specificity	Agriculture (light)	-24.5	-43.7	2.1	6	75
N. America	Low specificity	Agriculture (intense)	-23.7	-47.3	7.3	4	20
N. America	Prop. non-native	Primary vegetation	0.0	NA	NA	20	395
N. America	Prop. non-native	Secondary vegetation	29.0	5.4	61.4	18	258
N. America	Prop. non-native	Agriculture (minimal)	48.3	11.7	114.3	5	60
N. America	Prop. non-native	Agriculture (light)	54.6	13.1	138.3	13	94
N. America	Prop. non-native	Agriculture (intense)	62.1	3.7	174.2	8	25

Table S11: Responses of total abundance to land use for Europe and North America, relative to primary vegetation (median, 2.5% and 97.5% percentiles of model responses), and number of studies and sites per coefficient. Prop. non-native: The proportion of non-native species as a fraction of total abundance at a site.

Region	Category	Land use	Median	2.5%	97.5%	nStudies	nSites
Europe	Narrow range	Primary vegetation	0.0	NA	NA	13	105
Europe	Narrow range	Secondary vegetation	1.5	-38.2	62.7	39	395
Europe	Narrow range	Agriculture (minimal)	10.5	-32.6	69.2	35	559
Europe	Narrow range	Agriculture (light)	-22.3	-53.4	26.9	37	810
Europe	Narrow range	Agriculture (intense)	-15.1	-49.1	38.6	38	858
Europe	Wide range	Primary vegetation	0.0	NA	NA	13	105

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Region	Category	Land use	Median	2.5%	97.5%	nStudies	nSites
Europe	Wide range	Secondary vegetation	41.8	-10.1	129.7	45	466
Europe	Wide range	Agriculture (minimal)	63.9	0.3	164.1	36	567
Europe	Wide range	Agriculture (light)	39.6	-14.2	129.9	42	881
Europe	Wide range	Agriculture (intense)	17.0	-28.0	89.9	45	995
Europe	High specificity	Primary vegetation	0.0	NA	NA	6	73
Europe	High specificity	Secondary vegetation	-45.2	-66.4	-9.2	17	266
Europe	High specificity	Agriculture (minimal)	-25.4	-53.7	15.1	17	250
Europe	High specificity	Agriculture (light)	-16.1	-50.9	40.4	25	490
Europe	High specificity	Agriculture (intense)	-19.4	-51.3	34.3	27	499
Europe	Low specificity	Primary vegetation	0.0	NA	NA	5	62
Europe	Low specificity	Secondary vegetation	304.4	134.5	598.7	18	280
Europe	Low specificity	Agriculture (minimal)	549.8	285.6	993.7	15	229
Europe	Low specificity	Agriculture (light)	349.2	156.3	697.0	25	493
Europe	Low specificity	Agriculture (intense)	413.7	196.4	813.3	28	591
Europe	Prop. non-native	Primary vegetation	0.0	NA	NA	13	105
Europe	Prop. non-native	Secondary vegetation	-10.1	-33.2	25.2	46	441
Europe	Prop. non-native	Agriculture (minimal)	-13.5	-39.8	27.4	36	548
Europe	Prop. non-native	Agriculture (light)	7.3	-24.5	51.7	42	821
Europe	Prop. non-native	Agriculture (intense)	2.9	-23.8	47.9	45	922
N. America	Narrow range	Primary vegetation	0.0	NA	NA	19	405
N. America	Narrow range	Secondary vegetation	-23.8	-43.3	-0.6	18	270
N. America	Narrow range	Agriculture (minimal)	-46.4	-68.8	-12.4	6	62
N. America	Narrow range	Agriculture (light)	-55.5	-72.0	-28.9	10	52
N. America	Narrow range	Agriculture (intense)	-67.3	-82.5	-40.2	7	23
N. America	Wide range	Primary vegetation	0.0	NA	NA	20	409
N. America	Wide range	Secondary vegetation	16.2	-12.0	54.5	18	270
N. America	Wide range	Agriculture (minimal)	36.8	-12.7	115.0	6	62
N. America	Wide range	Agriculture (light)	-46.3	-64.7	-17.6	13	99
N. America	Wide range	Agriculture (intense)	-38.7	-66.2	8.0	8	25
N. America	High specificity	Primary vegetation	0.0	NA	NA	7	57
N. America	High specificity	Secondary vegetation	14.4	-28.6	85.0	7	112
N. America	High specificity	Agriculture (minimal)	40.9	-49.6	255.6	1	9
N. America	High specificity	Agriculture (light)	-65.9	-83.1	-36.5	4	18
N. America	High specificity	Agriculture (intense)	-84.0	-95.4	-59.6	2	8
N. America	Low specificity	Primary vegetation	0.0	NA	NA	8	73

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Region	Category	Land use	Median	2.5%	97.5%	nStudies	nSites
N. America	Low specificity	Secondary vegetation	-44.5	-64.8	-12.0	8	175
N. America	Low specificity	Agriculture (minimal)	-28.2	-63.3	37.5	2	48
N. America	Low specificity	Agriculture (light)	-56.3	-75.7	-21.6	6	75
N. America	Low specificity	Agriculture (intense)	-6.7	-57.0	113.3	3	10
N. America	Prop. non-native	Primary vegetation	0.0	NA	NA	20	395
N. America	Prop. non-native	Secondary vegetation	4.9	-25.6	49.2	18	258
N. America	Prop. non-native	Agriculture (minimal)	-14.2	-55.7	52.6	5	60
N. America	Prop. non-native	Agriculture (light)	63.6	-7.8	246.4	13	94
N. America	Prop. non-native	Agriculture (intense)	24.8	-47.4	299.0	8	25

B Figures

B.1 Taxonomic representation

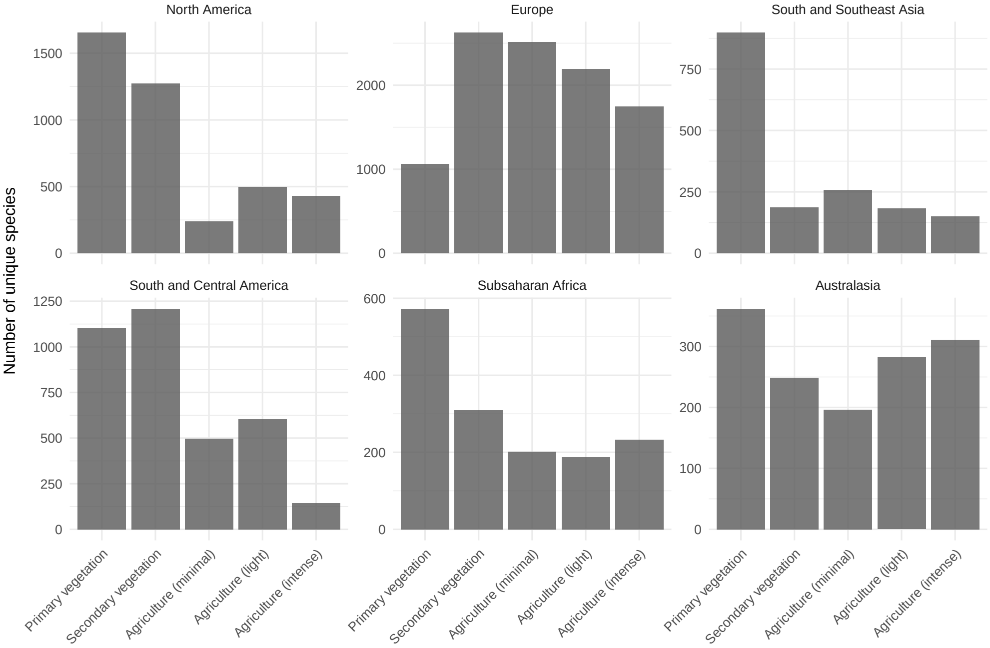


Figure S1: Number of unique arthropod species per land use and region in our dataset of the PREDICTS database.

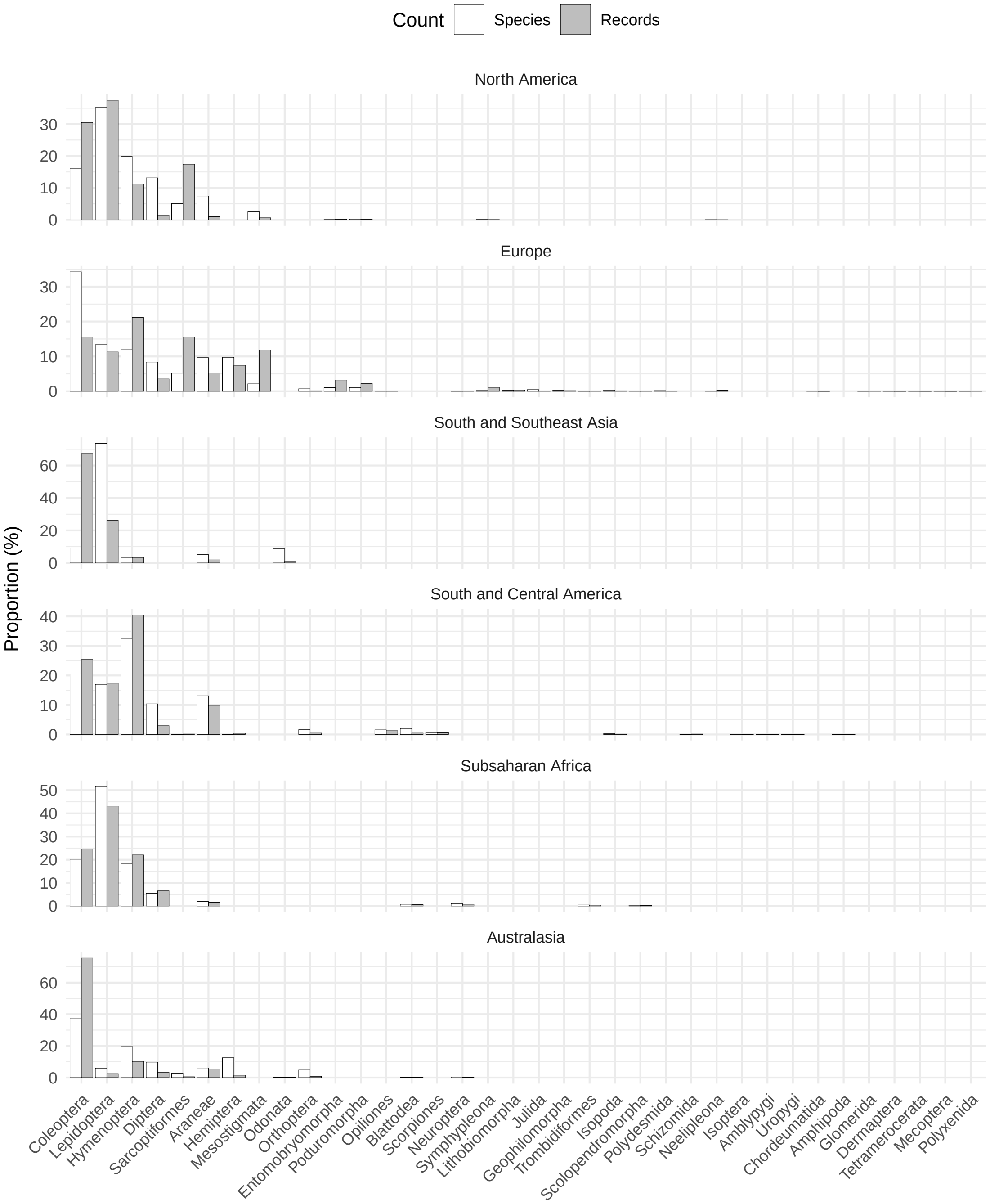


Figure S2: Percentages of unique arthropod species and records per taxonomic order and region, relative to the total per region, in our dataset of the PREDICTS database.

B.2 Vertebrate records

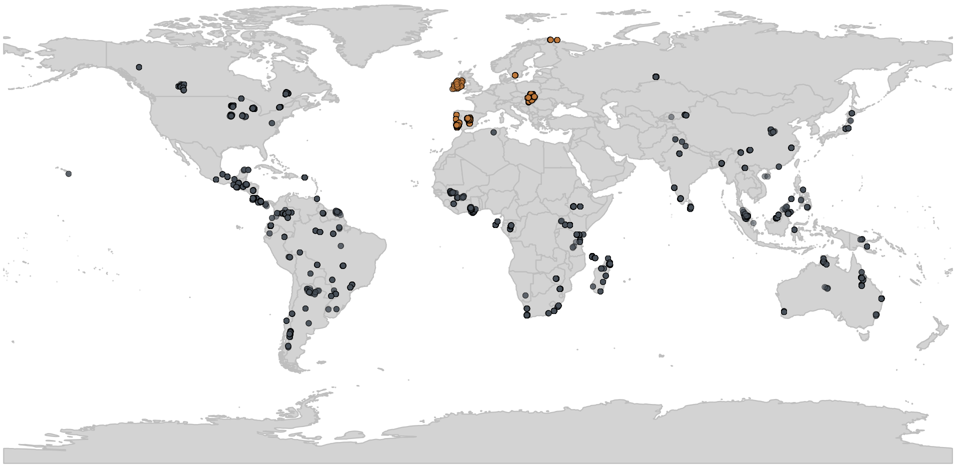


Figure S3: Sites with vertebrate records (phylum Chordata) from the PREDICTS database.

B.3 Natural habitat availability

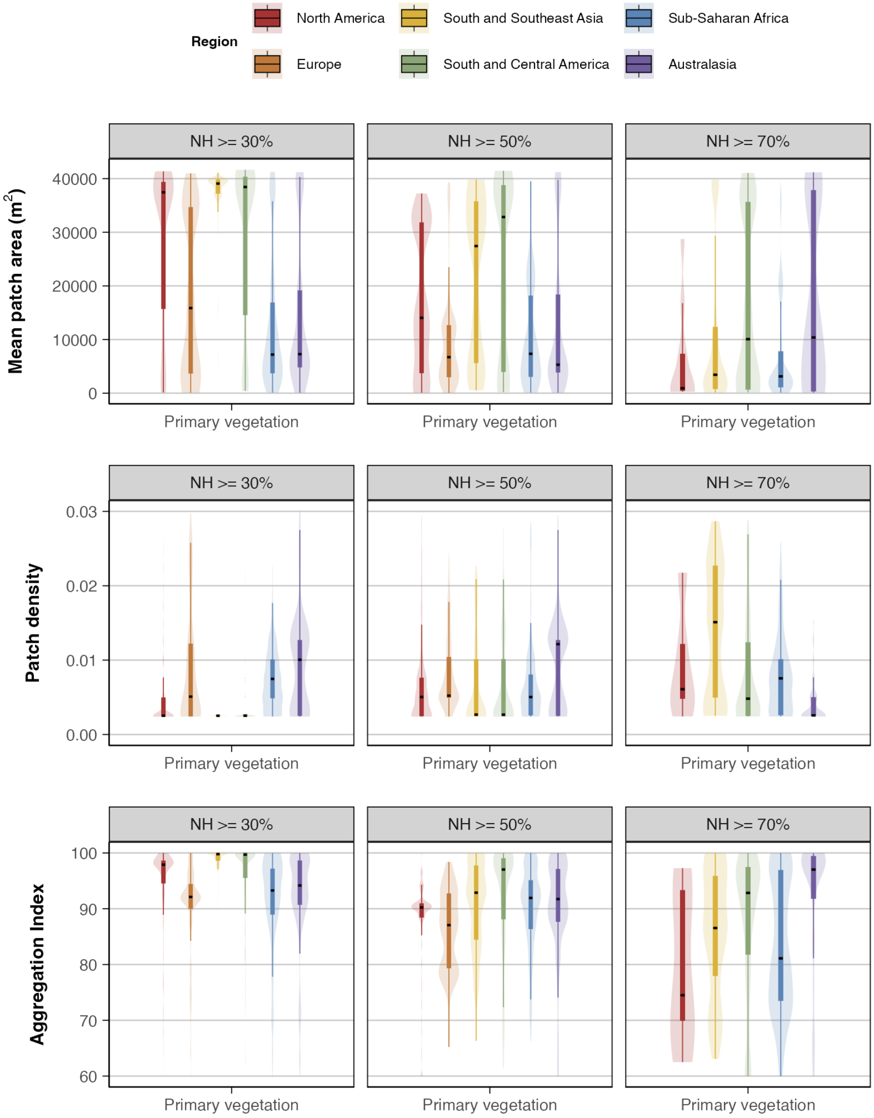


Figure S4: Connectivity of natural habitat (wilderness, forestry areas and open woodland grazing land) within 10km-radius buffers surrounding the primary vegetation sites from PREDICTS that were used in this study. Plotted are three standard habitat connectivity measures of categorical habitat layers: Mean patch area, patch density and aggregation index (He et al., 2000). Binary layers were obtained by converting continuous fractional layers to binary layers using a threshold of 0.5. In Europe, mean patch area tends to be lower, patch density higher and aggregation index lower, indicating more fragmentation. Differences are larger where the mean natural habitat in the buffer is higher, suggesting that it is particularly dense natural habitat that is more fragmented in Europe.

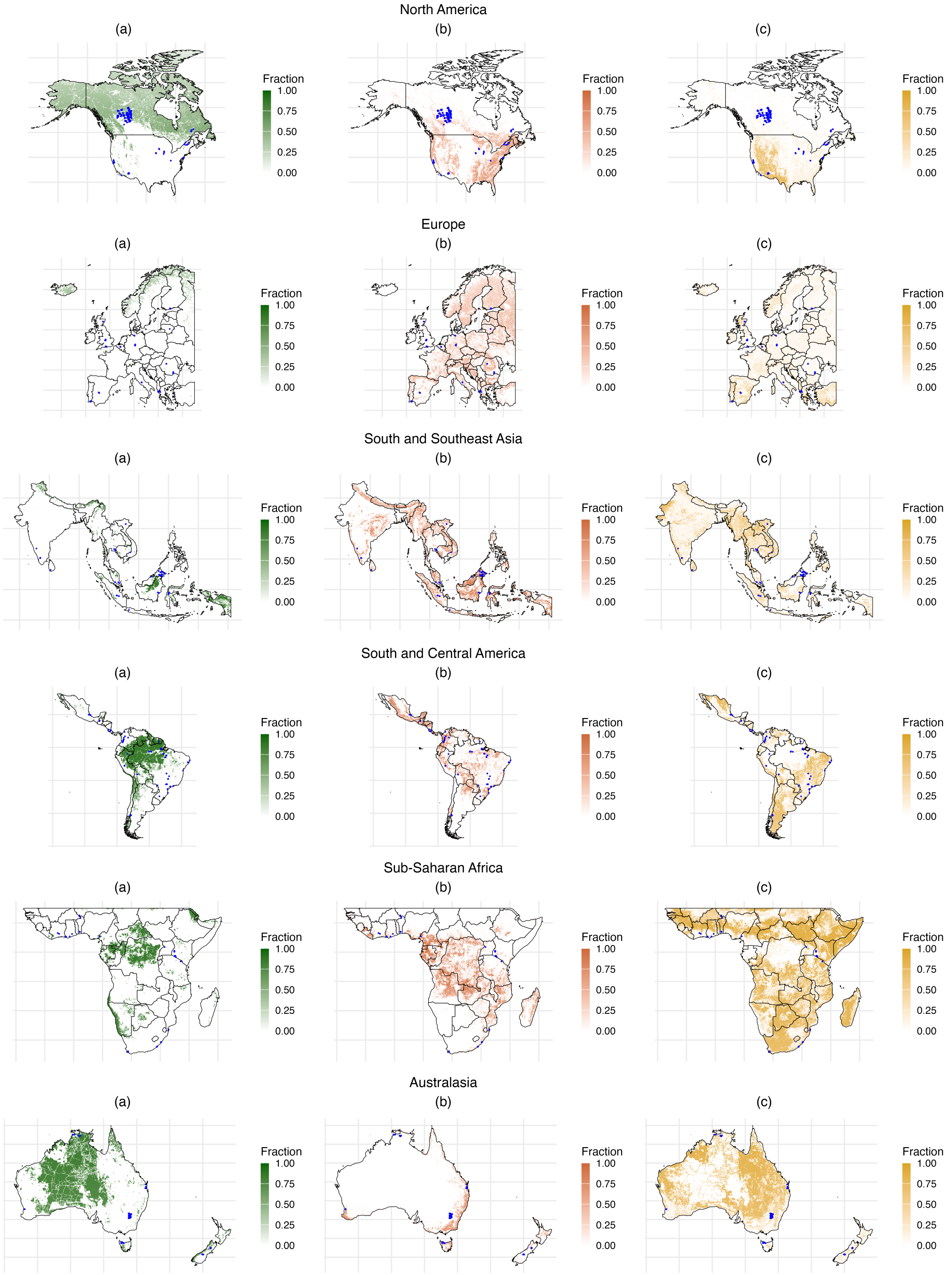


Figure S5: Maps of wilderness (a), forestry areas (b) and open woodland grazing land (c) in each region, plotted for the year 2005, and PREDICTS primary vegetation sites plotted in blue. Regions were cropped to exclude overseas territories like Hawaii from North America, or parts of a region in which no records were sampled in PREDICTS, such as Madagascar in sub-Saharan Africa or Iceland in Europe.

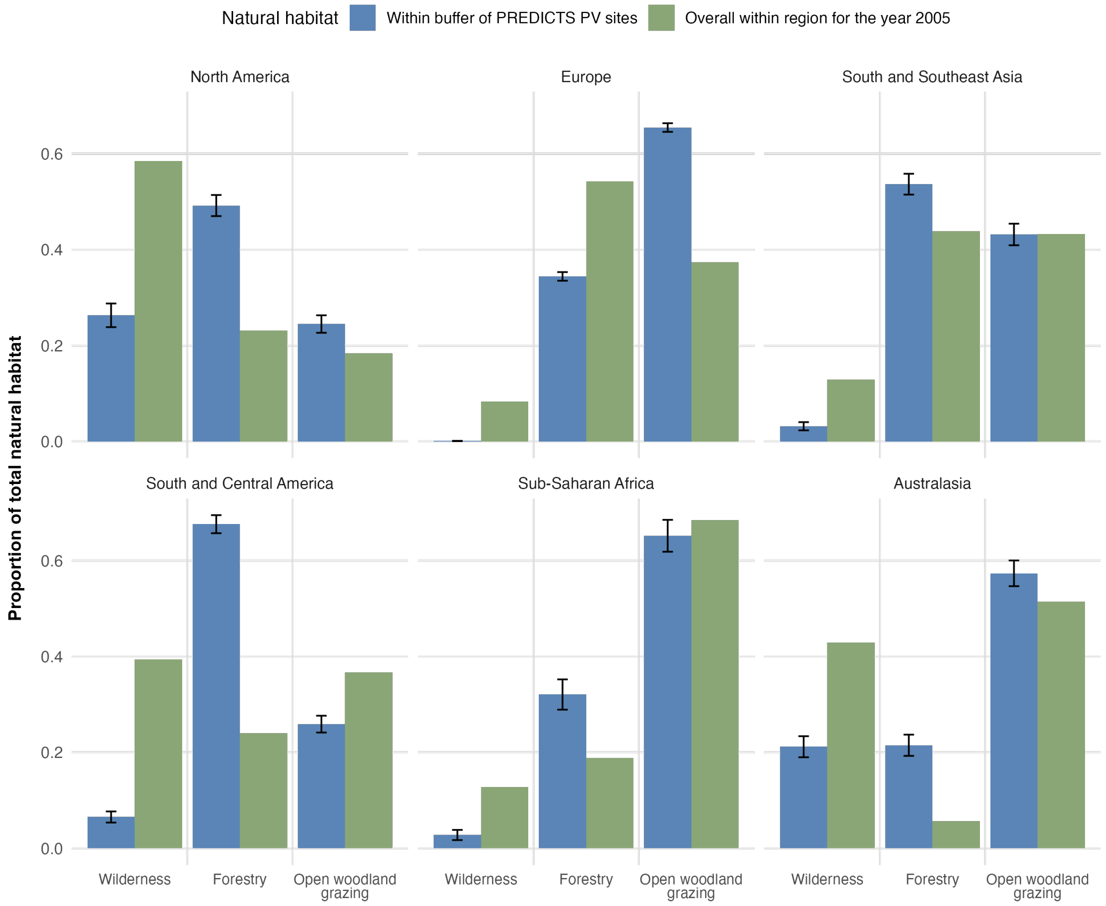


Figure S6: Proportions of wilderness, forestry areas and open woodland grazing land, of total natural habitat within 5-km buffers surrounding PREDICTS sites of primary vegetation (mean and 95% confidence interval), and overall within each region for the year 2005. The latter were computed directly from the natural habitat . The figure reveals a clear selection biases towards areas with lower proportions of wilderness. Regions were cropped to exclude overseas territories like Hawaii from North America, or parts of a region in which no records were sampled in PREDICTS, such as Madagascar in sub-Saharan Africa or Iceland in Europe. Corresponding maps are plotted in Fig. S5.

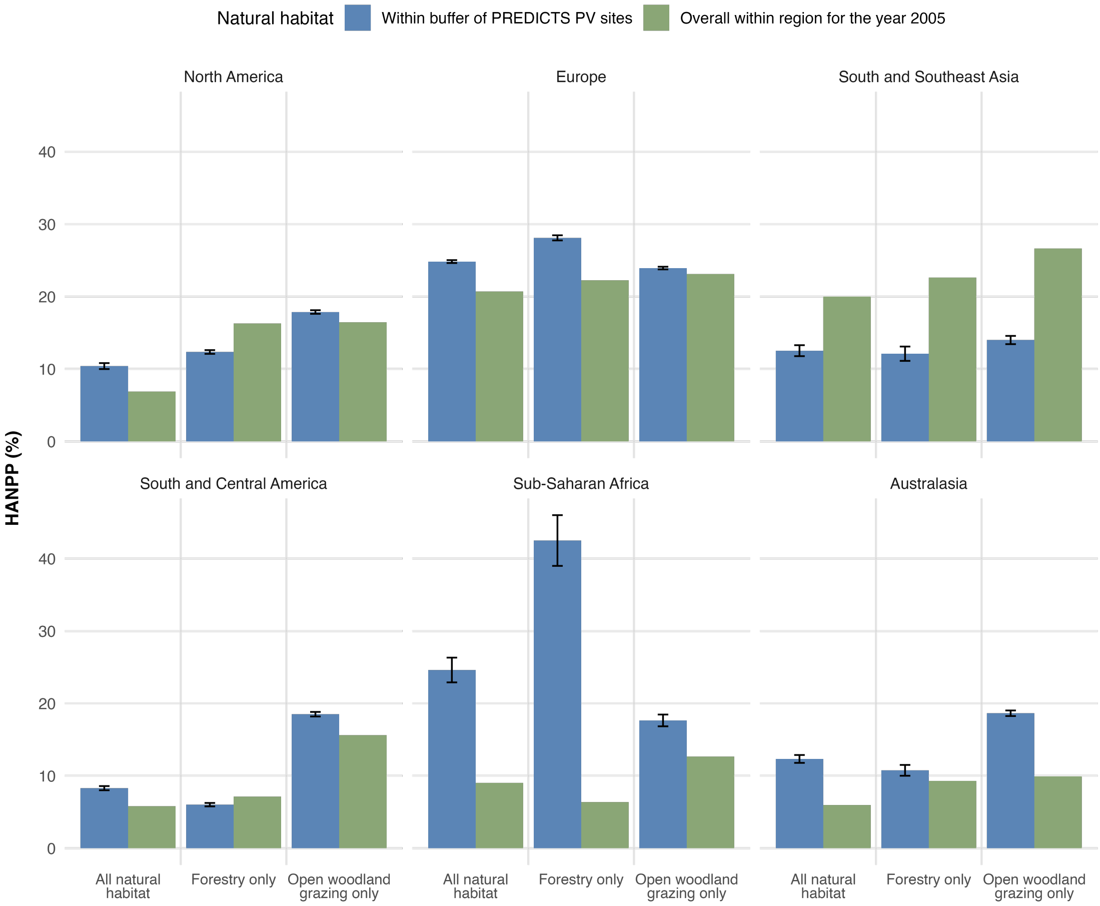


Figure S7: %HANPP per region within 5-km buffers surrounding PREDICTS sites of primary vegetation (mean and 95% confidence interval), and overall within each region for the year 2005. 'All natural habitat': Total HANPP as a percentage of the total potential NPP of the natural habitat. 'Forestry only': Forestry HANPP as a percentage of the potential NPP of forestry areas only. 'Open woodland grazing only': Open woodland grazing HANPP as a percentage of the potential NPP of open woodland grazing land only. The figure reveals a clear selection bias towards higher %HANPP in all region except South and Southeast Asia. This bias is particularly evident for forestry in sub-Saharan Africa, where sampled primary vegetation sites in the PREDICTS database (for arthropods) are sampled in forestry that is subject to almost 6.38 times the %HANPP of forestry areas overall in the region. Regions were cropped to exclude overseas territories like Hawaii from North America, or parts of a region in which no records were sampled in PREDICTS, such as Madagascar in sub-Saharan Africa or Iceland in Europe. Corresponding maps can be found in Fig. S5.

B.4 Compositional dissimilarity

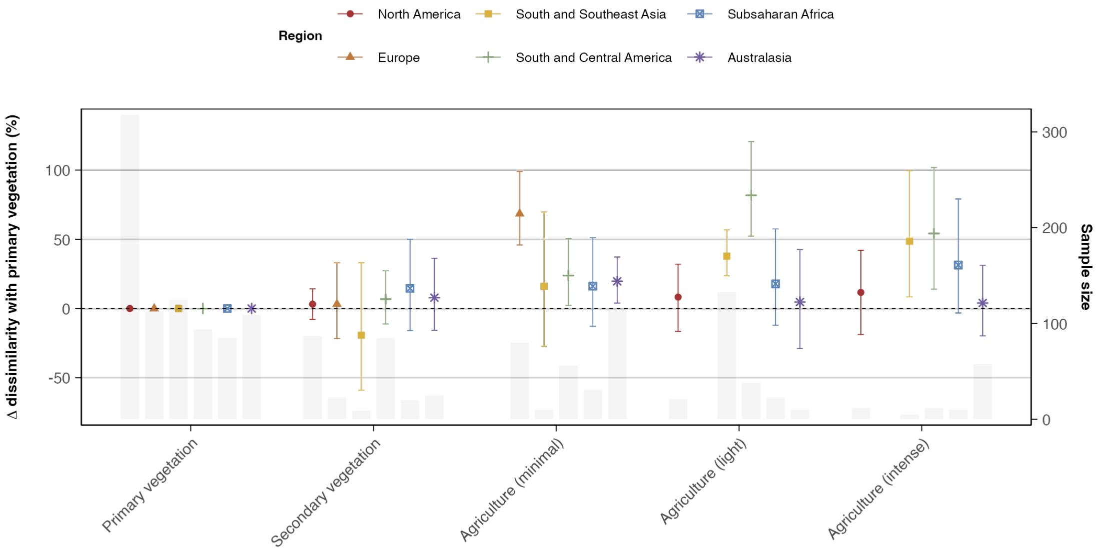


Figure S8: Compositional dissimilarity (Sørensen's Index) of each land use with primary vegetation per region, shown relative to the dissimilarity of primary vegetation with other primary vegetation sites (%). Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown.

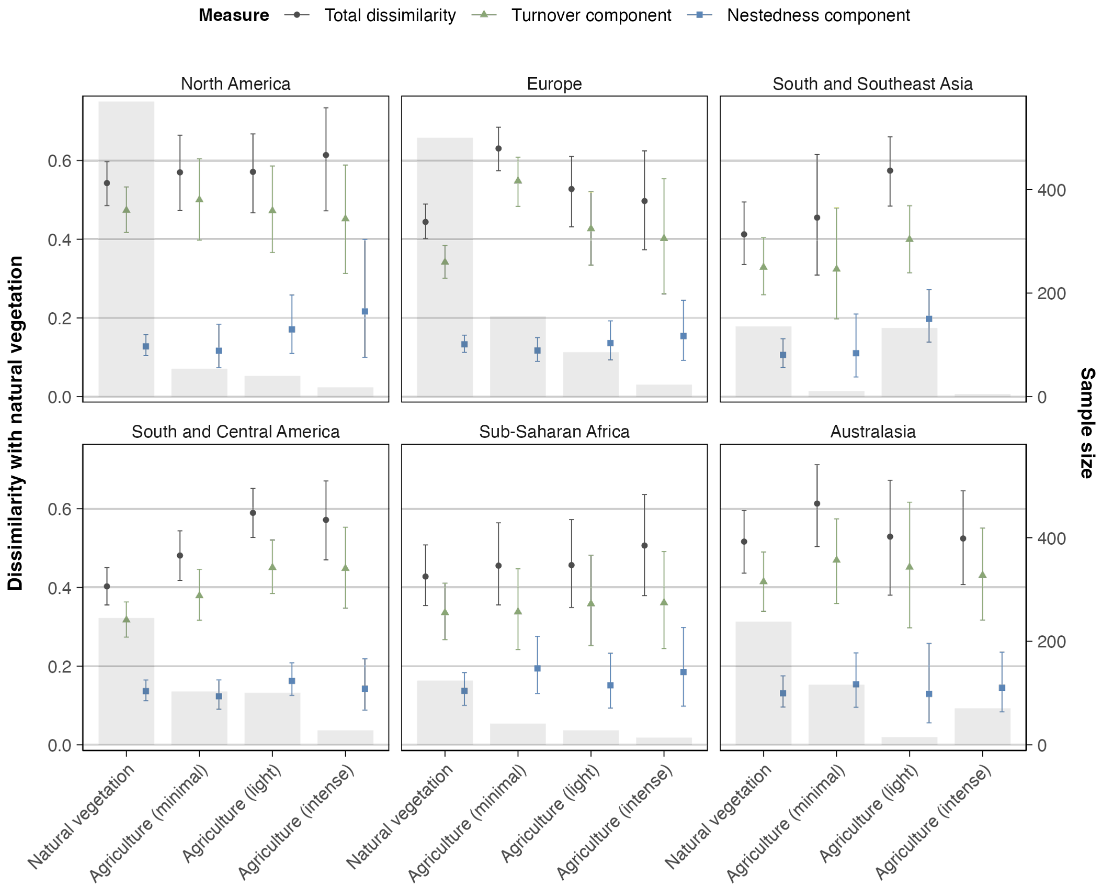


Figure S9: Absolute predictions of compositional dissimilarity (Sørensen's Index) of each land use with natural vegetation per region (%). Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown.

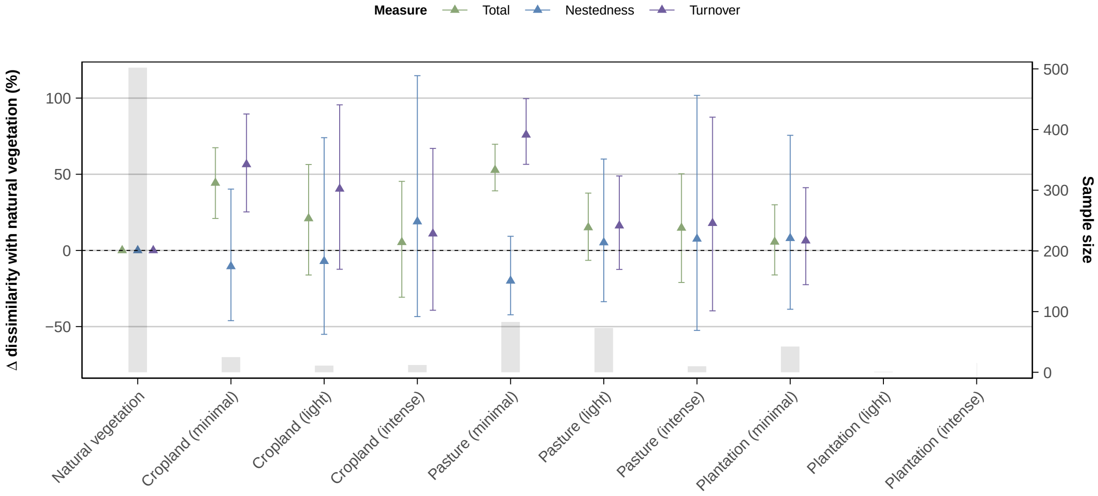


Figure S10: Compositional dissimilarity (Sørensen's Index) of each land use with natural vegetation in Europe, shown relative to the dissimilarity of natural vegetation with other natural vegetation sites (%). Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites), plotted as grey bars. Only model coefficients computed from at least 10 sites are shown. The figure shows that species turnover in minimal-use agriculture stems from cropland and pasture sites. It also shows that direct, within-study comparisons of agricultural sites with primary or secondary vegetation are very low, despite the large number of PREDICTS records in agricultural sites in Europe, highlighting an important data deficiency.

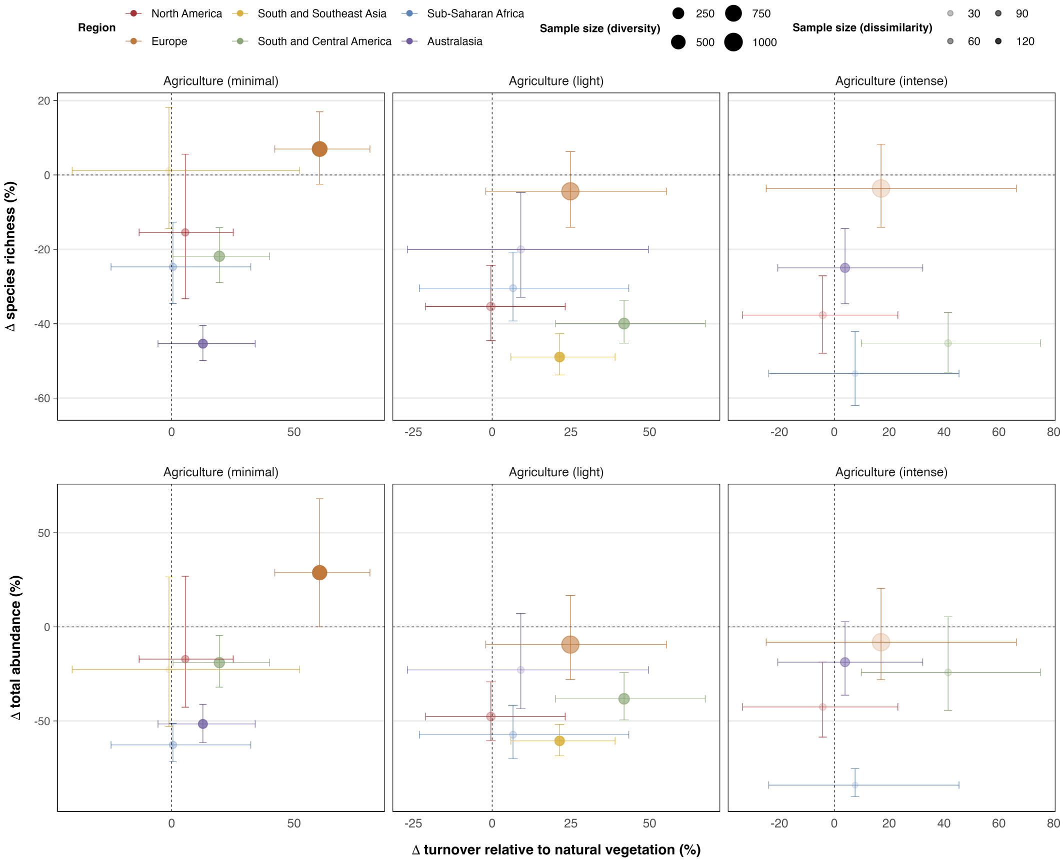


Figure S11: Turnover relative to natural vegetation (primary and secondary vegetation) of main text Fig. 4 plotted against the responses of species richness and total abundance (relative to primary vegetation) of main text Fig. 1. Points indicate median modelled responses and error bars represent 95% credible intervals. The sample sizes (number of sites) of diversity coefficients are indicated by the size of the points while the sample sizes of turnover coefficients are indicated by the transparency of the points.

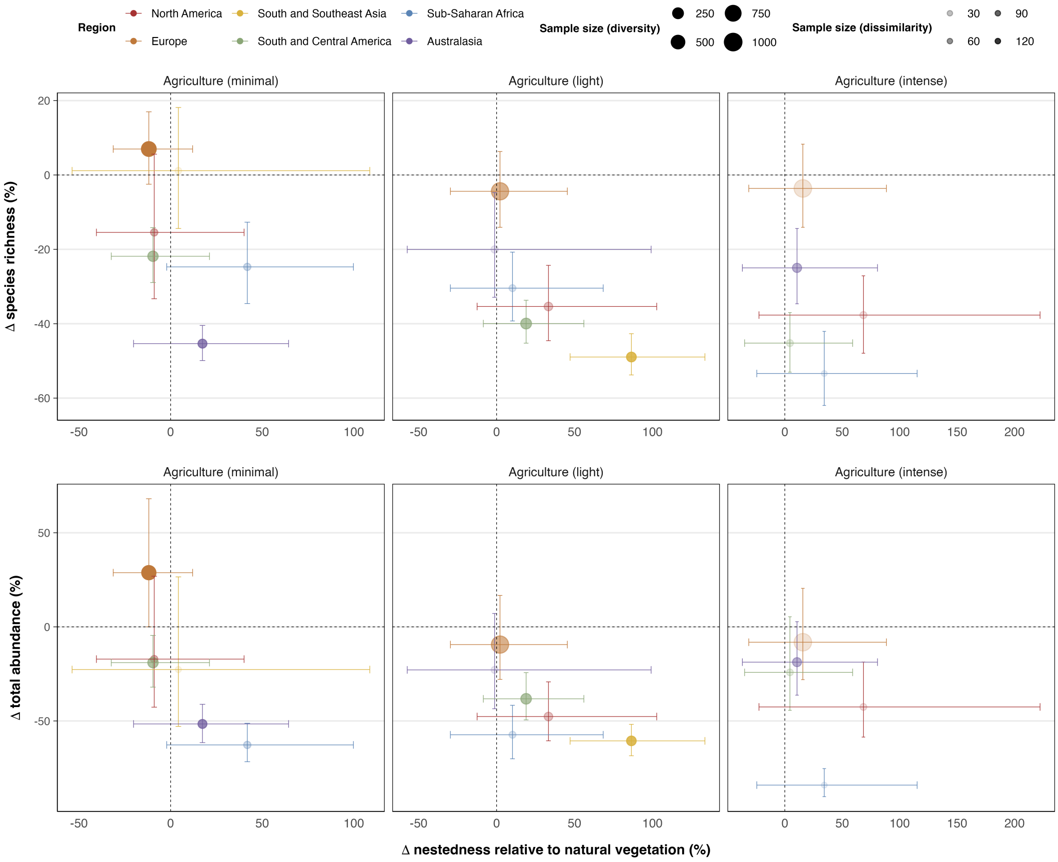


Figure S12: Nestedness relative to natural vegetation (primary and secondary vegetation) of main text Fig. 4 plotted against the responses of species richness and total abundance (relative to primary vegetation) of main text Fig. 1. Points indicate median modelled responses and error bars represent 95% credible intervals. The sample sizes (number of sites) of diversity coefficients are indicated by the size of the points while the sample sizes of nestedness coefficients are indicated by the transparency of the points.

B.5 Effects of range extent, habitat specificity and non-native species

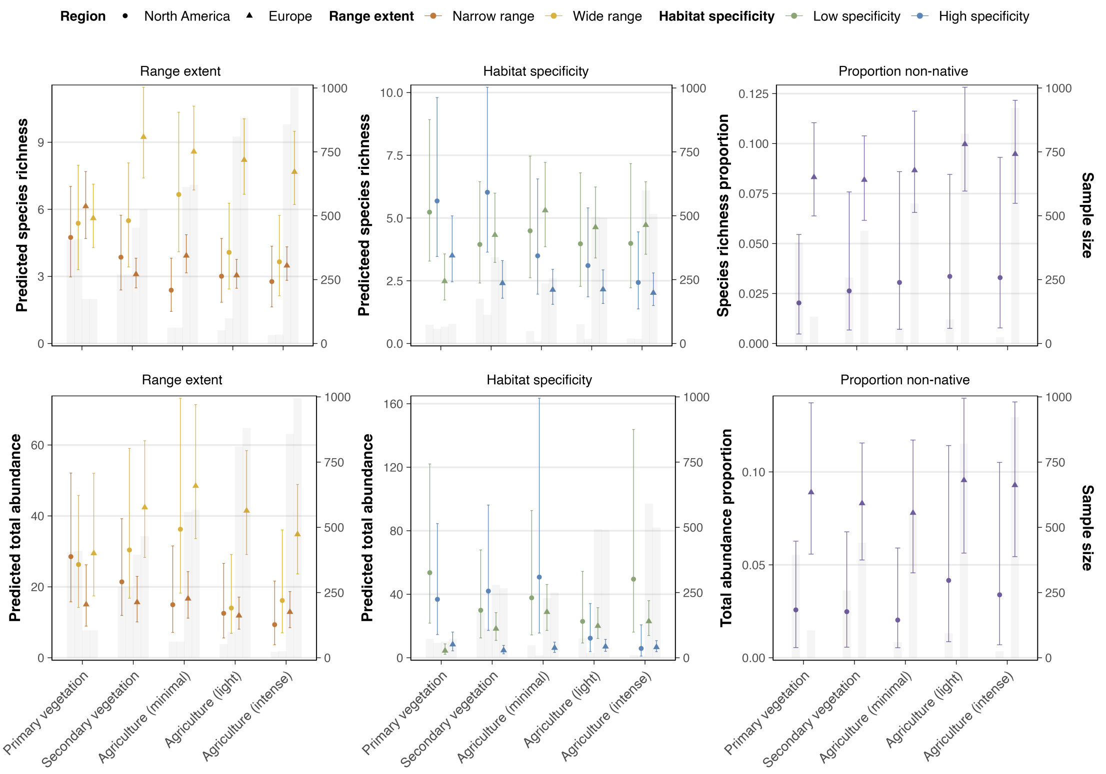


Figure S13: Absolute predictions of species richness and total abundance per land use in Europe and North America, comparing responses of species with narrow and wide range extent, and high and low habitat specificity. Non-native proportion: The proportion of non-native species in a site, as a fraction of species richness or total abundance. Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites). Only model coefficients computed from at least 10 sites are shown.

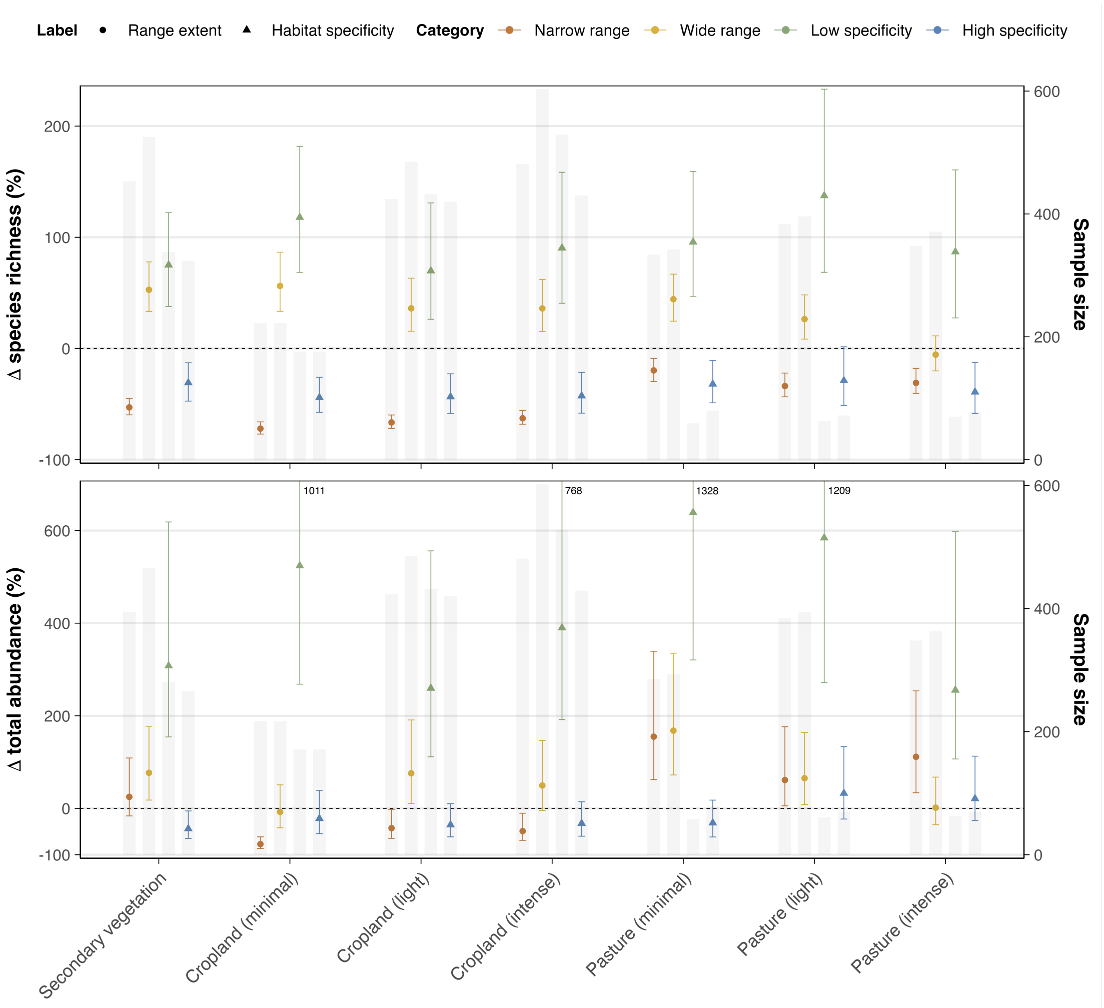


Figure S14: Arthropod diversity responses (species richness and total abundance) to individual agricultural land use types in Europe, relative to primary vegetation, comparing species with narrow and wide range extent, and high and low habitat specificity. Points indicate median modelled responses and error bars represent 95% credible intervals. The right y-axis shows sample sizes (number of sites). Only model coefficients computed from at least 10 sites are shown.

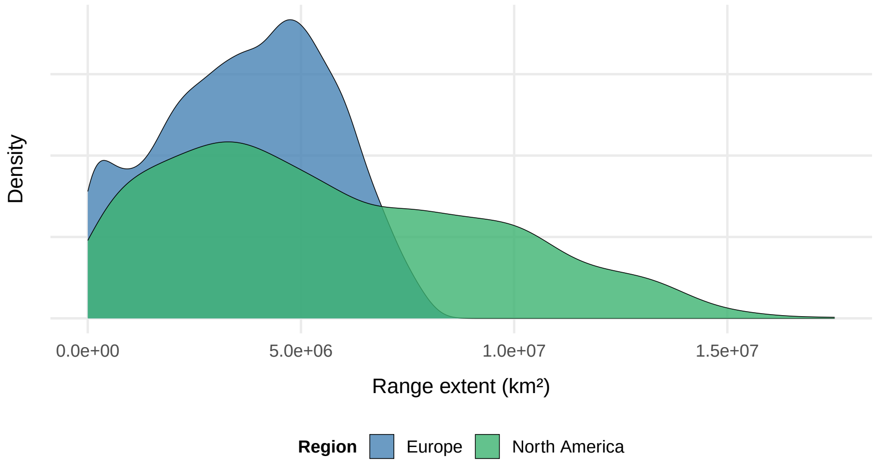


Figure S15: Densities of range extents for Europe and North America.

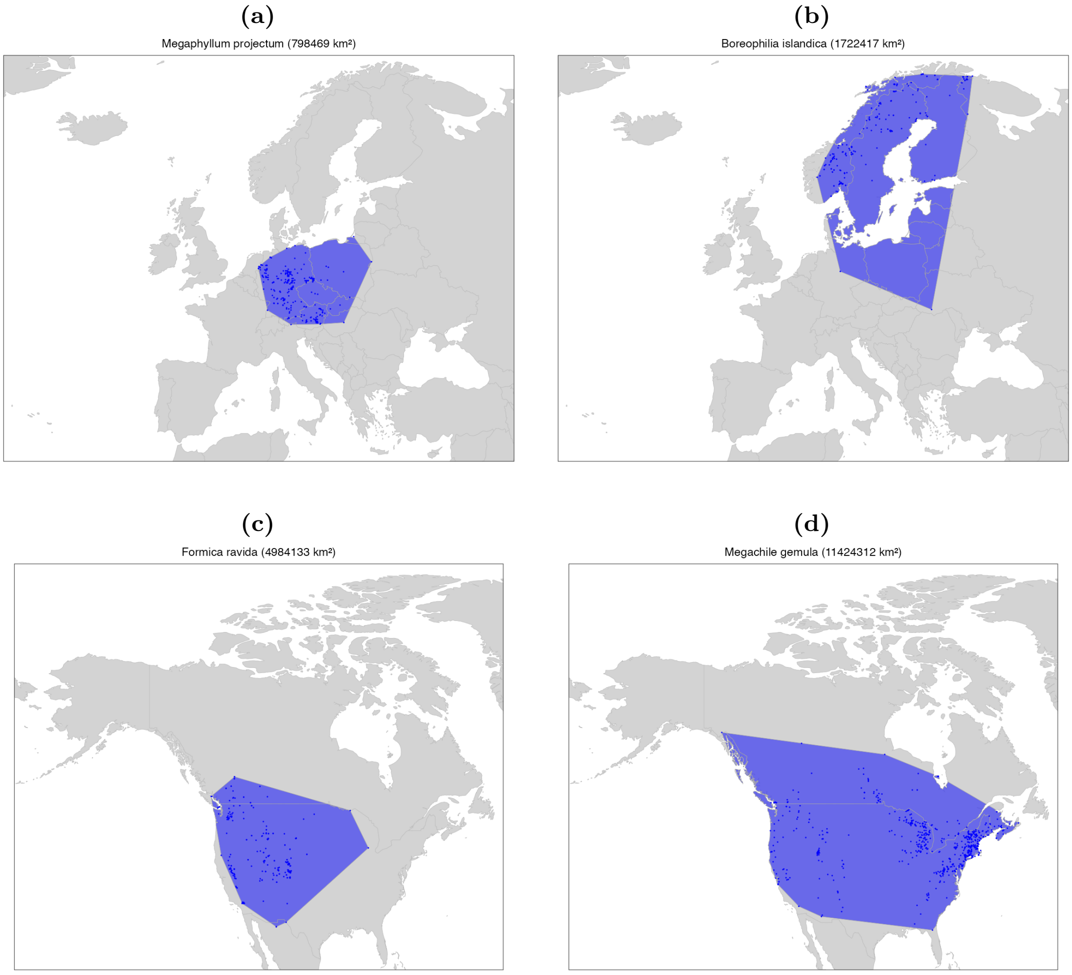
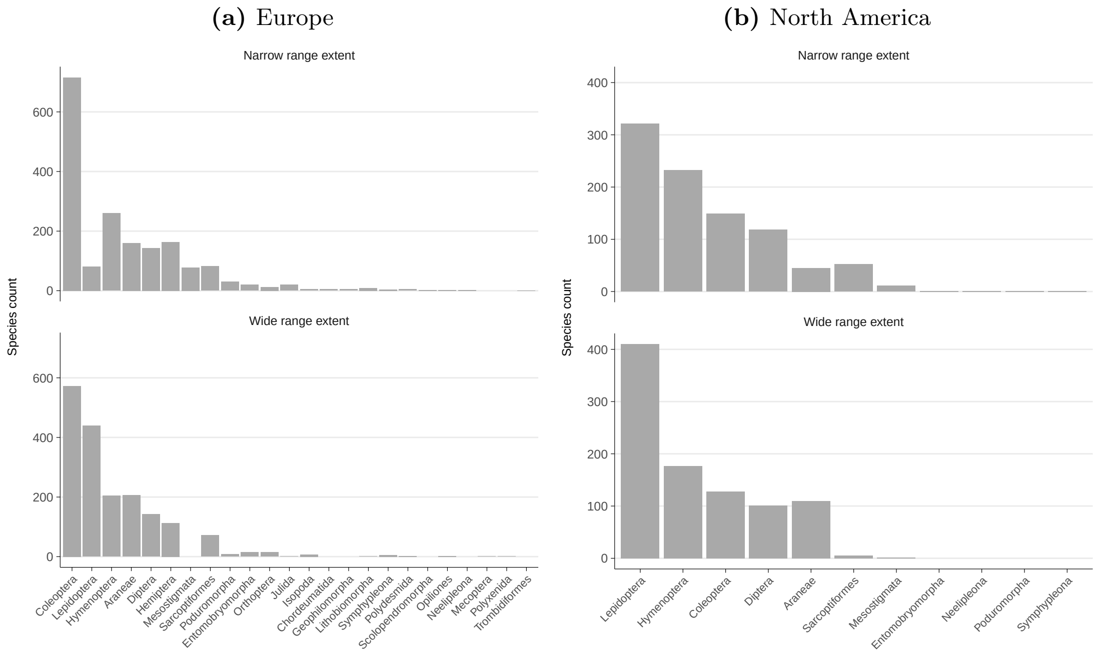


Figure S16: Examples of range extents for Europe (a, b) and North America (c, d).


(a) Europe

(b) North America

Figure S17: Species counts for taxonomic orders per range extent category in Europe (a) and North America (b).

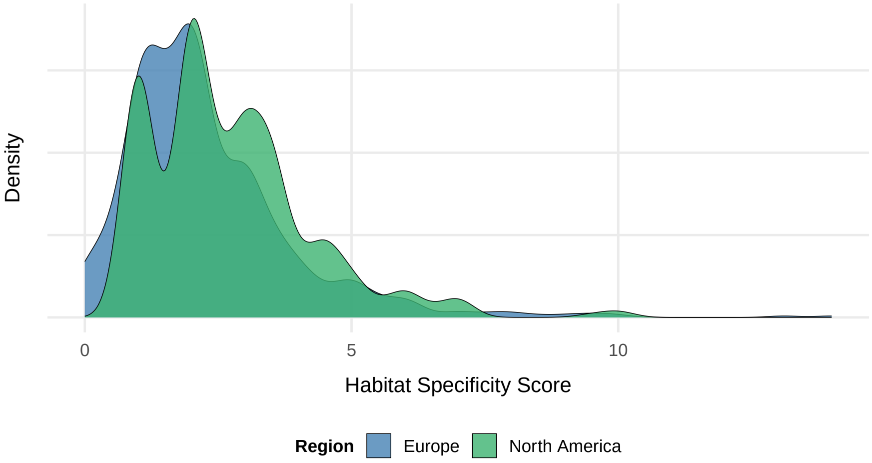
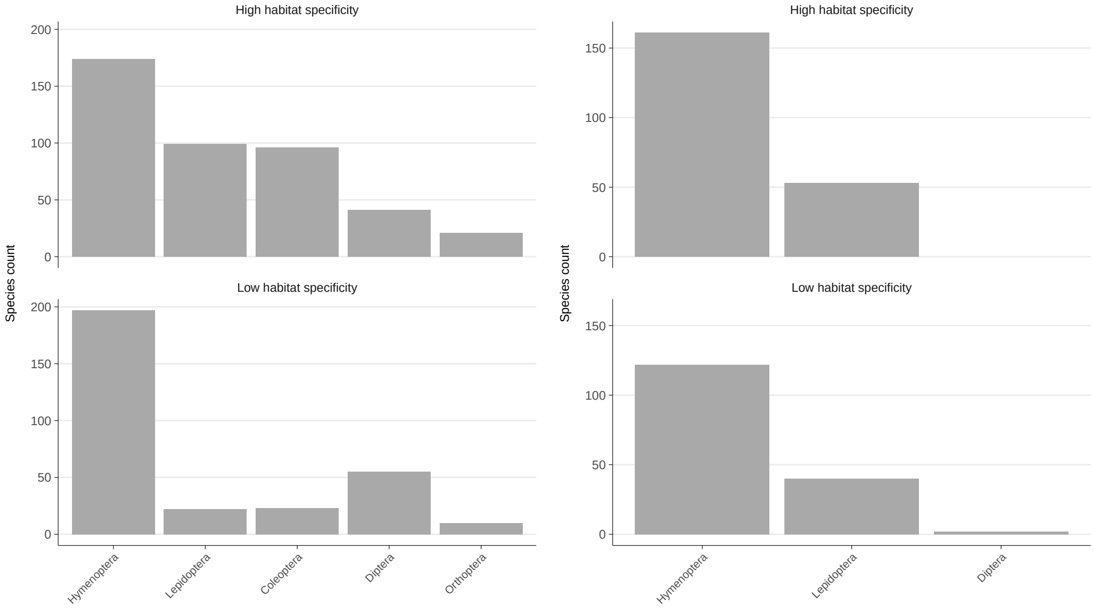


Figure S18: Densities of habitat specificity score for Europe and North America. A higher score implies less habitat specificity.



(a) Europe **(b)** North America

Figure S19: Species counts for taxonomic orders per habitat specificity category in Europe (a) and North America (b).

B.6 Abundance model comparison

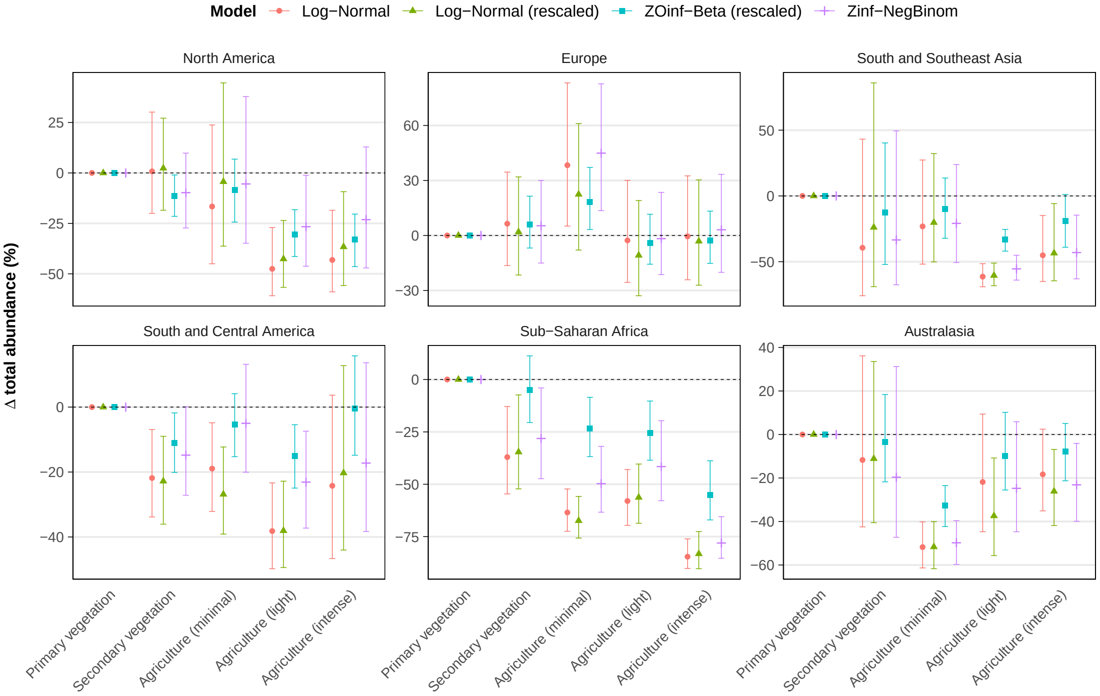
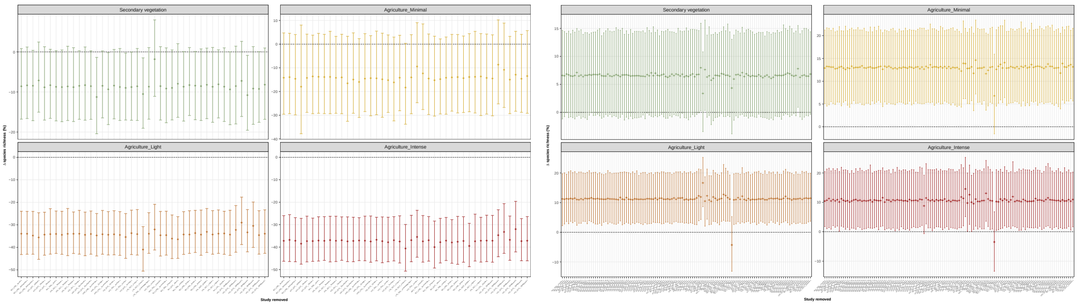


Figure S20: Comparison of model responses of abundance per land use and region as percentage change from primary vegetation. Points indicate median modelled responses and error bars represent 95% credible intervals. Shifted from left-to-right: Rescaled abundance modelled with a zero-and-one inflated beta distribution (red), log-transformed rescaled abundance modelled with a Gaussian distribution (green), and log-transformed total abundance (unscaled) modelled with a Gaussian distribution (blue). Although there is approximate agreement between the models, responses from the beta model tend to be more conservative.

B.7 Sensitivity analysis

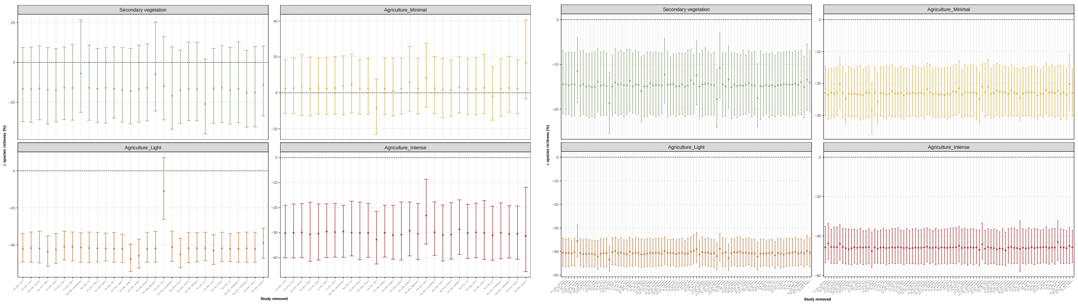
To test the robustness of the regional responses to agricultural land use shown in Figure 1, we conducted a sensitivity analysis on the model coefficients by removing individual studies from the model data and refitting the models of species richness and total abundance (Fig. S21 and Fig. S22). Due to the high computational cost of refitting Bayesian `brms` models, we used the R package `glmmTMB` (Brooks et al., 2017) to fit these models. Major changes in coefficients due to the removal of a study were further investigated but disregarded if the changes were not consistent across land uses and/or if the study in question corresponded to the largest study in that region (in which case large changes in coefficients are to be expected). For example, whilst the Australasian study `CC1_2007__Ewers 1` (New Zealand) results to substantially more negative diversity change across minimal-, light- and intense-use agriculture, this study is the largest PREDICTS study in Australasia and was therefore not removed from the analysis. This does suggest, however, that diversity declines in agricultural landscapes in Australasia may be less pronounced in Australia than in New Zealand.

For Europe, a consistent change in coefficients of species richness and total abundance was observed for the study `SC1_2011__Meijer 1`, which corresponds to one of two arthropod studies in the PREDICTS database that stem from the Azores islands. Due to the disproportionate impact of the Azores on European biodiversity responses, their geographical isolation as a small island group in the Atlantic ocean, and their substantial distance from the European mainland, we decided to remove the Azores records from the analysis. To be consistent, we removed studies from islands of similar size from other regions, which resulted in the removal of studies from Puerto Rico (South and Central America) and Comoros (Subsaharan Africa).



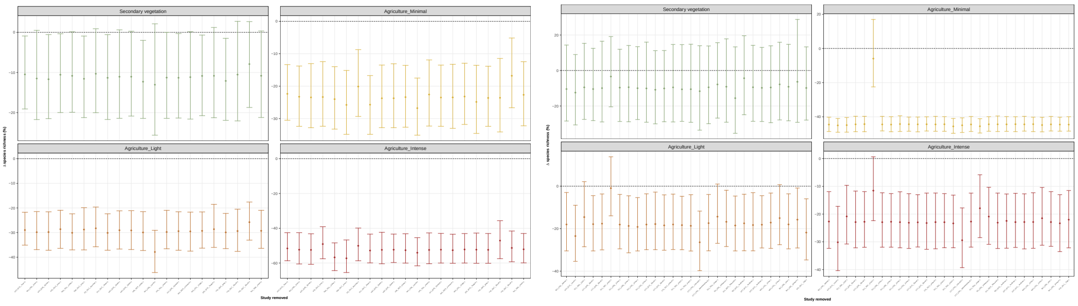
(a) North America

(b) Europe



(c) South and Southeast Asia

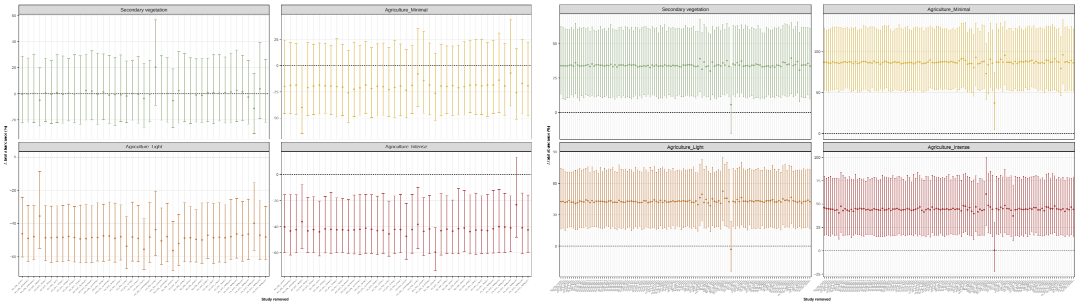
(d) South and Central America



(e) Subsaharan Africa

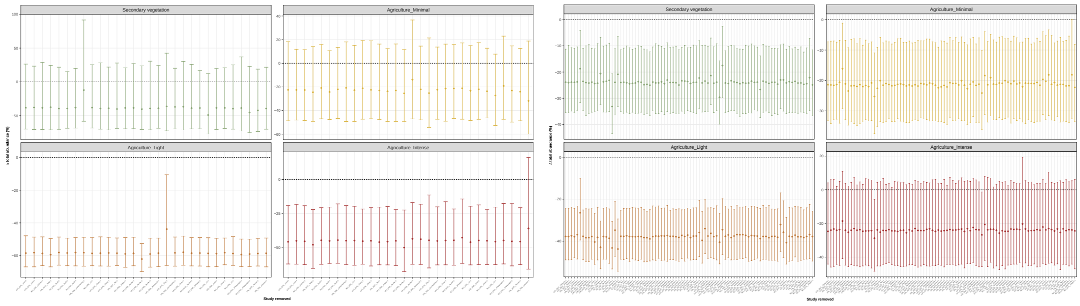
(f) Australasia

Figure S21: Sensitivity test of individual studies (through their individual removal from the dataset) on the regional model coefficients of species richness in secondary vegetation and minimal-, light- and intense-use agriculture, relative to primary vegetation. Points indicate median modelled responses and error bars represent 95% confidence intervals. In Europe, we observe a consistent bias across land use coefficients for the study `SC1_2011__Meijer 1` (located in the Azores island group), which results in substantially more positive coefficients of diversity change if the study is included.



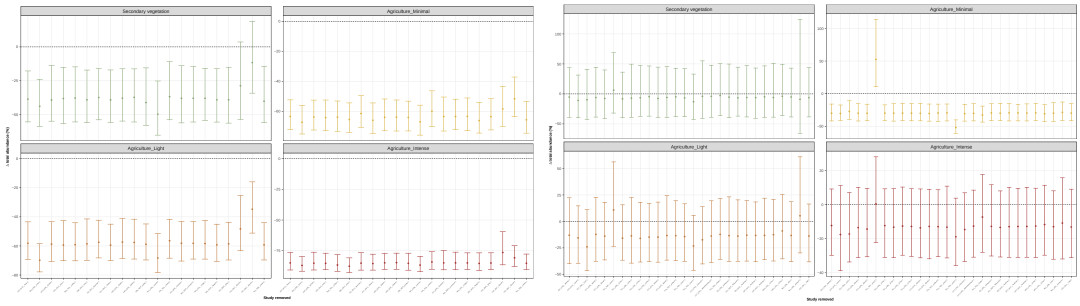
(a) North America

(b) Europe



(c) South and Southeast Asia

(d) South and Central America



(e) Subsaharan Africa

(f) Australasia

Figure S22: Sensitivity test of individual studies (through their individual removal from the dataset) on the regional model coefficients of total abundance in secondary vegetation and minimal-, light- and intense-use agriculture, relative to primary vegetation. Points indicate median modelled responses and error bars represent 95% confidence intervals. In Europe, we observe a consistent bias across land use coefficients for the study `SC1_2011__Meijer 1` (located in the Azores island group), which results in substantially more positive coefficients of diversity change if the study is included.

B.8 Influence of soil-core samples

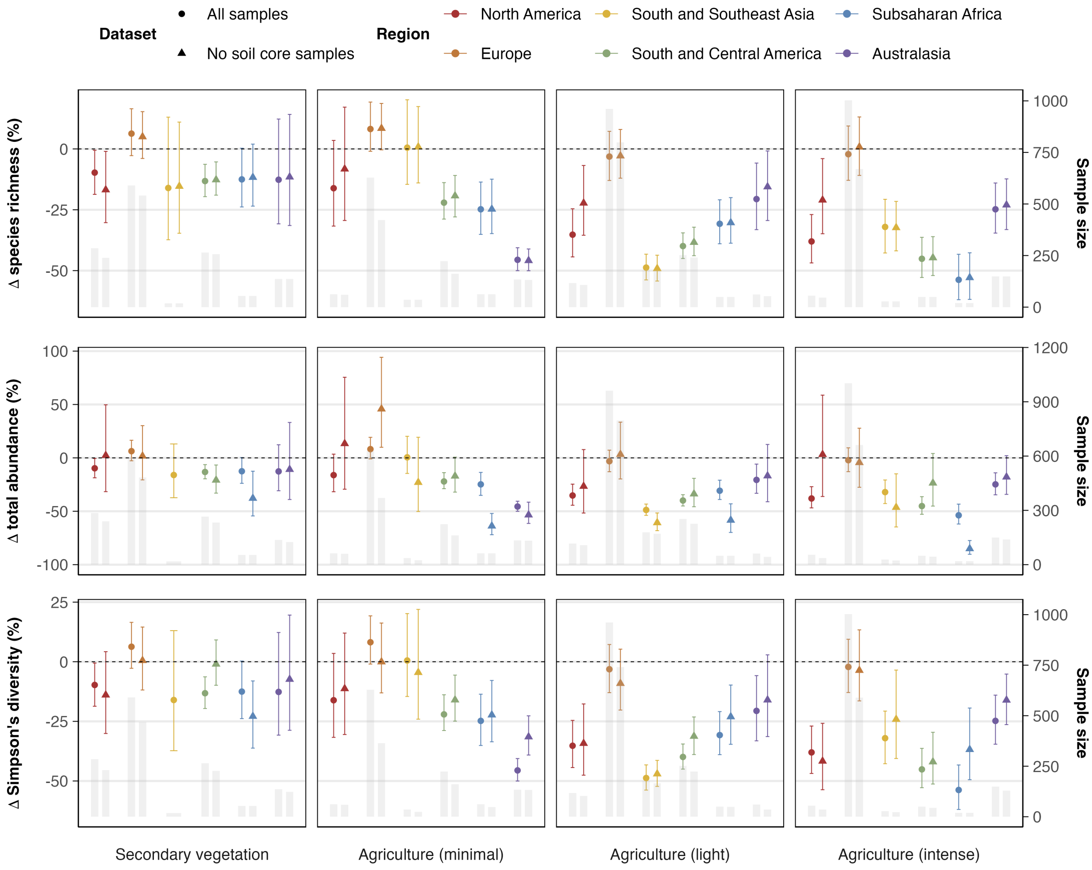


Figure S23: Comparison of the PREDICTS dataset used in this study with and without soil-core samples, comparing regional responses of species richness, total abundance and Simpson's diversity index to agricultural land use, relative to primary vegetation. Points indicate median modelled responses and error bars represent 95% confidence intervals. The figure shows that the removal of soil core samples does not substantially change diversity responses, with the exception that the response of total abundance in sub-Saharan Africa is more negative without soil core samples.

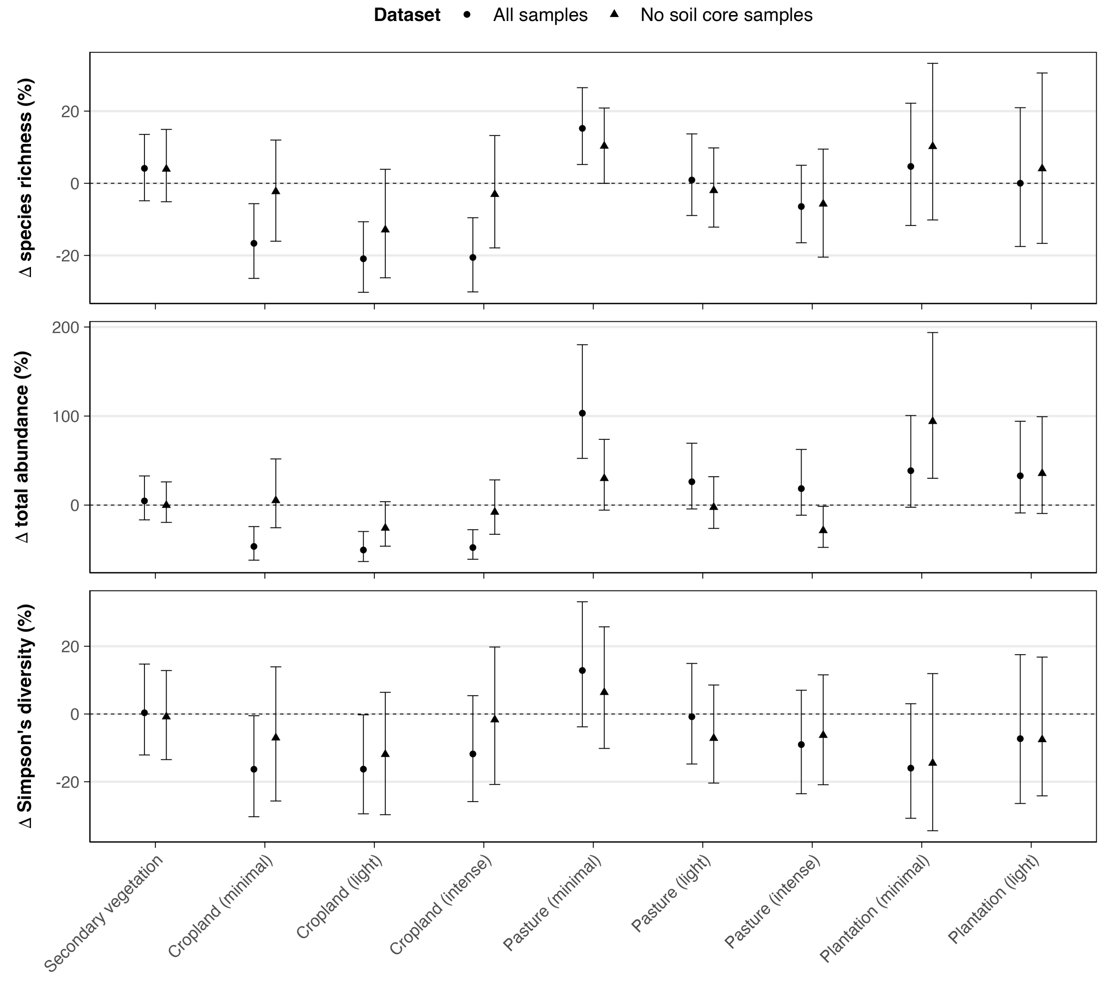


Figure S24: Comparison of the PREDICTS dataset used in this study with and without soil-core samples, comparing European responses of species richness, total abundance and Simpson's diversity index relative to primary vegetation, per individual land-use type and intensity. Points indicate median modelled responses for Europe and error bars represent 95% confidence intervals. The figure shows that the removal of soil core samples does not substantially change diversity responses, although responses in cropland are slightly less negative without core samples.

References

Brooks, M. E., Kristensen, K., van Benthem, K. J., Magnusson, A., Berg, C. W., Nielsen, A., Skaug, H. J., Maechler, M., and Bolker, B. M. (2017). “glmmTMB Balances Speed and Flexibility Among Packages for Zero-inflated Generalized Linear Mixed Modeling”. In: *The R Journal* 9.2, pp. 378–400. DOI: `10.32614/RJ-2017-066`.

He, H. S., DeZonia, B. E., and Mladenoff, D. J. (Oct. 2000). “An aggregation index (AI) to quantify spatial patterns of landscapes”. In: *Landscape Ecology* 15.7, pp. 591–601. ISSN: 1572-9761. DOI: `10.1023/A:1008102521322`.

Hudson, L. N. et al. (2017). “The database of the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project”. In: *Ecology and Evolution* 7.1, pp. 145–188. DOI: `https://doi.org/10.1002/ece3.2579`.

Supplementary Information B

Model Fits and Diagnostics Plots

Contents

A Regional responses

The following model diagnostic plots refer to the comparison of regional responses of biodiversity in primary vegetation, secondary vegetation and agricultural land use (Fig. 1).

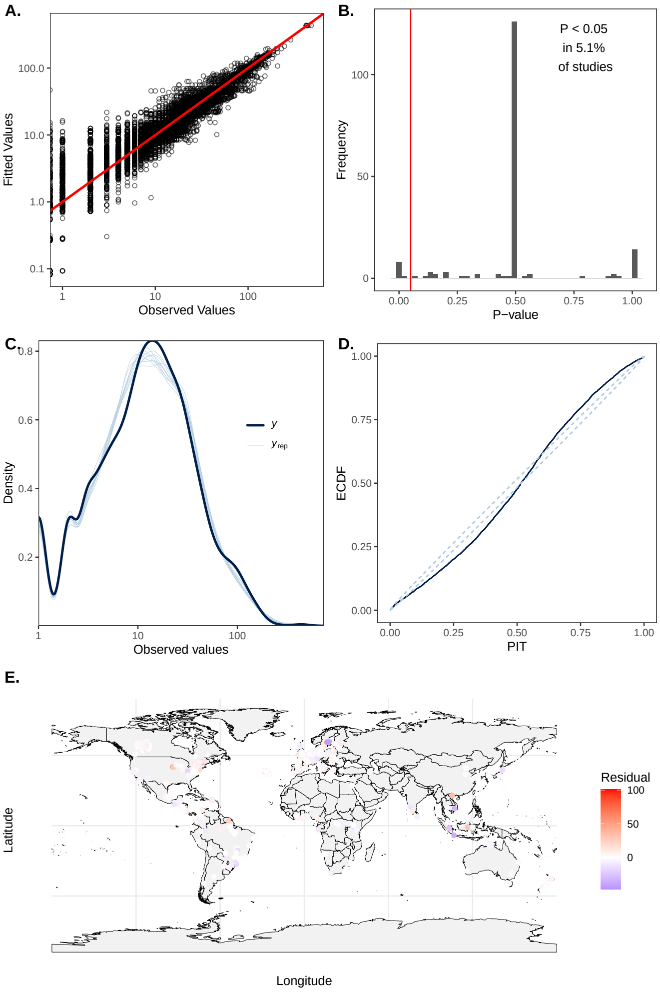


Figure M1: Model diagnostic plots for the zero-inflated negative binomial model of global species richness responses to land use: Richness $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

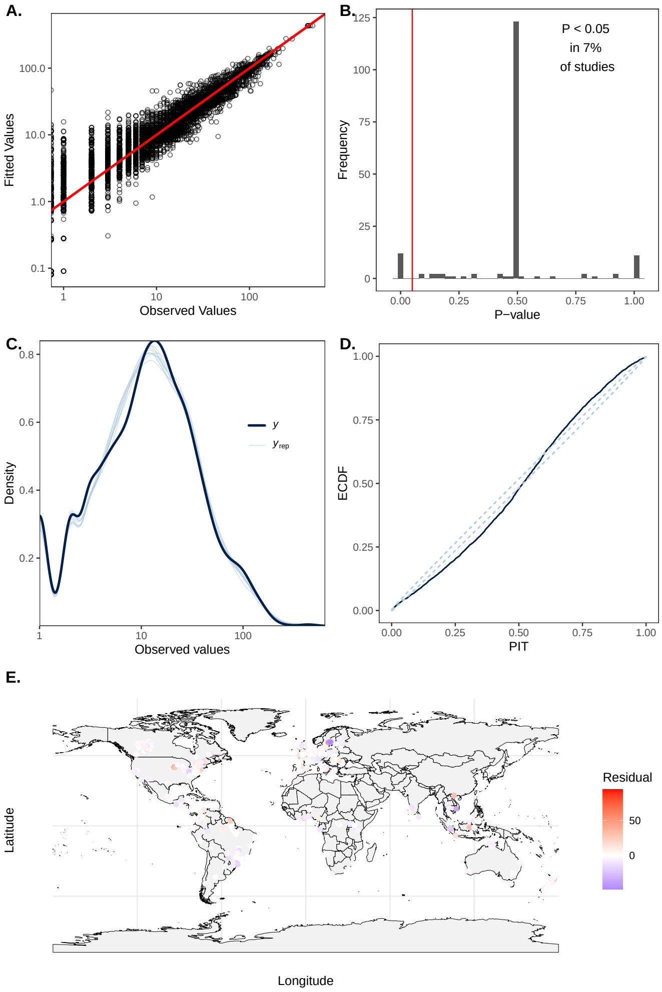


Figure M2: Model diagnostic plots for the zero-inflated negative binomial model of regional species richness responses to land use: Richness $\sim$ LandUse $\times$ Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M1: Posterior summary of the global model of species richness (Fig. M1).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 7604)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 341)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.24      0.05     1.15     1.35 1.00     1224     2943

~SS:SSB (Number of levels: 1696)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.21      0.01     0.19     0.24 1.00     5120     9570

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                  2.84      0.07     2.70     2.97 1.01      632     1234
zi_Intercept              -5.37      0.22    -5.84    -4.97 1.00    24669    13954
UI2Secondaryvegetation    -0.13      0.02    -0.17    -0.09 1.00    13895    15118
UI2Agriculture_Minimal    -0.22      0.02    -0.27    -0.18 1.00    15282    14596
UI2Agriculture_Light      -0.33      0.02    -0.37    -0.28 1.00    11134    13619
UI2Agriculture_Intense    -0.36      0.03    -0.41    -0.31 1.00    12246    14491

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    14.80      0.55    13.74    15.92 1.00    14225    14438

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.905 (95% CI [0.894, 0.912])
     Marginal R2: 0.005 (95% CI [0.003, 0.007])
```

Table M2: Posterior summary of the regional model of species richness (Fig. M2).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 * Region + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 7188)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 323)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.27      0.05     1.17     1.38 1.00     3432     6393

~SS:SSB (Number of levels: 1632)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.21      0.01     0.19     0.23 1.00     5617    10817

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                               2.49      0.12     2.25     2.73 1.00     1216     2423
zi_Intercept                                           -5.32      0.22    -5.79    -4.92 1.00    40384    13614
UI2Secondaryvegetation                                  0.06      0.05    -0.03     0.15 1.00     5995    11716
UI2Agriculture_Minimal                                  0.08      0.05    -0.01     0.16 1.00     5938    10724
UI2Agriculture_Light                                   -0.04      0.05    -0.14     0.07 1.00     4923     9310
UI2Agriculture_Intense                                 -0.03      0.06    -0.14     0.08 1.00     5053     9350
RegionNorthAmerica                                      0.37      0.24    -0.08     0.84 1.00     1701     3614
RegionSouthandSoutheastAsia                             0.90      0.27     0.37     1.43 1.00     2123     3712
RegionSouthandCentralAmerica                            0.39      0.19     0.02     0.75 1.00     1388     3233
RegionSubsaharanAfrica                                  0.21      0.31    -0.40     0.82 1.00     2536     4568
RegionAustralasia                                       0.36      0.28    -0.18     0.90 1.00     2166     3794
UI2Secondaryvegetation:RegionNorthAmerica              -0.16      0.07    -0.31    -0.02 1.00     9631    13407
UI2Agriculture_Minimal:RegionNorthAmerica              -0.25      0.12    -0.48    -0.02 1.00    16968    16148
```

```
UI2Agriculture_Light:RegionNorthAmerica                -0.40      0.09    -0.58    -0.22 1.00    10111    14428
UI2Agriculture_Intense:RegionNorthAmerica              -0.45      0.10    -0.65    -0.25 1.00    11462    14597
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.23      0.15    -0.52     0.06 1.00    22859    15124
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.07      0.09    -0.25     0.12 1.00    15094    15125
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.63      0.08    -0.78    -0.48 1.00     7978    13286
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.36      0.10    -0.55    -0.17 1.00    11207    13845
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.20      0.06    -0.32    -0.08 1.00     7910    13236
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.32      0.07    -0.45    -0.19 1.00     9353    14920
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.47      0.07    -0.61    -0.34 1.00     7024    12012
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.58      0.09    -0.76    -0.39 1.00     9220    13961
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.18      0.09    -0.35    -0.01 1.00    12434    15682
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -0.36      0.09    -0.53    -0.19 1.00    12645    15148
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.33      0.09    -0.49    -0.16 1.00     9166    14359
UI2Agriculture_Intense:RegionSubsaharanAfrica          -0.74      0.12    -0.97    -0.50 1.00    13992    14771
UI2Secondaryvegetation:RegionAustralasia               -0.19      0.14    -0.47     0.07 1.00    17174    15374
UI2Agriculture_Minimal:RegionAustralasia               -0.68      0.06    -0.80    -0.56 1.00     9210    13255
UI2Agriculture_Light:RegionAustralasia                 -0.19      0.10    -0.39     0.01 1.00    10897    14221
UI2Agriculture_Intense:RegionAustralasia               -0.26      0.09    -0.43    -0.09 1.00     8904    13779

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    17.37      0.74    15.96    18.86 1.00    16775    15686

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.918 (95% CI [0.908, 0.925])
     Marginal R2: 0.025 (95% CI [0.006, 0.058])
```

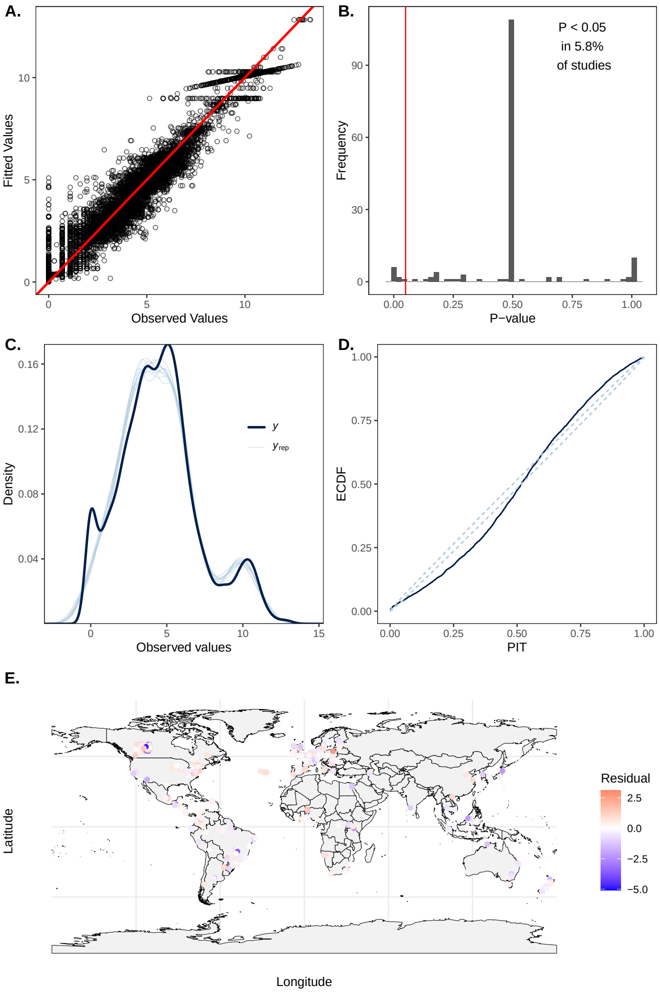


Figure M3: Model diagnostic plots for the Gaussian model of global total abundance responses to land use: Log(Abundance+1) ∼ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

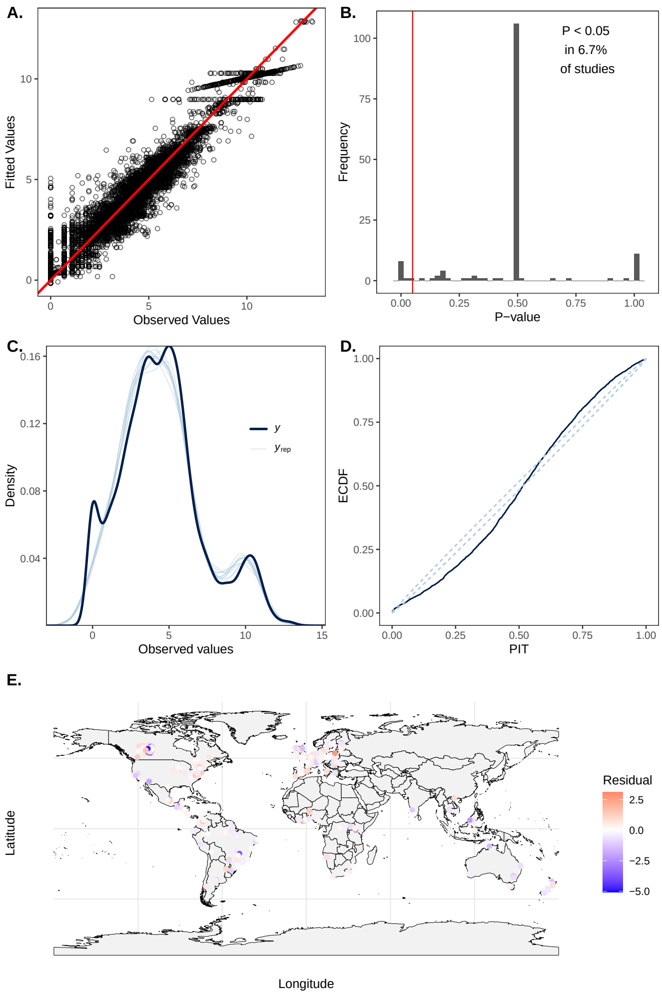


Figure M4: Model diagnostic plots for the Gaussian model of regional total abundance responses to land use: Log(Abundance+1) $\sim$ LandUse $\times$ Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M3: Posterior summary of the global model of total abundance (Fig. M3).

```
                                      BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 + (1 | SS/SSB)
   Data: model_data (Number of observations: 7122)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 314)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.11      0.09     1.94     2.29 1.00     2258     4282

~SS:SSB (Number of levels: 1624)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.42      0.02     0.37     0.47 1.00     5368    10618

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                  5.26      0.12     5.02     5.51 1.01     1174     2780
UI2Secondaryvegetation    -0.24      0.05    -0.33    -0.15 1.00    23249    17202
UI2Agriculture_Minimal    -0.27      0.05    -0.36    -0.18 1.00    23482    17854
UI2Agriculture_Light      -0.46      0.05    -0.55    -0.37 1.00    18742    17183
UI2Agriculture_Intense    -0.45      0.05    -0.55    -0.34 1.00    20184    15549

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.82      0.01     0.81     0.84 1.00    18357    14190

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.905 (95% CI [0.903, 0.907])
     Marginal R2: 0.005 (95% CI [0.003, 0.006])
```

Table M4: Posterior summary of the regional model of total abundance (Fig. M4).

```
                                      BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Region + (1 | SS/SSB)
   Data: model_data (Number of observations: 6751)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.11      0.09     1.93     2.29 1.00     2086     4042

~SS:SSB (Number of levels: 1561)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.43      0.02     0.38     0.47 1.00     5203     9227

Regression Coefficients:
                                                   Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                              4.51      0.23     4.04     4.96 1.00      964     1878
UI2Secondaryvegetation                                 0.07      0.13    -0.18     0.31 1.00     2325     4719
UI2Agriculture_Minimal                                 0.32      0.14     0.05     0.59 1.00     2335     5283
UI2Agriculture_Light                                  -0.02      0.13    -0.29     0.24 1.00     2058     4385
UI2Agriculture_Intense                                 0.00      0.14    -0.28     0.27 1.00     2092     4468
RegionNorthAmerica                                     0.45      0.41    -0.35     1.27 1.00     1158     2590
RegionSouthandSoutheastAsia                            1.76      0.52     0.74     2.76 1.01     1341     3162
RegionSouthandCentralAmerica                           0.97      0.34     0.32     1.65 1.00     1169     2742
RegionSubsaharanAfrica                                 0.66      0.54    -0.41     1.70 1.00     1630     3831
RegionAustralasia                                      2.03      0.51     1.05     3.05 1.00     1467     3164
UI2Secondaryvegetation:RegionNorthAmerica             -0.06      0.17    -0.39     0.28 1.00     3383     7314
UI2Agriculture_Minimal:RegionNorthAmerica             -0.51      0.24    -0.97    -0.05 1.00     4427     9051
UI2Agriculture_Light:RegionNorthAmerica               -0.62      0.21    -1.03    -0.22 1.00     3433     7454
UI2Agriculture_Intense:RegionNorthAmerica             -0.55      0.23    -0.99    -0.11 1.00     3902     8626
UI2Secondaryvegetation:RegionSouthandSoutheastAsia    -0.57      0.45    -1.47     0.31 1.00    13338    14827
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia    -0.58      0.28    -1.14    -0.02 1.00     6903    11526
```

```
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.92      0.17    -1.26    -0.58 1.00     3069     6629
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.61      0.28    -1.16    -0.07 1.00     5940    10905
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.31      0.15    -0.61    -0.02 1.00     2922     6142
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.54      0.16    -0.86    -0.22 1.00     2980     6595
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.46      0.17    -0.79    -0.13 1.00     2805     6150
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.28      0.22    -0.72     0.15 1.00     4031     8593
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.53      0.21    -0.94    -0.11 1.00     4588     9345
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -1.32      0.20    -1.71    -0.93 1.00     3860     8551
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.84      0.21    -1.25    -0.43 1.00     3742     8848
UI2Agriculture_Intense:RegionSubsaharanAfrica          -1.85      0.26    -2.35    -1.33 1.00     5248    10283
UI2Secondaryvegetation:RegionAustralasia               -0.19      0.26    -0.69     0.31 1.00     5753     9603
UI2Agriculture_Minimal:RegionAustralasia               -1.05      0.18    -1.40    -0.71 1.00     3413     7710
UI2Agriculture_Light:RegionAustralasia                 -0.24      0.22    -0.66     0.19 1.00     4013     8438
UI2Agriculture_Intense:RegionAustralasia               -0.21      0.18    -0.56     0.16 1.00     2959     6459

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.81      0.01     0.80     0.83 1.00    13326    12249

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.910 (95% CI [0.908, 0.912])
     Marginal R2: 0.053 (95% CI [0.023, 0.086])
```

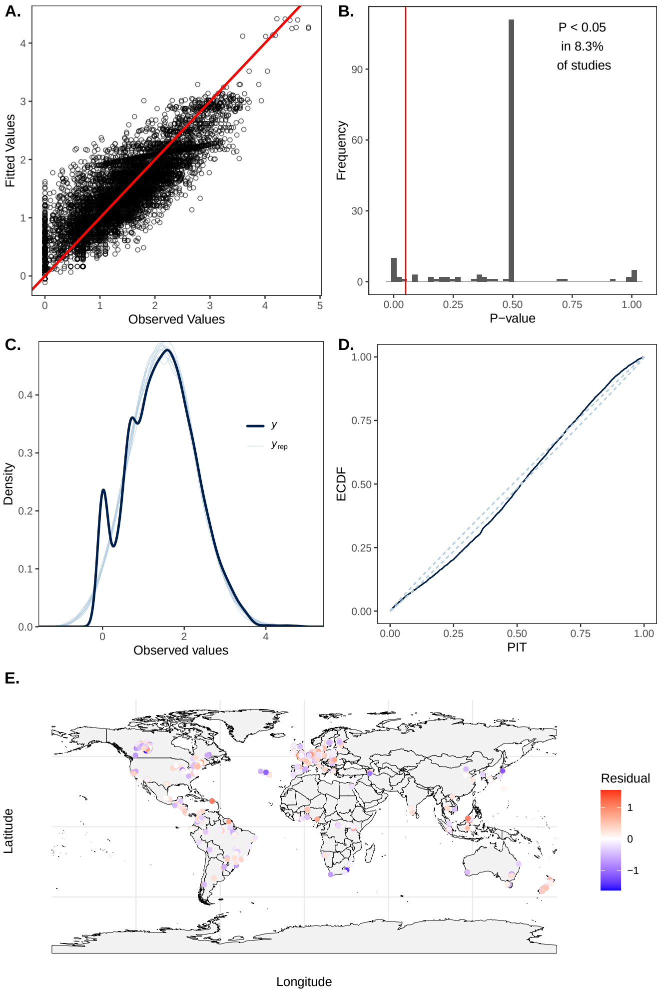


Figure M5: Model diagnostic plots for the Gaussian model of global Simpson's diversity responses to land use: Log(Simpson) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

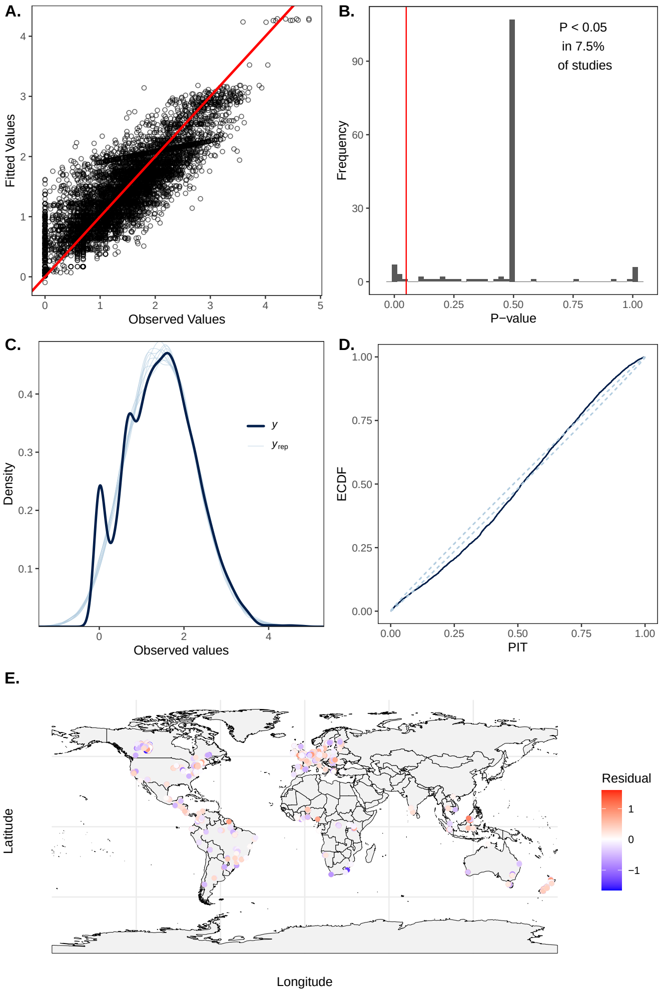


Figure M6: Model diagnostic plots for the Gaussian model of regional Simpson's diversity responses to land use: Log(Simpson) ∼ LandUse × Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M5: Posterior summary of the global model of Simpson's diversity index (Fig. M5).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ UI2 + (1 | SS/SSB)
   Data: model_data (Number of observations: 6726)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 314)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.72      0.03     0.66     0.78 1.00     4243     7967

~SS:SSB (Number of levels: 1589)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.21      0.01     0.18     0.23 1.00     5581    10057

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                  1.70      0.04     1.61     1.79 1.00     2570     5044
UI2Secondaryvegetation    -0.14      0.03    -0.19    -0.09 1.00    19685    15914
UI2Agriculture_Minimal    -0.28      0.03    -0.33    -0.23 1.00    19862    16476
UI2Agriculture_Light      -0.37      0.03    -0.42    -0.32 1.00    16391    14549
UI2Agriculture_Intense    -0.38      0.03    -0.44    -0.32 1.00    19441    16033

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.45      0.00     0.44     0.46 1.00    17170    14736

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.694 (95% CI [0.685, 0.702])
     Marginal R2: 0.035 (95% CI [0.027, 0.043])
```

Table M6: Posterior summary of the regional model of Simpson's diversity index (Fig. M6).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ UI2 * Region + (1 | SS/SSB)
   Data: model_data (Number of observations: 6355)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.73      0.03     0.67     0.80 1.00     4843     8369

~SS:SSB (Number of levels: 1526)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.20      0.01     0.18     0.23 1.00     6174    11261

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                               1.54      0.09     1.36     1.73 1.00     2414     4768
UI2Secondaryvegetation                                  0.00      0.07    -0.13     0.13 1.00     3621     6816
UI2Agriculture_Minimal                                 -0.03      0.07    -0.17     0.11 1.00     3522     7354
UI2Agriculture_Light                                   -0.09      0.07    -0.23     0.04 1.00     3137     6415
UI2Agriculture_Intense                                 -0.10      0.07    -0.25     0.04 1.00     3273     6664
RegionNorthAmerica                                      0.20      0.16    -0.11     0.50 1.00     2848     5792
RegionSouthandSoutheastAsia                             0.44      0.19     0.07     0.81 1.00     3897     7016
RegionSouthandCentralAmerica                            0.01      0.13    -0.24     0.26 1.00     2785     5903
RegionSubsaharanAfrica                                  0.08      0.20    -0.31     0.47 1.00     3546     7044
RegionAustralasia                                      -0.05      0.19    -0.43     0.33 1.00     3409     6850
UI2Secondaryvegetation:RegionNorthAmerica              -0.12      0.09    -0.30     0.06 1.00     5193     9339
UI2Agriculture_Minimal:RegionNorthAmerica              -0.16      0.13    -0.41     0.09 1.00     7145    12140
UI2Agriculture_Light:RegionNorthAmerica                -0.49      0.11    -0.71    -0.28 1.00     5699    10021
UI2Agriculture_Intense:RegionNorthAmerica              -0.63      0.12    -0.87    -0.39 1.00     6236    11806
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.15      0.25    -0.64     0.33 1.00    21751    15055
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.01      0.15    -0.31     0.29 1.00    10156    13999
```

```
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.54      0.09    -0.72    -0.36 1.00     4695     8612
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.18      0.15    -0.47     0.11 1.00     9234    11576
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.01      0.08    -0.17     0.15 1.00     4591     8688
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.17      0.09    -0.34     0.00 1.00     4591     9232
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.25      0.09    -0.42    -0.07 1.00     4334     9006
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.45      0.12    -0.68    -0.22 1.00     6293    11740
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.26      0.11    -0.48    -0.03 1.00     7884    12780
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -0.21      0.11    -0.43    -0.00 1.00     6023    11434
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.17      0.11    -0.39     0.05 1.00     5808    11481
UI2Agriculture_Intense:RegionSubsaharanAfrica          -0.36      0.14    -0.64    -0.09 1.00     8289    12953
UI2Secondaryvegetation:RegionAustralasia               -0.07      0.14    -0.34     0.20 1.00     9137    12772
UI2Agriculture_Minimal:RegionAustralasia               -0.35      0.09    -0.53    -0.16 1.00     4956    10133
UI2Agriculture_Light:RegionAustralasia                 -0.09      0.12    -0.33     0.15 1.00     6697    11970
UI2Agriculture_Intense:RegionAustralasia               -0.07      0.10    -0.27     0.12 1.00     4895    10045

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.44      0.00     0.43     0.45 1.00    19210    14800

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.707 (95% CI [0.699, 0.716])
     Marginal R2: 0.056 (95% CI [0.036, 0.084])
```

B Regional responses per land use type and intensity

The following model diagnostic plots refer to the comparison of global and Europe-specific responses to individual land use types and intensities, for the three taxonomic groups Arthropoda, Chordata and Plantae (Fig. 2).

B.1 Arthropoda

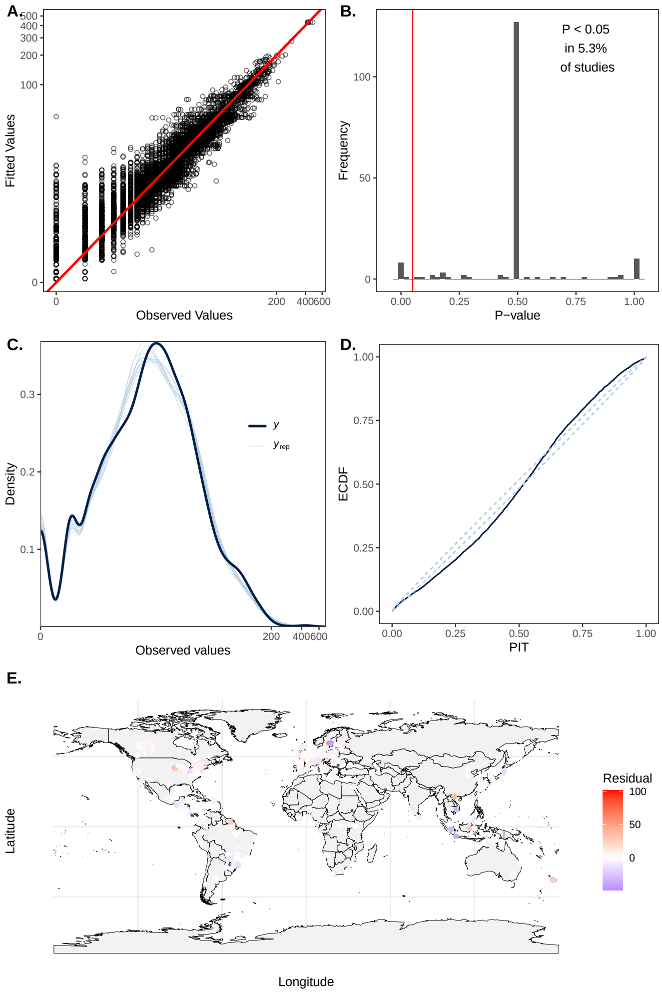


Figure M7: Model diagnostic plots for the zero-inflated negative binomial model of global species richness responses to land use: Richness $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

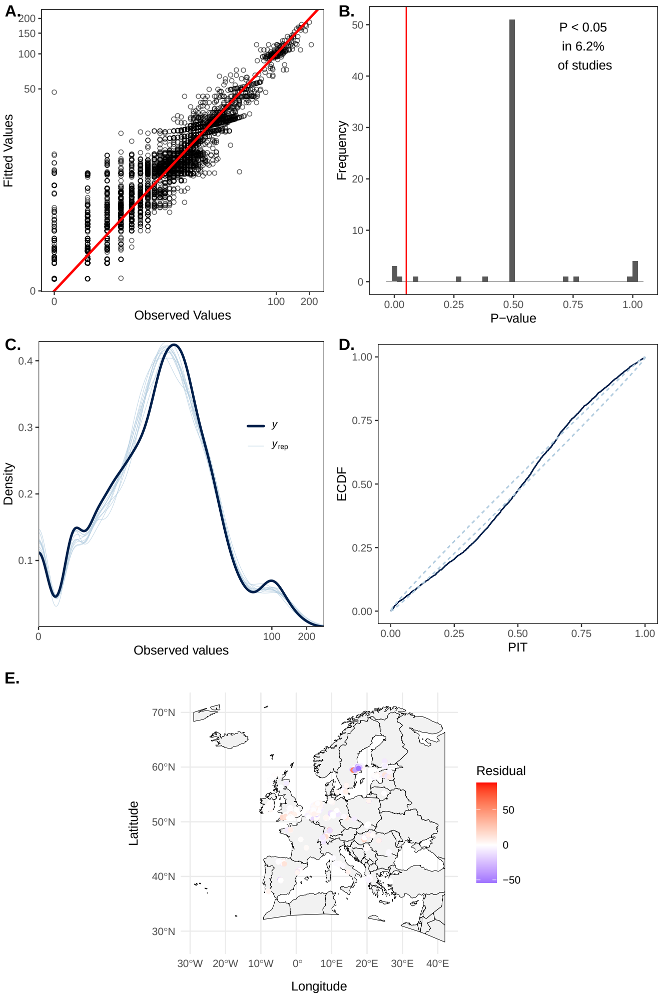


Figure M8: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use in Europe: Richness $\sim$ LandUse + $(1|\text{SS}/\text{SSB})$. Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M7: Posterior summary of the global model of species richness (Fig. M7).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ LU + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 7604)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 341)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.25      0.05     1.16     1.35 1.00     1678     3445

~SS:SSB (Number of levels: 1696)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.19      0.01     0.17     0.22 1.00     5479    10314

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      2.85      0.07     2.71     2.99 1.01      565     1502
zi_Intercept                  -5.34      0.22    -5.79    -4.94 1.00    32271    14439
LUSecondaryvegetation         -0.13      0.02    -0.17    -0.08 1.00    16543    15550
LUCropland_Minimal            -0.32      0.04    -0.40    -0.24 1.00    18845    16656
LUCropland_Light              -0.50      0.04    -0.57    -0.43 1.00    12102    14779
LUCropland_Intense            -0.54      0.04    -0.61    -0.47 1.00    12150    14509
LUPasture_Minimal             -0.22      0.03    -0.27    -0.17 1.00    19322    16125
LUPasture_Light               -0.25      0.03    -0.30    -0.19 1.00    13961    14473
LUPasture_Intense             -0.39      0.03    -0.46    -0.32 1.00    13757    15129
LUPlantationforest_Minimal    -0.10      0.04    -0.18    -0.02 1.00    24793    16319
LUPlantationforest_Light      -0.37      0.03    -0.44    -0.30 1.00    21402    15936
LUPlantationforest_Intense    -0.10      0.04    -0.18    -0.01 1.00    18243    16009

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    15.01      0.56    13.94    16.15 1.00    17382    13094

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.903 (95% CI [0.892, 0.911])
     Marginal R2: 0.008 (95% CI [0.005, 0.011])
```

Table M8: Posterior summary of the model of species richness for Europe (Fig. M8).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ LU + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 3412)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 118)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.37      0.09     1.20     1.57 1.00     3463     6871

~SS:SSB (Number of levels: 897)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.15      0.01     0.12     0.18 1.00     6293    11021

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      2.56      0.13     2.30     2.83 1.00     1405     2502
zi_Intercept                  -5.07      0.27    -5.66    -4.59 1.00    38999    13164
LUSecondaryvegetation          0.04      0.05    -0.05     0.13 1.00    14463    16164
LUCropland_Minimal            -0.18      0.06    -0.30    -0.06 1.00    16937    16715
LUCropland_Light              -0.23      0.06    -0.36    -0.10 1.00    11119    14853
LUCropland_Intense            -0.23      0.06    -0.35    -0.11 1.00    11474    14306
LUPasture_Minimal              0.14      0.05     0.05     0.24 1.00    14487    16566
```

```
LUPasture_Light                0.02      0.05    -0.09     0.12 1.00    11248    14082
LUPasture_Intense             -0.06      0.06    -0.18     0.05 1.00    10769    13479
LUPlantationforest_Minimal     0.04      0.09    -0.13     0.21 1.00    23539    16593
LUPlantationforest_Light       0.01      0.10    -0.19     0.20 1.00    31103    16369
LUPlantationforest_Intense     0.72      0.08     0.57     0.88 1.00    13519    15080

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    19.38      1.39    16.83    22.30 1.00    14984    14998

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.917 (95% CI [0.908, 0.924])
     Marginal R2: 0.007 (95% CI [0.003, 0.012])
```

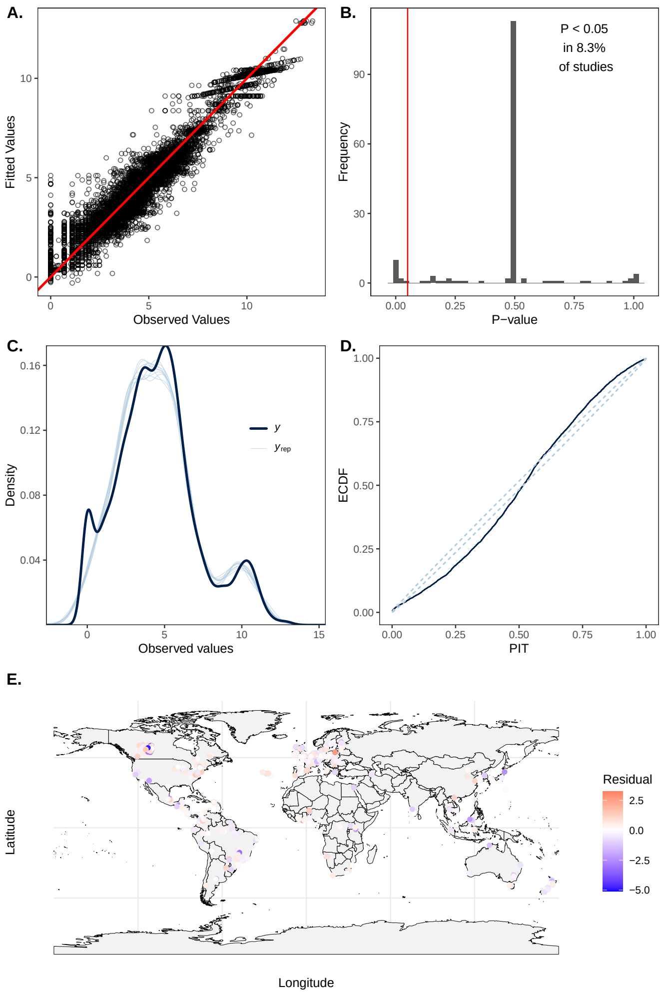


Figure M9: Model diagnostic plots for the Gaussian model of global total abundance responses to land use: Log(Abundance+1) ∼ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

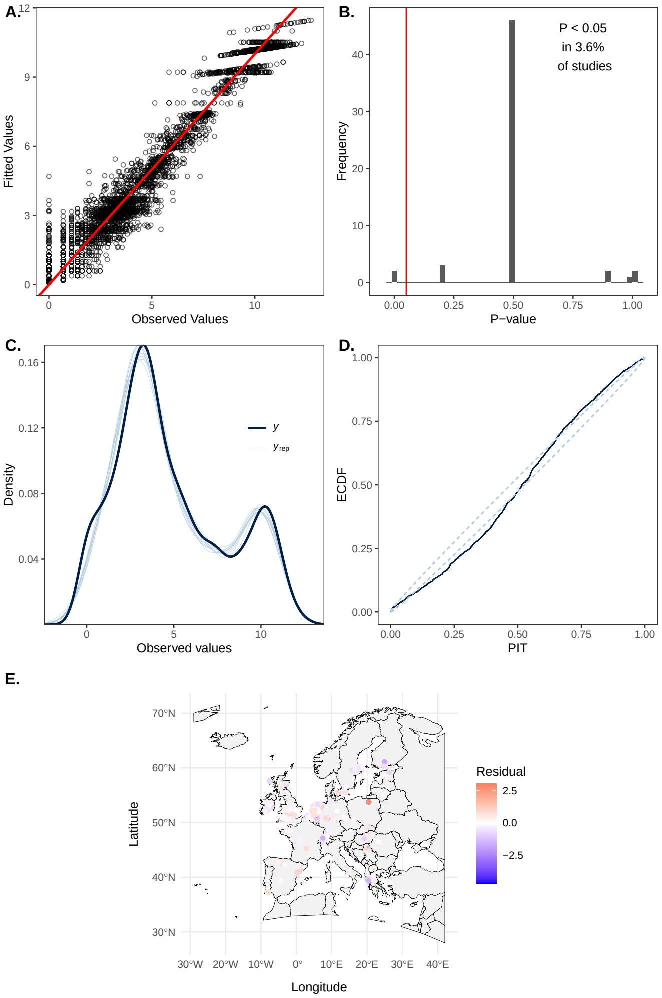


Figure M10: Model diagnostic plots for the Gaussian model of total abundance responses to land use in Europe: Log(Abundance+1) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M9: Posterior summary of the global model of total abundance (Fig. M9).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 7122)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 314)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.09      0.09     1.92     2.26 1.00     1809     4331

~SS:SSB (Number of levels: 1624)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.41      0.02     0.37     0.45 1.00     5925    11912

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      5.30      0.12     5.06     5.54 1.01      897     2327
LUSecondaryvegetation         -0.22      0.05    -0.31    -0.13 1.00    13832    14589
LUCropland_Minimal            -0.80      0.07    -0.95    -0.66 1.00    17671    16103
LUCropland_Light              -0.91      0.07    -1.05    -0.76 1.00    11117    14650
LUCropland_Intense            -0.93      0.07    -1.08    -0.78 1.00    12122    13991
LUPasture_Minimal             -0.07      0.06    -0.18     0.05 1.00    17254    15105
LUPasture_Light               -0.20      0.06    -0.32    -0.08 1.00    13161    14900
LUPasture_Intense             -0.30      0.07    -0.44    -0.16 1.00    13665    16240
LUPlantationforest_Minimal    -0.00      0.09    -0.18     0.17 1.00    22838    15678
LUPlantationforest_Light      -0.55      0.07    -0.68    -0.41 1.00    21637    16108
LUPlantationforest_Intense     0.06      0.10    -0.13     0.25 1.00    23689    15508

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.81      0.01     0.80     0.83 1.00    19874    14735

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.907 (95% CI [0.905, 0.909])
     Marginal R2: 0.018 (95% CI [0.014, 0.022])
```

Table M10: Posterior summary of the model of total abundance for Europe (Fig. M10).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 3211)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 111)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.13      0.15     1.85     2.46 1.00     1759     3174

~SS:SSB (Number of levels: 876)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.31      0.03     0.25     0.38 1.00     4148     8416

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      4.67      0.24     4.20     5.14 1.00     1088     2121
LUSecondaryvegetation          0.06      0.13    -0.18     0.30 1.00     3822     8141
LUCropland_Minimal            -0.61      0.16    -0.93    -0.29 1.00     4391     9601
LUCropland_Light              -0.68      0.16    -0.99    -0.35 1.00     3066     6797
LUCropland_Intense            -0.62      0.15    -0.92    -0.32 1.00     3286     7139
LUPasture_Minimal              0.72      0.15     0.42     1.02 1.00     3597     8666
LUPasture_Light                0.24      0.14    -0.04     0.52 1.00     3130     7309
LUPasture_Intense              0.18      0.15    -0.11     0.48 1.00     3091     6657
LUPlantationforest_Minimal     0.34      0.19    -0.03     0.70 1.00     6741    11355
LUPlantationforest_Light       0.29      0.20    -0.09     0.68 1.00    11575    15096
```

```
LUPlantationforest_Intense     1.26      0.22     0.83     1.69 1.00     5209    10657

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.79      0.01     0.77     0.82 1.00    12548    13361

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.938 (95% CI [0.937, 0.940])
     Marginal R2: 0.025 (95% CI [0.019, 0.032])
```

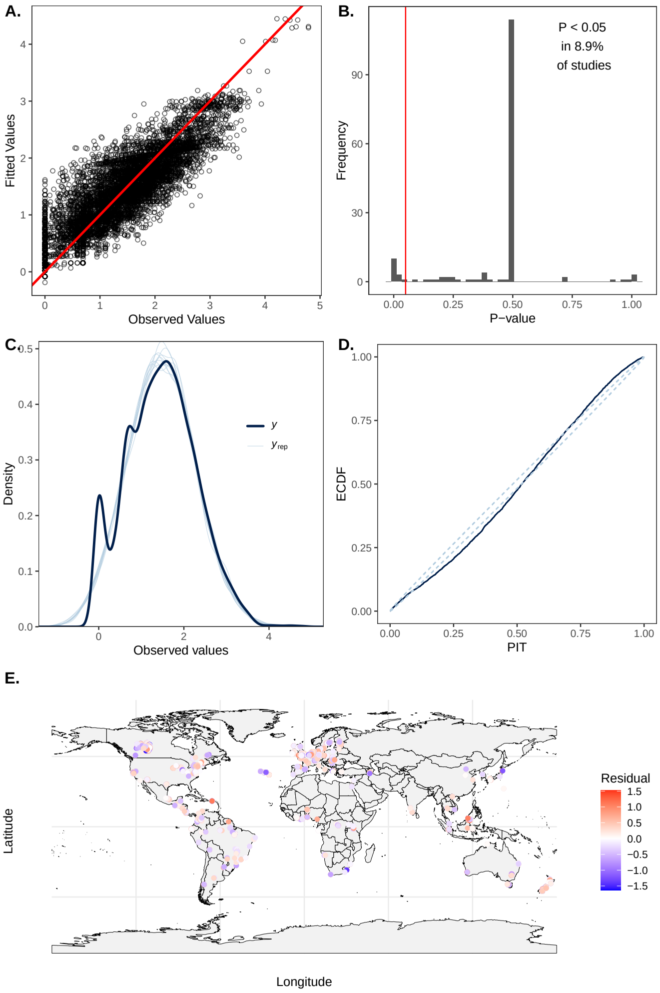


Figure M11: Model diagnostic plots for the Gaussian model of global Simpson's diversity responses to land use: Log(Simpson) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

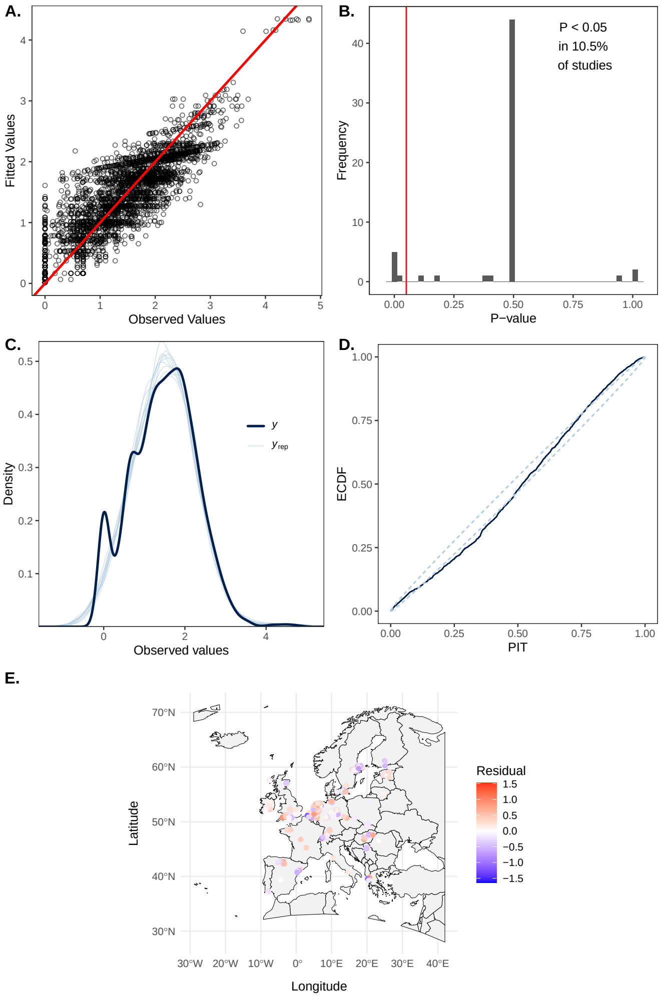


Figure M12: Model diagnostic plots for the Gaussian model of Simpson's diversity responses to land use in Europe: Log(Simpson) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M11: Posterior summary of the global model of Simpson's diversity index (Fig. M11).

```
                                        BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 6726)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 314)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.72      0.03     0.66     0.79 1.00     2370     4781

~SS:SSB (Number of levels: 1589)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.20      0.01     0.18     0.22 1.00     4678     9207

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      1.70      0.05     1.61     1.79 1.01     1301     2503
LUSecondaryvegetation         -0.14      0.03    -0.19    -0.09 1.00    11008    13901
LUCropland_Minimal            -0.37      0.04    -0.46    -0.29 1.00    11418    14441
LUCropland_Light              -0.45      0.04    -0.53    -0.37 1.00     8191    11489
LUCropland_Intense            -0.45      0.04    -0.54    -0.37 1.00     8241    12190
LUPasture_Minimal             -0.23      0.03    -0.30    -0.17 1.00    12631    14704
LUPasture_Light               -0.30      0.03    -0.37    -0.24 1.00     9823    13644
LUPasture_Intense             -0.40      0.04    -0.48    -0.32 1.00    10096    14376
LUPlantationforest_Minimal    -0.24      0.05    -0.34    -0.14 1.00    16751    14853
LUPlantationforest_Light      -0.43      0.04    -0.50    -0.35 1.00    14275    14196
LUPlantationforest_Intense    -0.20      0.05    -0.30    -0.09 1.00    15825    16041

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.45      0.00     0.44     0.46 1.00    14353    14046

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.694 (95% CI [0.686, 0.702])
     Marginal R2: 0.044 (95% CI [0.034, 0.055])
```

Table M12: Posterior summary of the model of Simpson's diversity index for Europe (Fig. M12).

```
                                        BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 3032)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 111)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.79      0.06     0.68     0.91 1.00     6265     9955

~SS:SSB (Number of levels: 853)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.19      0.02     0.15     0.23 1.00     5619    10698

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      1.55      0.10     1.35     1.75 1.00     4361     8155
LUSecondaryvegetation          0.00      0.07    -0.13     0.14 1.00    11446    15568
LUCropland_Minimal            -0.18      0.09    -0.36    -0.01 1.00    12156    15524
LUCropland_Light              -0.18      0.09    -0.36    -0.01 1.00     9570    13592
LUCropland_Intense            -0.13      0.09    -0.30     0.04 1.00     9566    12947
LUPasture_Minimal              0.12      0.08    -0.05     0.28 1.00    10640    14536
LUPasture_Light               -0.01      0.08    -0.17     0.14 1.00     9529    13244
LUPasture_Intense             -0.10      0.08    -0.26     0.06 1.00     9469    13533
LUPlantationforest_Minimal    -0.17      0.11    -0.39     0.04 1.00    18237    16782
```

```
LUPlantationforest_Light      -0.08      0.11    -0.29      0.15 1.00    27318    16927
LUPlantationforest_Intense     0.40      0.12     0.16      0.64 1.00    13332    15760

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.44      0.01     0.43     0.45 1.00    18178    14228

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.690 (95% CI [0.677, 0.703])
     Marginal R2: 0.020 (95% CI [0.010, 0.032])
```

B.2 Chordata

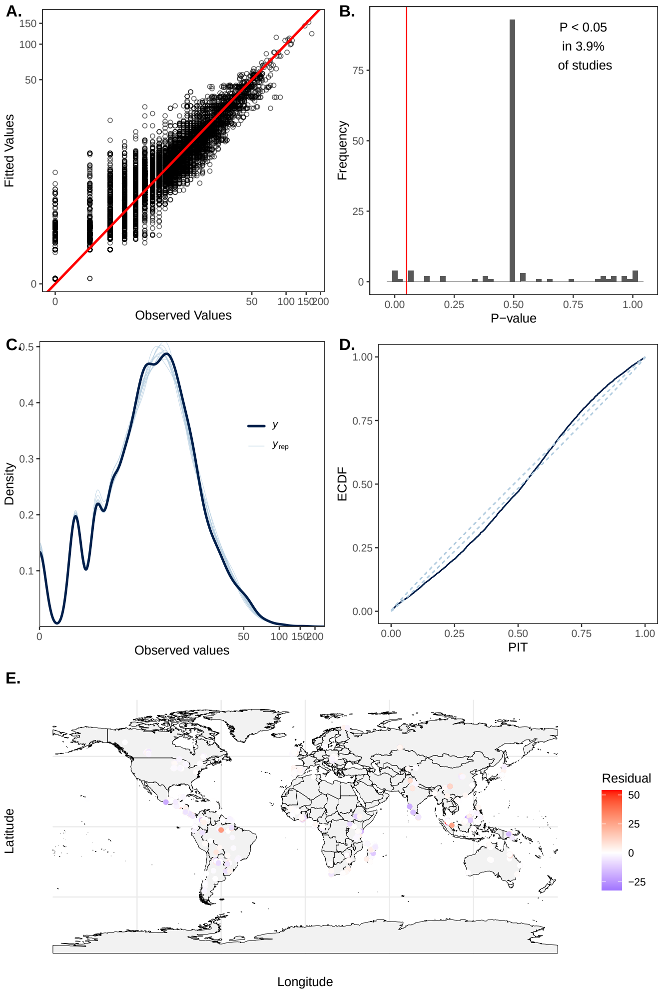


Figure M13: Model diagnostic plots for the zero-inflated negative binomial model of global species richness responses to land use: Richness $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

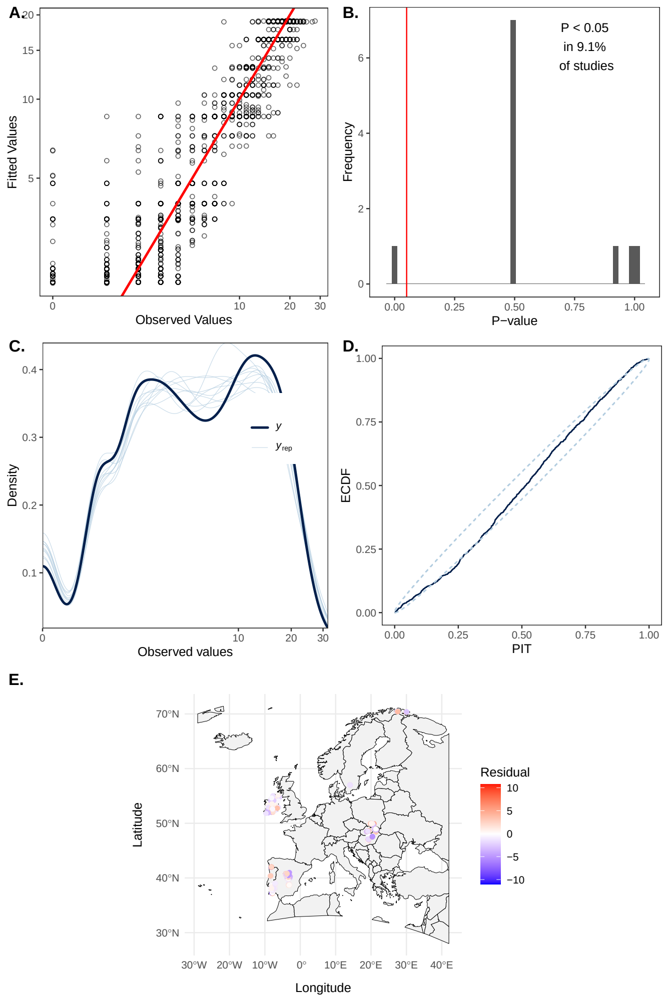


Figure M14: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use in Europe: Richness $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M13: Posterior summary of the global model of species richness (Fig. M13).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ LU + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 7842)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 224)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.07      0.06     0.97     1.19 1.00     2378     5275

~SS:SSB (Number of levels: 855)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.22      0.01     0.19     0.24 1.00     6180    11195

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      2.44      0.07     2.30     2.59 1.01     1006     2371
zi_Intercept                  -8.88      1.25   -11.88    -7.05 1.00    23800    11167
LUSecondaryvegetation         -0.09      0.02    -0.12    -0.05 1.00    24133    16956
LUCropland_Minimal            -0.17      0.03    -0.23    -0.11 1.00    33215    16169
LUCropland_Light              -0.20      0.03    -0.27    -0.13 1.00    36759    15186
LUCropland_Intense            -0.23      0.10    -0.42    -0.04 1.00    37110    15235
LUPasture_Minimal             -0.24      0.04    -0.32    -0.17 1.00    30795    16130
LUPasture_Light               -0.31      0.03    -0.37    -0.26 1.00    30864    16740
LUPasture_Intense             -0.19      0.05    -0.29    -0.09 1.00    22248    16565
LUPlantationforest_Minimal    -0.07      0.03    -0.12    -0.02 1.00    23920    16106
LUPlantationforest_Light      -0.22      0.02    -0.26    -0.18 1.00    24204    16937
LUPlantationforest_Intense    -0.46      0.04    -0.53    -0.39 1.00    30199    15965

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    31.42      1.87    27.94    35.32 1.00    31326    14006

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.855 (95% CI [0.848, 0.862])
     Marginal R2: 0.011 (95% CI [0.007, 0.015])
```

Table M14: Posterior summary of the model of species richness for Europe (Fig. M14).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ LU + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 1157)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 15)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.69      0.17     0.43     1.08 1.00     8141    11199

~SS:SSB (Number of levels: 113)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.29      0.06     0.18     0.42 1.00     5098    10136

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      2.33      0.20     1.94     2.72 1.00     6423     8930
zi_Intercept                  -5.26      0.97    -7.81    -4.05 1.00     9163     7633
LUSecondaryvegetation         -0.15      0.04    -0.23    -0.07 1.00    18047    15462
LUCropland_Minimal             0.19      0.09     0.01     0.36 1.00    23136    15474
LUCropland_Intense            -0.22      0.12    -0.46     0.02 1.00    28209    15648
LUPasture_Minimal             -0.55      0.13    -0.80    -0.29 1.00    21141    15364
LUPasture_Light               -0.32      0.08    -0.47    -0.17 1.00    19260    16543
```

```
LUPasture_Intense             -0.01      0.31    -0.63     0.56 1.00    32256    13428
LUPlantationforest_Minimal     0.00      0.06    -0.11     0.11 1.00    19519    16181
LUPlantationforest_Light      -0.23      0.05    -0.33    -0.13 1.00    22194    15704
LUPlantationforest_Intense    -0.61      0.07    -0.74    -0.48 1.00    24867    16728

Further Distributional Parameters:
           Estimate       Est.Error l-95% CI    u-95% CI Rhat Bulk_ESS Tail_ESS
shape 6322954526.55 290719243411.97   487.10 13141967.76 1.00    14777     8381

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.850 (95% CI [0.837, 0.861])
     Marginal R2: 0.083 (95% CI [0.029, 0.158])
```

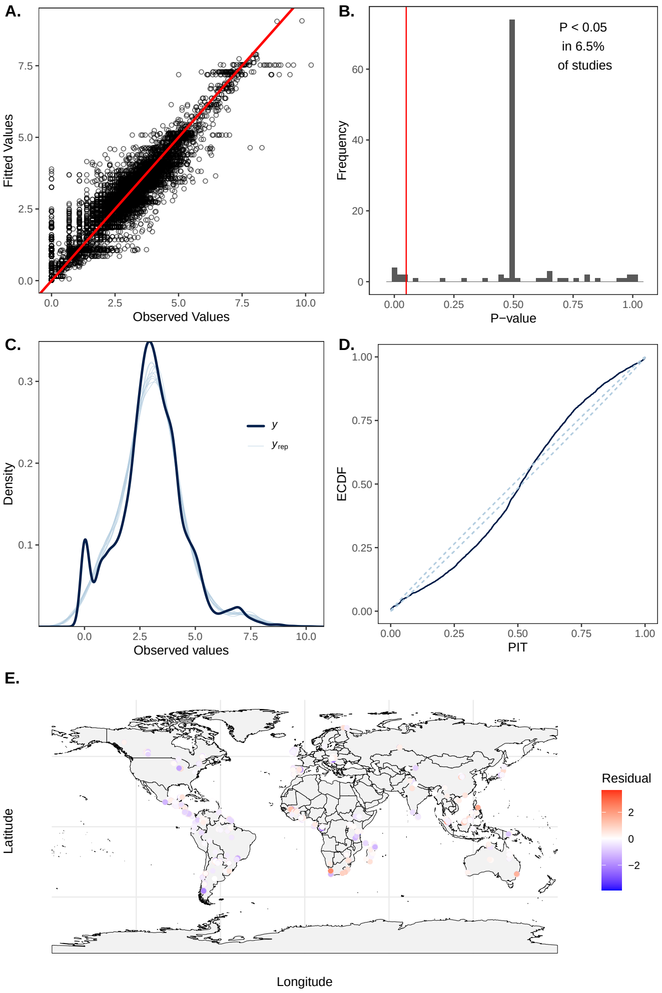


Figure M15: Model diagnostic plots for the Gaussian model of global total abundance responses to land use: Log(Abundance+1) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

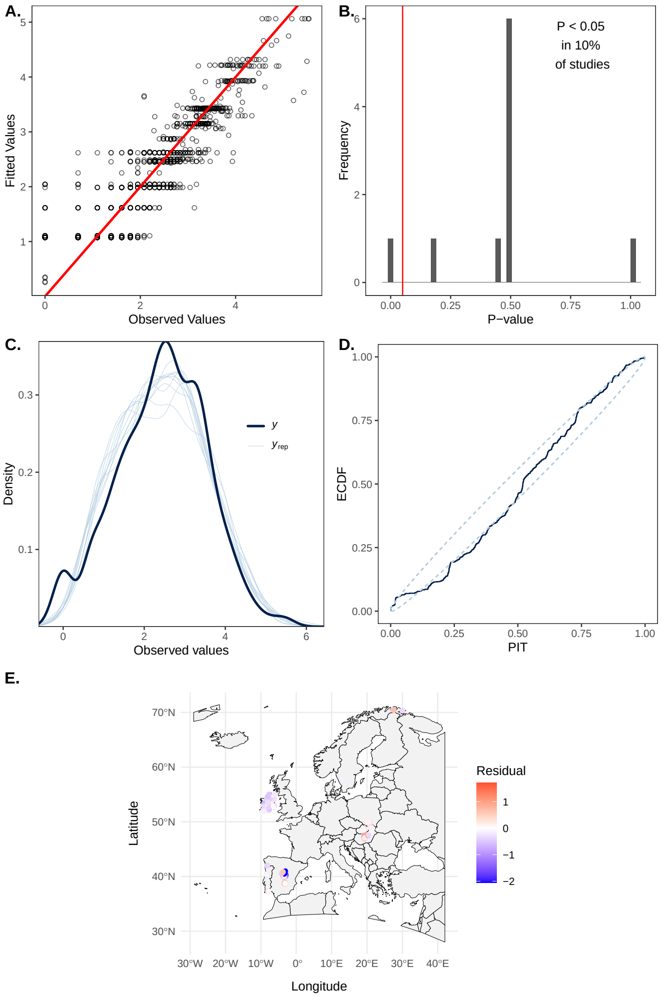


Figure M16: Model diagnostic plots for the Gaussian model of total abundance responses to land use in Europe: Log(Abundance+1) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M15: Posterior summary of the global model of total abundance (Fig. M15).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 7007)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 199)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.73      0.09     1.56     1.92 1.00     2471     5066

~SS:SSB (Number of levels: 751)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.33      0.02     0.29     0.37 1.00     6843    12431

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      3.83      0.12     3.59     4.07 1.01      983     2029
LUSecondaryvegetation         -0.04      0.03    -0.10     0.02 1.00    20326    16038
LUCropland_Minimal             0.01      0.05    -0.08     0.11 1.00    32767    15044
LUCropland_Light              -0.20      0.06    -0.32    -0.07 1.00    36154    15222
LUCropland_Intense            -0.04      0.09    -0.23     0.15 1.00    31540    15829
LUPasture_Minimal             -0.12      0.06    -0.25     0.00 1.00    30492    16358
LUPasture_Light               -0.52      0.05    -0.61    -0.43 1.00    29056    15774
LUPasture_Intense             -0.13      0.10    -0.32     0.06 1.00    25215    15414
LUPlantationforest_Minimal    -0.02      0.04    -0.10     0.07 1.00    23613    17202
LUPlantationforest_Light      -0.24      0.04    -0.31    -0.17 1.00    22643    16276
LUPlantationforest_Intense    -0.26      0.05    -0.36    -0.15 1.00    28902    15481

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.60      0.01     0.59     0.61 1.00    30488    14143

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.838 (95% CI [0.834, 0.841])
     Marginal R2: 0.008 (95% CI [0.006, 0.010])
```

Figure M17: Posterior summary of the model of total abundance for Europe (Fig. M16).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 966)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 14)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.41      0.31     0.02     1.14 1.03      160       71

~SS:SSB (Number of levels: 35)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.13      0.16     0.86     1.47 1.01     2123     7896

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      3.36      0.28     2.80     3.90 1.01     3048     5019
LUSecondaryvegetation         -0.27      0.08    -0.43    -0.11 1.02      255      758
LUCropland_Minimal             0.16      0.11    -0.06     0.37 1.01     1120    13231
LUCropland_Intense            -0.30      0.12    -0.53    -0.08 1.01      386     7667
LUPasture_Minimal             -0.34      0.18    -0.71     0.01 1.01     1155     7831
LUPasture_Light               -0.43      0.11    -0.65    -0.20 1.00     5675     8496
LUPasture_Intense              0.04      0.55    -1.03     1.13 1.00    16908    13144
LUPlantationforest_Minimal     0.10      0.10    -0.09     0.29 1.02      219      179
LUPlantationforest_Light      -0.28      0.11    -0.48    -0.03 1.03      125       25
LUPlantationforest_Intense    -0.92      0.13    -1.16    -0.68 1.03      151       74
```

```
Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.51      0.01     0.49     0.54 1.02      267      185

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.790 (95% CI [0.777, 0.800])
     Marginal R2: 0.051 (95% CI [0.036, 0.070])
```

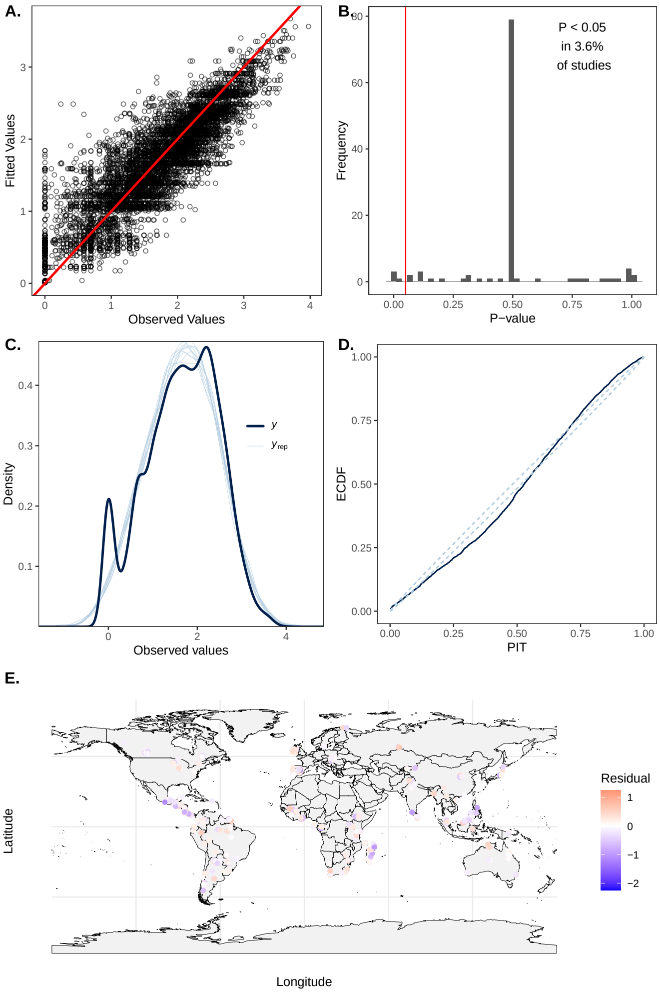


Figure M18: Model diagnostic plots for the Gaussian model of global Simpson's diversity responses to land use: Log(Simpson) ∼ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

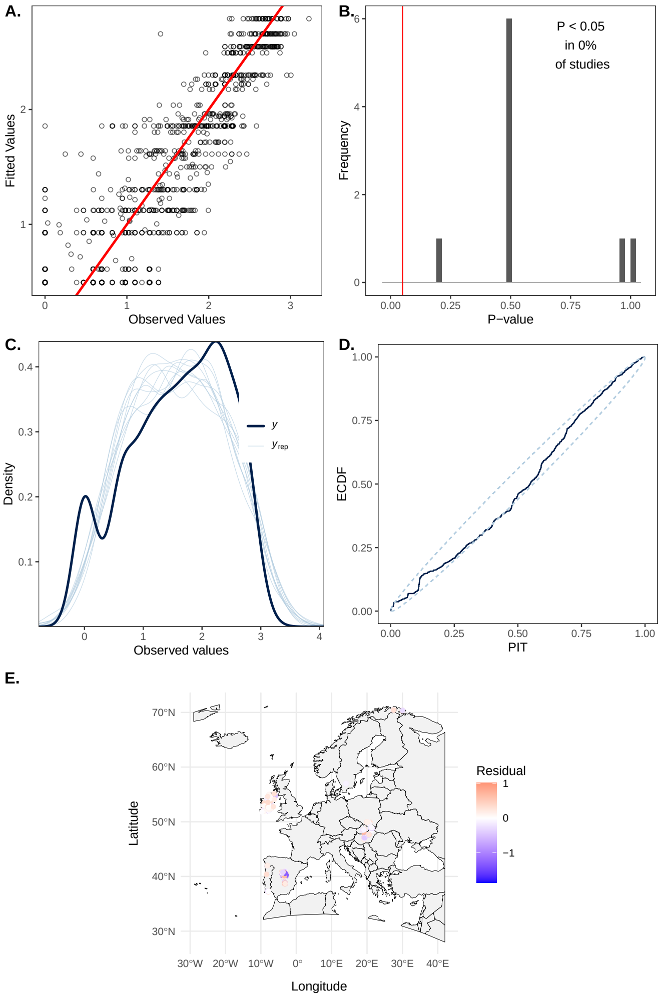


Figure M19: Model diagnostic plots for the Gaussian model of Simpson's diversity responses to land use in Europe: Log(Simpson) $\sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Figure M20: Posterior summary of the global model of Simpson's diversity index (Fig. M18).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 6708)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 199)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.82      0.05     0.73     0.91 1.00     5216     9227

~SS:SSB (Number of levels: 742)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.22      0.01     0.20     0.25 1.00     7211    11805

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      1.80      0.06     1.68     1.92 1.00     2555     5477
LUSecondaryvegetation         -0.11      0.02    -0.15    -0.07 1.00    28142    18557
LUCropland_Minimal            -0.18      0.03    -0.24    -0.11 1.00    39875    17040
LUCropland_Light              -0.30      0.04    -0.39    -0.22 1.00    45355    15905
LUCropland_Intense            -0.25      0.07    -0.38    -0.12 1.00    41140    16051
LUPasture_Minimal             -0.31      0.05    -0.40    -0.23 1.00    38275    16438
LUPasture_Light               -0.27      0.03    -0.34    -0.21 1.00    35881    15628
LUPasture_Intense             -0.33      0.06    -0.46    -0.20 1.00    33476    16888
LUPlantationforest_Minimal    -0.11      0.03    -0.17    -0.05 1.00    31383    16441
LUPlantationforest_Light      -0.18      0.03    -0.23    -0.13 1.00    30372    17262
LUPlantationforest_Intense    -0.36      0.04    -0.43    -0.28 1.00    36510    16790

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.41      0.00     0.40     0.42 1.00    30952    14920

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.749 (95% CI [0.743, 0.755])
     Marginal R2: 0.019 (95% CI [0.014, 0.024])
```

Figure M21: Posterior summary of the model of Simpson's diversity index for Europe (Fig. M19).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogSimp ~ LU + (1 | SS/SSB)
   Data: model_data (Number of observations: 923)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 14)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.51      0.19     0.12     0.90 1.00     5069     3798

~SS:SSB (Number of levels: 33)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.30      0.11     0.08     0.53 1.00     3666     5649

Regression Coefficients:
                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                      2.04      0.17     1.70     2.38 1.00    11948    13019
LUSecondaryvegetation         -0.24      0.06    -0.37    -0.12 1.00    13029    14983
LUCropland_Minimal             0.13      0.09    -0.05     0.31 1.00    16062    16549
LUCropland_Intense            -0.36      0.09    -0.54    -0.17 1.00    17482    15810
LUPasture_Minimal             -0.80      0.15    -1.09    -0.50 1.00    20455    15872
LUPasture_Light               -0.49      0.09    -0.67    -0.30 1.00    17064    16462
LUPasture_Intense             -0.37      0.45    -1.26     0.51 1.00    31683    14779
LUPlantationforest_Minimal    -0.05      0.08    -0.20     0.10 1.00    14322    16492
LUPlantationforest_Light      -0.32      0.07    -0.47    -0.18 1.00    20009    16533
```

```
LUPlantationforest_Intense    -0.46      0.09    -0.64    -0.28 1.00    25689    14591

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.40      0.01     0.39     0.42 1.00    29767    14504

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.769 (95% CI [0.756, 0.782])
     Marginal R2: 0.057 (95% CI [0.036, 0.082])
```

C Compositional dissimilarity

Here we provide an example model diagnostics plot from one of the 100 models fitted on different permutations of compositional dissimilarity between natural vegetation and other land uses (Fig. 4). These diagnostics are from the model of total dissimilarity, but diagnostics from the turnover and nestedness components are similar.

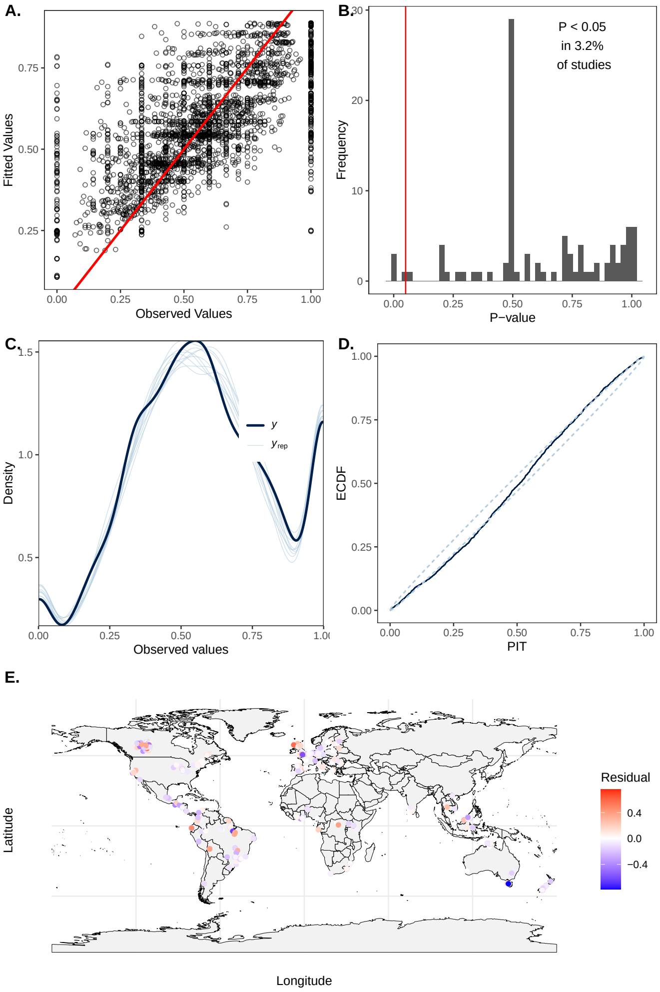


Figure M22: Model diagnostic plots for the zero-and-one inflated beta model of total compositional dissimilarity (Sørensen's Index): Dissimilarity ∼ LandUse * Region + (1|SS). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

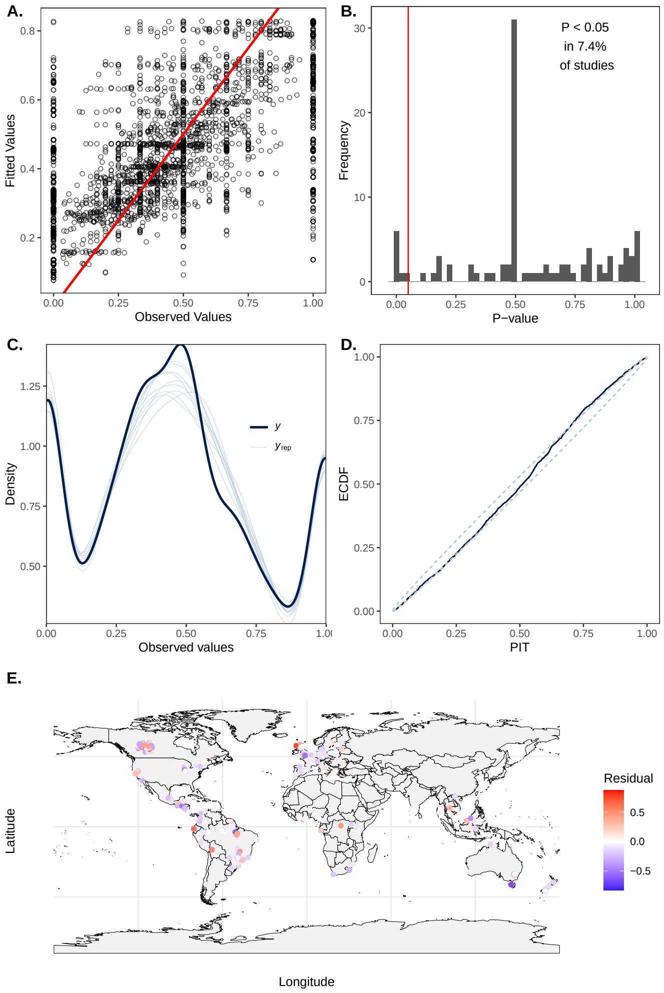


Figure M23: Model diagnostic plots for the zero-and-one inflated beta model of species turnover (Sørensen's Index): Turnover $\sim$ LandUse * Region + (1|SS). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

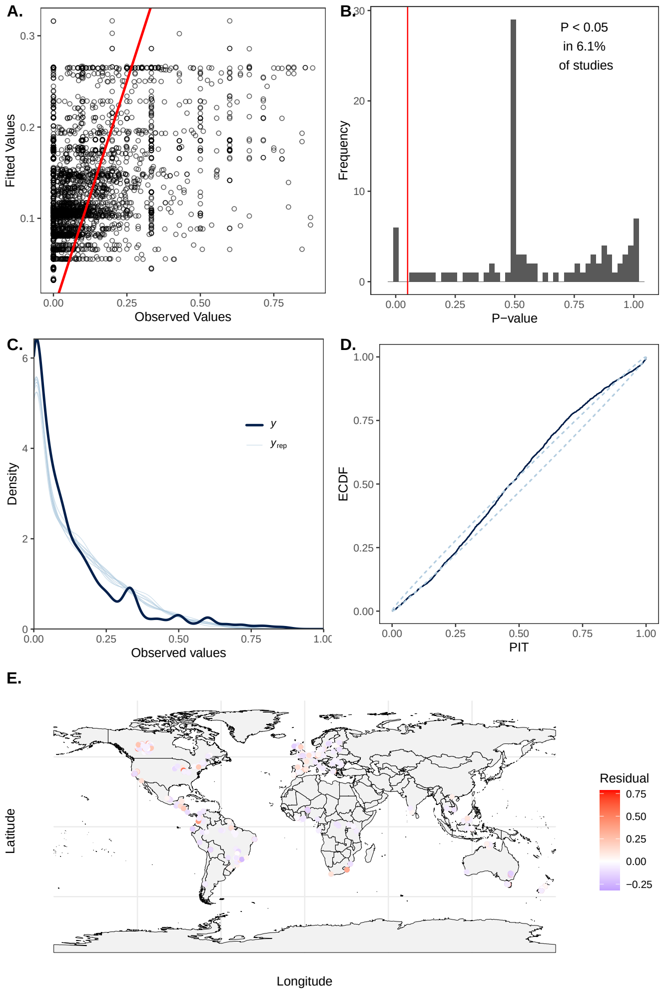


Figure M24: Model diagnostic plots for the zero-and-one inflated beta model of species nestedness (Sørensen's Index): Nestedness ∼ LandUse * Region + (1|SS). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M16: Posterior summary of the model of total compositional dissimilarity (Fig. M22).

```
                                          BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit; phi = log; zoi = logit; coi = logit
Formula: Dissimilarity ~ LU * Region + Dist_geo + (1 | SS)
         phi ~ 1
         zoi ~ (1 | SS)
         coi ~ (1 | SS)
   Data: model_data (Number of observations: 2858)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 187)
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         0.55      0.04     0.48     0.63 1.00     4093     8313
sd(zoi_Intercept)     2.80      0.34     2.22     3.54 1.00     2997     5966
sd(coi_Intercept)     3.55      0.78     2.31     5.37 1.00     5005     8751

Regression Coefficients:
                                                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                           -0.27      0.09    -0.44    -0.10 1.00     1995     4476
phi_Intercept                                        2.43      0.03     2.38     2.49 1.00    21620    13743
zoi_Intercept                                       -3.53      0.36    -4.30    -2.88 1.00     2651     5135
coi_Intercept                                        1.92      0.58     0.86     3.14 1.00     3270     6305
LUAgriculture_Minimal                                0.75      0.09     0.58     0.93 1.00     5485     9451
LUAgriculture_Light                                  0.28      0.14     0.01     0.55 1.00     3876     7036
LUAgriculture_Intense                                0.55      0.19     0.18     0.92 1.00     4280     9516
RegionNorthAmerica                                   0.40      0.14     0.11     0.68 1.00     2085     4501
RegionSouthandSoutheastAsia                         -0.29      0.19    -0.67     0.09 1.00     3473     6496
RegionSouthandCentralAmerica                        -0.17      0.13    -0.42     0.09 1.00     2518     4834
RegionSubsaharanAfrica                              -0.07      0.19    -0.44     0.30 1.00     3234     5406
RegionAustralasia                                    0.27      0.19    -0.10     0.64 1.00     2043     4714
Dist_geo                                             0.12      0.02     0.08     0.16 1.00    12869    15537
LUAgriculture_Minimal:RegionNorthAmerica            -0.73      0.15    -1.03    -0.43 1.00     9854    13640
LUAgriculture_Light:RegionNorthAmerica              -0.15      0.20    -0.54     0.24 1.00     5883    10883
LUAgriculture_Intense:RegionNorthAmerica            -0.19      0.29    -0.75     0.38 1.00     6873    12517
LUAgriculture_Minimal:RegionSouthandSoutheastAsia   -0.40      0.32    -1.04     0.23 1.00     9962    13721
LUAgriculture_Light:RegionSouthandSoutheastAsia      0.40      0.16     0.08     0.72 1.00     4684     8863
LUAgriculture_Intense:RegionSouthandSoutheastAsia    0.70      0.36    -0.01     1.42 1.00     9138    12652
LUAgriculture_Minimal:RegionSouthandCentralAmerica  -0.53      0.12    -0.78    -0.29 1.00     7520    11689
LUAgriculture_Light:RegionSouthandCentralAmerica     0.49      0.18     0.14     0.84 1.00     4797     9274
LUAgriculture_Intense:RegionSouthandCentralAmerica   0.13      0.25    -0.35     0.63 1.00     5399    11412
LUAgriculture_Minimal:RegionSubsaharanAfrica        -0.64      0.16    -0.94    -0.32 1.00     8290    12643
LUAgriculture_Light:RegionSubsaharanAfrica          -0.44      0.22    -0.86    -0.02 1.00     5837    11520
LUAgriculture_Intense:RegionSubsaharanAfrica        -0.30      0.27    -0.83     0.22 1.00     6129    11011
LUAgriculture_Minimal:RegionAustralasia             -0.45      0.16    -0.75    -0.13 1.00    10221    13590
LUAgriculture_Light:RegionAustralasia                0.14      0.29    -0.43     0.70 1.00     7867    12357
LUAgriculture_Intense:RegionAustralasia             -0.41      0.24    -0.88     0.06 1.00     5722    10523

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.434 (95% CI [0.412, 0.457])
     Marginal R2: 0.102 (95% CI [0.071, 0.136])
```

Table M17: Posterior summary of the model of species turnover (Fig. M23).

```
                                          BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit; phi = log; zoi = logit; coi = logit
Formula: Dissimilarity ~ LU * Region + Dist_geo + (1 | SS)
         phi ~ 1
         zoi ~ (1 | SS)
         coi ~ (1 | SS)
   Data: model_data (Number of observations: 2858)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 187)
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         0.54      0.04     0.46     0.62 1.00     5435     9801
```

```
sd(zoi_Intercept)     3.20      0.33     2.61     3.91 1.00     4454     8184
sd(coi_Intercept)     2.51      0.40     1.85     3.38 1.00     4760     8903

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                              -0.62      0.09    -0.80    -0.44 1.00     3074     5555
phi_Intercept                                           2.37      0.03     2.30     2.43 1.00    24875    14479
zoi_Intercept                                          -2.38      0.32    -3.07    -1.80 1.00     2460     5087
coi_Intercept                                          -0.92      0.34    -1.63    -0.29 1.00     3072     6288
LUAgriculture_Minimal                                   0.93      0.09     0.75     1.12 1.00     8512    12063
LUAgriculture_Light                                     0.42      0.16     0.11     0.73 1.00     5473     9255
LUAgriculture_Intense                                   0.57      0.25     0.08     1.06 1.00     5535     8982
RegionNorthAmerica                                      0.61      0.15     0.31     0.90 1.00     3038     5513
RegionSouthandSoutheastAsia                            -0.27      0.20    -0.67     0.11 1.00     5332     8952
RegionSouthandCentralAmerica                           -0.16      0.13    -0.42     0.11 1.00     4132     8688
RegionSubsaharanAfrica                                  0.01      0.20    -0.37     0.39 1.00     4863     8355
RegionAustralasia                                       0.33      0.19    -0.04     0.70 1.00     3903     6910
Dist_geo                                                0.10      0.02     0.06     0.14 1.00    17213    16189
LUAgriculture_Minimal:RegionNorthAmerica               -0.76      0.19    -1.12    -0.39 1.00    12820    14461
LUAgriculture_Light:RegionNorthAmerica                 -0.38      0.23    -0.83     0.07 1.00     7942    12577
LUAgriculture_Intense:RegionNorthAmerica               -0.53      0.35    -1.21     0.16 1.00     7998    11420
LUAgriculture_Minimal:RegionSouthandSoutheastAsia      -0.75      0.34    -1.42    -0.09 1.00    13998    14496
LUAgriculture_Light:RegionSouthandSoutheastAsia        -0.04      0.18    -0.40     0.31 1.00     6188    11190
LUAgriculture_Intense:RegionSouthandSoutheastAsia       0.66      0.40    -0.12     1.46 1.00     8792    13027
LUAgriculture_Minimal:RegionSouthandCentralAmerica     -0.82      0.14    -1.10    -0.54 1.00    11913    14634
LUAgriculture_Light:RegionSouthandCentralAmerica        0.29      0.20    -0.10     0.68 1.00     6654    11079
LUAgriculture_Intense:RegionSouthandCentralAmerica      0.18      0.30    -0.41     0.76 1.00     6632    11044
LUAgriculture_Minimal:RegionSubsaharanAfrica           -0.98      0.19    -1.36    -0.61 1.00    13361    15589
LUAgriculture_Light:RegionSubsaharanAfrica             -0.58      0.28    -1.13    -0.05 1.00     9439    13802
LUAgriculture_Intense:RegionSubsaharanAfrica           -0.57      0.33    -1.23     0.08 1.00     7501    11545
LUAgriculture_Minimal:RegionAustralasia                -0.74      0.16    -1.05    -0.42 1.00    14440    14477
LUAgriculture_Light:RegionAustralasia                  -0.03      0.31    -0.64     0.59 1.00    11471    13452
LUAgriculture_Intense:RegionAustralasia                -0.61      0.32    -1.23     0.01 1.00     6772    10432

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.368 (95% CI [0.344, 0.391])
     Marginal R2: 0.074 (95% CI [0.049, 0.104])
```

Table M18: Posterior summary of the model of species nestedness (Fig. M24).

```
                                     BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit; phi = log; zoi = logit; coi = logit
Formula: Dissimilarity ~ LU * Region + Dist_geo + (1 | SS)
         phi ~ 1
         zoi ~ (1 | SS)
         coi ~ (1 | SS)
   Data: model_data (Number of observations: 2858)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 187)
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         0.50      0.04     0.42     0.58 1.00     6790    10891
sd(zoi_Intercept)     1.75      0.18     1.43     2.12 1.00     5031     9780
sd(coi_Intercept)     0.82      0.65     0.03     2.43 1.00    12742    10078

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                              -1.68      0.09    -1.86    -1.49 1.00     4749     8736
phi_Intercept                                           2.01      0.03     1.95     2.08 1.00    27789    13724
zoi_Intercept                                          -1.96      0.19    -2.34    -1.61 1.00     4504     8444
coi_Intercept                                          -7.52      1.46   -11.03    -5.37 1.00    25369    10802
LUAgriculture_Minimal                                  -0.09      0.12    -0.33     0.16 1.00     8612    12507
LUAgriculture_Light                                    -0.11      0.18    -0.48     0.25 1.00     6803    11065
LUAgriculture_Intense                                   0.07      0.25    -0.43     0.55 1.00     7242    11493
RegionNorthAmerica                                     -0.09      0.15    -0.39     0.20 1.00     4888     9063
RegionSouthandSoutheastAsia                            -0.23      0.21    -0.65     0.18 1.00     8372    11862
RegionSouthandCentralAmerica                            0.01      0.14    -0.27     0.28 1.00     6240    10677
RegionSubsaharanAfrica                                  0.01      0.19    -0.38     0.38 1.00     7448    12146
RegionAustralasia                                      -0.08      0.19    -0.45     0.30 1.00     5723    10142
Dist_geo                                               -0.01      0.03    -0.07     0.04 1.00    18472    16433
LUAgriculture_Minimal:RegionNorthAmerica               -0.14      0.22    -0.58     0.29 1.00    14692    14910
LUAgriculture_Light:RegionNorthAmerica                  0.18      0.28    -0.37     0.71 1.00     9861    14863
LUAgriculture_Intense:RegionNorthAmerica                0.87      0.39     0.09     1.63 1.00    10321    15146
```

```
LUAgriculture_Minimal:RegionSouthandSoutheastAsia     -0.06      0.46    -0.97     0.80 1.00    17060    15998
LUAgriculture_Light:RegionSouthandSoutheastAsia        0.87      0.22     0.44     1.30 1.00     8162    13206
LUAgriculture_Intense:RegionSouthandSoutheastAsia     -0.32      0.59    -1.57     0.76 1.00    16648    14728
LUAgriculture_Minimal:RegionSouthandCentralAmerica     0.00      0.18    -0.34     0.35 1.00    12097    15015
LUAgriculture_Light:RegionSouthandCentralAmerica       0.41      0.23    -0.05     0.87 1.00     8131    11671
LUAgriculture_Intense:RegionSouthandCentralAmerica    -0.25      0.33    -0.90     0.41 1.00     9525    14377
LUAgriculture_Minimal:RegionSubsaharanAfrica           0.50      0.22     0.07     0.93 1.00    12767    15703
LUAgriculture_Light:RegionSubsaharanAfrica             0.46      0.30    -0.12     1.05 1.00    10156    13478
LUAgriculture_Intense:RegionSubsaharanAfrica           0.16      0.37    -0.58     0.89 1.00    10221    14098
LUAgriculture_Minimal:RegionAustralasia                0.29      0.22    -0.14     0.71 1.00    15343    14689
LUAgriculture_Light:RegionAustralasia                 -0.46      0.42    -1.32     0.35 1.00    15268    14034
LUAgriculture_Intense:RegionAustralasia                0.13      0.32    -0.49     0.78 1.00     9619    13227

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.155 (95% CI [0.134, 0.177])
     Marginal R2: 0.036 (95% CI [0.019, 0.061])
```

D Effects of range extent, habitat specificity and non-native species

D.1 Range extent

The following model diagnostic plots refer to the comparison of biodiversity responses in primary vegetation, secondary vegetation and agricultural land use between species with different range extents, comparing Europe and North America (Fig. 5).

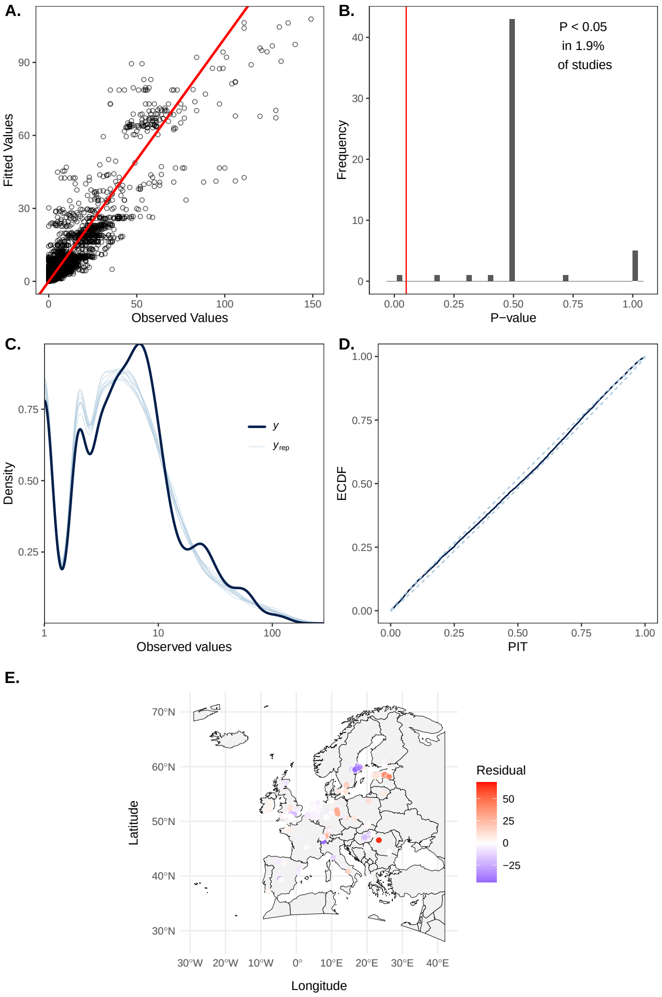


Figure M25: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use and range extent in Europe: Richness $\sim$ LandUse $\times$ RangeExtent + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

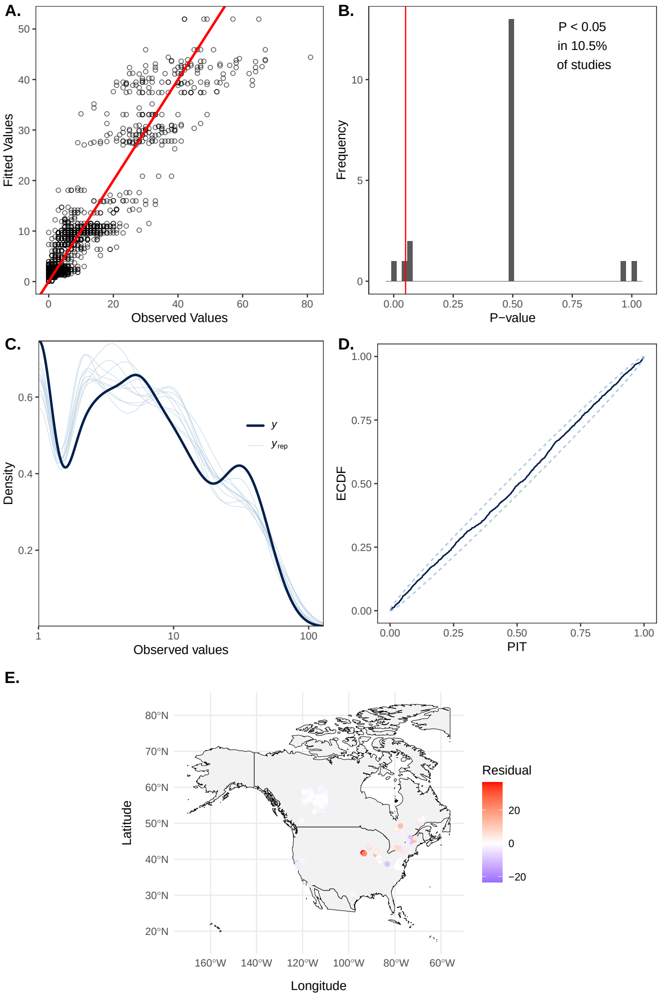


Figure M26: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use and range extent in North America: Richness $\sim$ LandUse $\times$ RangeExtent + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M19: Posterior summary of the model of species richness for Europe (Fig. M25).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 * Quants + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 6114)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 105)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.26      0.09     1.10     1.45 1.00     1177     2323

~SS:SSB (Number of levels: 861)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.16      0.02     0.12     0.20 1.00     3016     5291

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          1.89      0.14     1.61     2.17 1.01      661     1581
zi_Intercept                      -3.28      0.14    -3.59    -3.02 1.00    12695     6953
UI2Secondaryvegetation            -0.69      0.09    -0.87    -0.51 1.00     3734     6049
UI2Agriculture_Minimal            -0.45      0.08    -0.60    -0.30 1.00     3485     5708
UI2Agriculture_Light              -0.70      0.09    -0.88    -0.53 1.00     3136     5116
UI2Agriculture_Intense            -0.57      0.09    -0.75    -0.39 1.00     3378     5739
Quants2                           -0.09      0.07    -0.23     0.05 1.00     2739     5151
UI2Secondaryvegetation:Quants2     1.19      0.08     1.02     1.36 1.00     3108     5742
UI2Agriculture_Minimal:Quants2     0.87      0.08     0.71     1.04 1.00     3263     5836
UI2Agriculture_Light:Quants2       1.08      0.08     0.92     1.24 1.00     3002     5300
UI2Agriculture_Intense:Quants2     0.88      0.08     0.73     1.04 1.00     3031     5730

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape     4.57      0.21     4.16     5.00 1.00     9437     7300

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.800 (95% CI [0.780, 0.820])
     Marginal R2: 0.037 (95% CI [0.021, 0.056])
```

Table M20: Posterior summary of the model of species richness for North America (Fig. ??).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 * Quants + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 1697)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 36)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.51      0.19     1.19     1.95 1.00     1859     3630

~SS:SSB (Number of levels: 120)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.11      0.04     0.04     0.18 1.00     2555     3301

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          1.50      0.26     1.00     2.02 1.00      819     1833
zi_Intercept                      -6.00      1.13    -8.81    -4.46 1.00     7993     4232
UI2Secondaryvegetation            -0.21      0.07    -0.35    -0.07 1.00     9649     7390
UI2Agriculture_Minimal            -0.70      0.15    -0.99    -0.41 1.00     8618     7219
UI2Agriculture_Light              -0.45      0.12    -0.69    -0.22 1.00     9699     7985
UI2Agriculture_Intense            -0.54      0.15    -0.84    -0.26 1.00     9776     8143
Quants2                            0.12      0.04     0.04     0.20 1.00     8959     7692
UI2Secondaryvegetation:Quants2     0.23      0.06     0.10     0.35 1.00    10205     7734
```

```
UI2Agriculture_Minimal:Quants2     0.92      0.15     0.62     1.20 1.00    11101     7846
UI2Agriculture_Light:Quants2       0.17      0.13    -0.09     0.43 1.00    11960     8060
UI2Agriculture_Intense:Quants2     0.15      0.15    -0.15     0.45 1.00    12104     7908

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape     8.13      0.78     6.73     9.81 1.00    12088     7071

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.848 (95% CI [0.831, 0.861])
     Marginal R2: 0.005 (95% CI [0.001, 0.012])
```

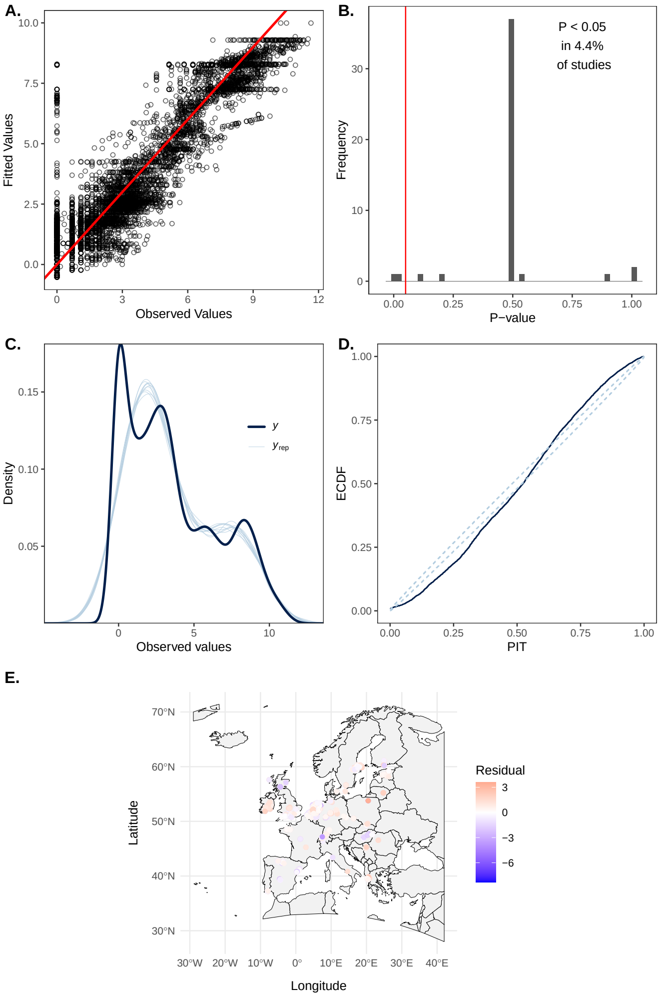


Figure M27: Model diagnostic plots for the Gaussian model of total abundance responses to land use and range extent in Europe: Log(Abundance+1) $\sim$ LandUse $\times$ RangeExtent + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

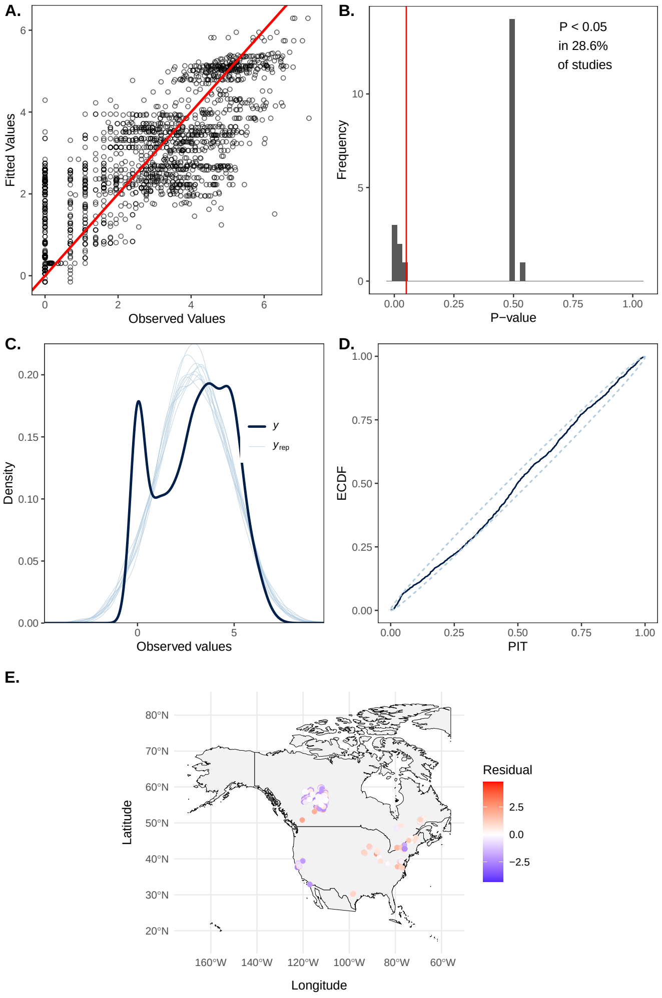


Figure M28: Model diagnostic plots for the Gaussian model of total abundance responses to land use and range extent in North America: Log(Abundance+1) ∼ LandUse × RangeExtent + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M21: Posterior summary of the model of total abundance for Europe (Fig. M27).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Quants + (1 | SS/SSB)
   Data: model_data (Number of observations: 5741)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 99)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.91      0.16     1.63     2.24 1.00     1443     3048

~SS:SSB (Number of levels: 847)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.73      0.05     0.63     0.83 1.00     2434     4230

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          2.83      0.29     2.25     3.41 1.00     1576     3417
UI2Secondaryvegetation             0.00      0.23    -0.45     0.45 1.00     2925     5271
UI2Agriculture_Minimal             0.08      0.23    -0.38     0.52 1.00     2880     5322
UI2Agriculture_Light              -0.25      0.24    -0.71     0.22 1.00     2818     4950
UI2Agriculture_Intense            -0.17      0.24    -0.65     0.30 1.00     2845     4790
Quants2                            0.62      0.17     0.27     0.95 1.00     2344     4293
UI2Secondaryvegetation:Quants2     0.34      0.20    -0.04     0.73 1.00     2802     4873
UI2Agriculture_Minimal:Quants2     0.42      0.19     0.05     0.80 1.00     2596     4812
UI2Agriculture_Light:Quants2       0.58      0.18     0.22     0.94 1.00     2619     4778
UI2Agriculture_Intense:Quants2     0.33      0.18    -0.03     0.69 1.00     2496     5031

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     1.27      0.01     1.25     1.30 1.00     6912     7135

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.825 (95% CI [0.820, 0.830])
     Marginal R2: 0.030 (95% CI [0.026, 0.034])
```

Table M22: Posterior summary of the model of total abundance for North America (Fig. M28).

```
BRMS Summary
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Quants + (1 | SS/SSB)
   Data: model_data (Number of observations: 1677)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 35)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.66      0.22     1.29     2.15 1.00     3236     5349

~SS:SSB (Number of levels: 119)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.38      0.07     0.25     0.52 1.00     3299     6328

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          3.39      0.30     2.81     3.97 1.00     2321     4106
UI2Secondaryvegetation            -0.28      0.14    -0.55    -0.01 1.00    13088     7844
UI2Agriculture_Minimal            -0.62      0.23    -1.08    -0.16 1.00    12505     7993
UI2Agriculture_Light              -0.77      0.22    -1.20    -0.35 1.00    13961     8184
UI2Agriculture_Intense            -1.04      0.30    -1.63    -0.45 1.00    15351     8048
Quants2                           -0.08      0.09    -0.24     0.09 1.00    12837     8193
UI2Secondaryvegetation:Quants2     0.42      0.13     0.15     0.67 1.00    13569     8593
UI2Agriculture_Minimal:Quants2     0.92      0.24     0.46     1.38 1.00    17378     7338
UI2Agriculture_Light:Quants2       0.18      0.25    -0.30     0.66 1.00    15600     8403
UI2Agriculture_Intense:Quants2     0.58      0.37    -0.14     1.29 1.00    15842     7552
```

```
Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     1.23      0.02     1.18     1.27 1.00    16728     7006

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.581 (95% CI [0.559, 0.600])
     Marginal R2: 0.023 (95% CI [0.011, 0.037])
```

D.2 Habitat specificity

The following model diagnostic plots refer to the comparison of biodiversity responses in primary vegetation, secondary vegetation and agricultural land use between species with different levels of habitat specificity, comparing Europe and North America (Fig. 5).

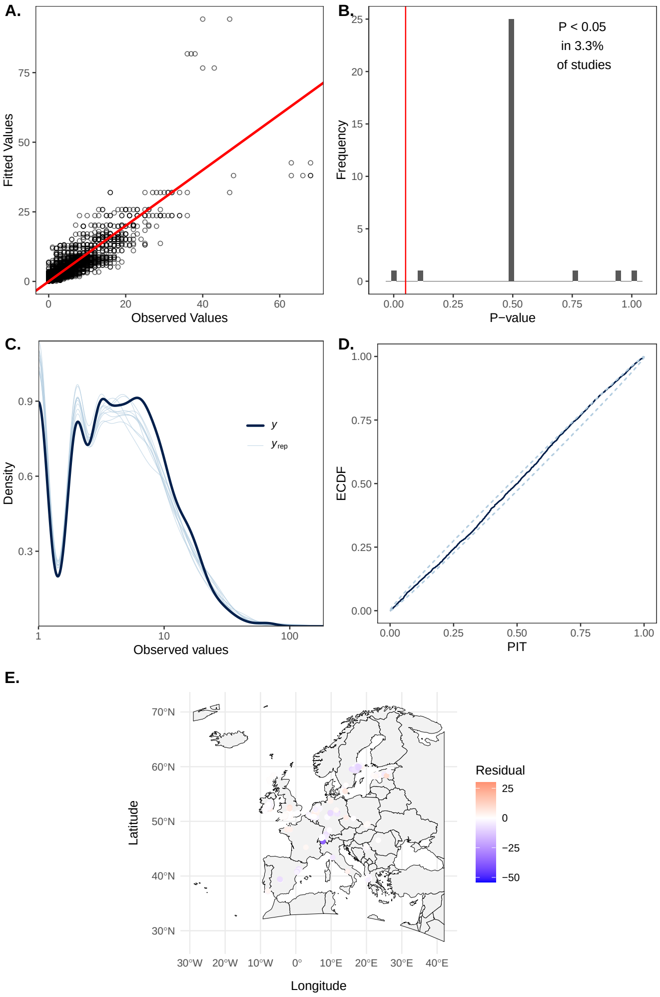


Figure M29: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use and habitat specificity in Europe: Richness $\sim$ LandUse $\times$ HabitatSpecificity + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

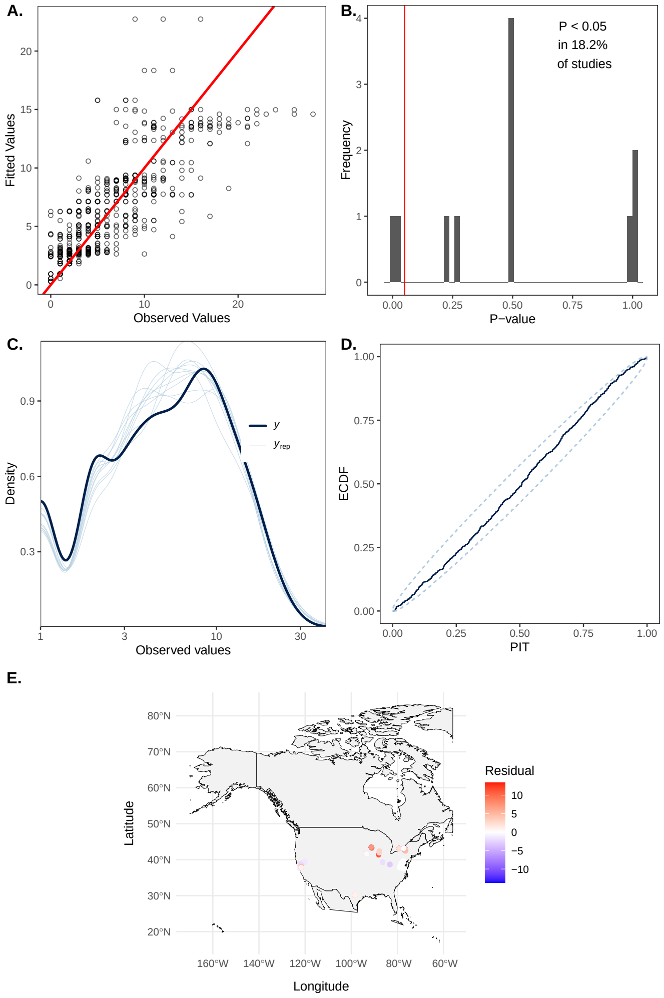


Figure M30: Model diagnostic plots for the zero-inflated negative binomial model of species richness responses to land use and habitat specificity in North America: Richness $\sim$ LandUse $\times$ HabitatSpecificity + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M23: Posterior summary of the model of species richness for Europe (Fig. M29).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 * Quants + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 3389)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 59)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.11      0.11     0.91     1.34 1.00     1537     3371

~SS:SSB (Number of levels: 280)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.23      0.03     0.17     0.29 1.00     2857     5086

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          1.28      0.19     0.91     1.64 1.00     1047     2295
zi_Intercept                      -6.30      1.14    -9.18    -4.75 1.00    10361     5057
UI2Secondaryvegetation            -0.37      0.13    -0.62    -0.12 1.00     4233     6135
UI2Agriculture_Minimal            -0.49      0.12    -0.74    -0.24 1.00     3928     6321
UI2Agriculture_Light              -0.49      0.14    -0.76    -0.21 1.00     3252     5350
UI2Agriculture_Intense            -0.54      0.14    -0.82    -0.26 1.00     3262     5604
Quants2                           -0.35      0.09    -0.53    -0.17 1.00     2811     4701
UI2Secondaryvegetation:Quants2     0.93      0.10     0.73     1.13 1.00     3133     5345
UI2Agriculture_Minimal:Quants2     1.25      0.11     1.05     1.46 1.00     3205     5745
UI2Agriculture_Light:Quants2       1.11      0.10     0.92     1.31 1.00     3028     4783
UI2Agriculture_Intense:Quants2     1.19      0.10     1.00     1.39 1.00     3015     4851

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    11.23      0.99     9.46    13.32 1.00    13751     7153

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.757 (95% CI [0.747, 0.767])
     Marginal R2: 0.044 (95% CI [0.023, 0.073])
```

Table M24: Posterior summary of the model of species richness for North America (Fig. ??).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Species_richness ~ UI2 * Quants + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 605)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 19)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.08      0.22     0.74     1.62 1.00     2260     4434

~SS:SSB (Number of levels: 76)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.11      0.06     0.01     0.22 1.00     1986     2904

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          1.74      0.26     1.22     2.27 1.00     1189     2643
zi_Intercept                      -5.68      1.15    -8.65    -4.11 1.00     8700     4197
UI2Secondaryvegetation             0.05      0.10    -0.15     0.26 1.00     8320     7457
UI2Agriculture_Minimal            -0.48      0.22    -0.92    -0.05 1.00     7286     6680
UI2Agriculture_Light              -0.60      0.16    -0.92    -0.29 1.00     6719     7571
UI2Agriculture_Intense            -0.85      0.19    -1.23    -0.47 1.00     7873     7677
Quants2                           -0.08      0.09    -0.25     0.09 1.00     5066     6650
UI2Secondaryvegetation:Quants2    -0.34      0.10    -0.54    -0.14 1.00     5425     6772
```

```
UI2Agriculture_Minimal:Quants2     0.33      0.21    -0.08     0.75 1.00     6831     6774
UI2Agriculture_Light:Quants2       0.32      0.18    -0.04     0.68 1.00     6379     7347
UI2Agriculture_Intense:Quants2     0.57      0.20     0.17     0.97 1.00     7772     7352

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape    17.33      3.92    11.49    26.63 1.00    10655     6845

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.646 (95% CI [0.610, 0.677])
     Marginal R2: 0.040 (95% CI [0.007, 0.102])
```

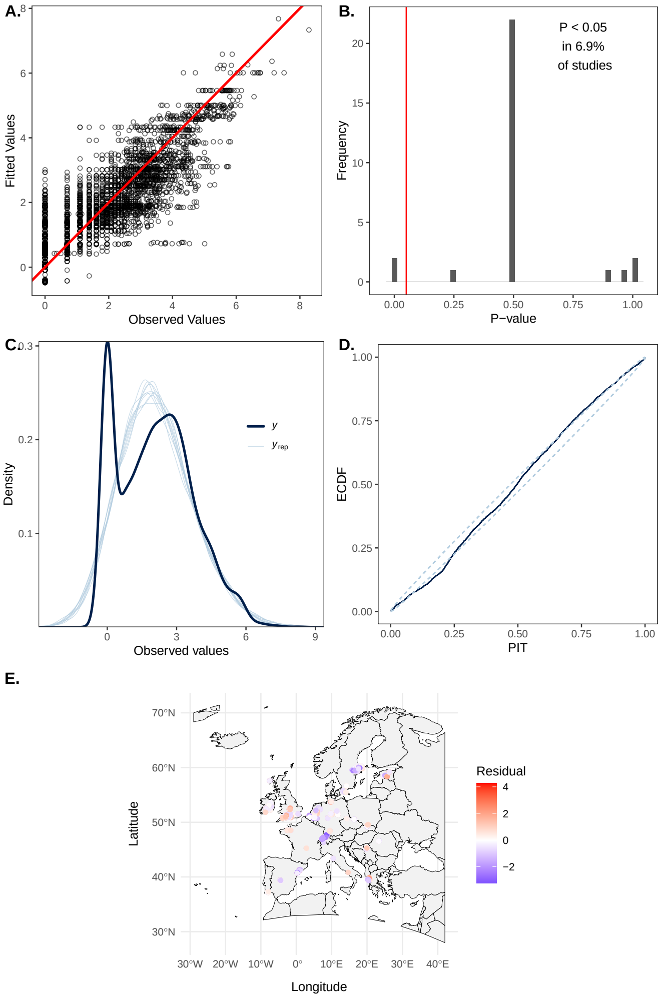


Figure M31: Model diagnostic plots for the Gaussian model of total abundance responses to land use and habitat specificity in Europe: Log(Abundance+1) $\sim$ LandUse × HabitatSpecificity + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

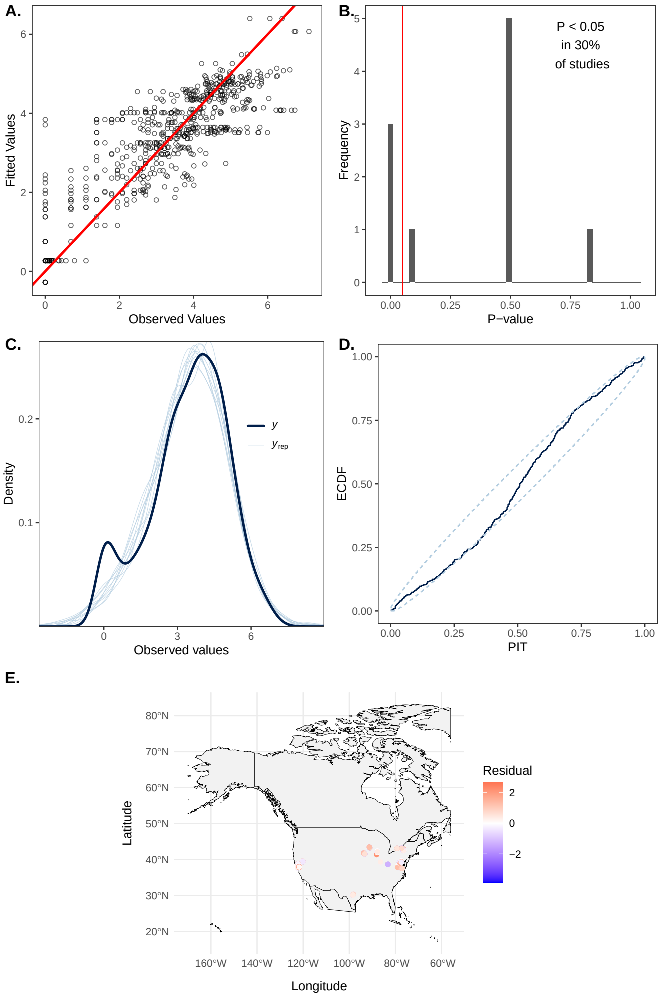


Figure M32: Model diagnostic plots for the Gaussian model of total abundance responses to land use and habitat specificity in North America: Log(Abundance+1) ∼ LandUse × HabitatSpecificity + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Figure M33: Posterior summary of the model of total abundance for Europe (Fig. M31).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Quants + (1 | SS/SSB)
   Data: model_data (Number of observations: 3233)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 55)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.52      0.16     1.25     1.87 1.00     1681     3195

~SS:SSB (Number of levels: 273)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.29      0.04     0.21     0.37 1.00     3096     5738

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          2.22      0.29     1.63     2.80 1.00     1315     2060
UI2Secondaryvegetation            -0.52      0.22    -0.96    -0.10 1.00     4192     5436
UI2Agriculture_Minimal            -0.28      0.21    -0.70     0.12 1.00     3990     6087
UI2Agriculture_Light              -0.17      0.23    -0.62     0.28 1.00     3442     5745
UI2Agriculture_Intense            -0.21      0.23    -0.66     0.23 1.00     3310     5244
Quants2                           -0.53      0.15    -0.83    -0.23 1.00     3410     5373
UI2Secondaryvegetation:Quants2     1.75      0.17     1.41     2.09 1.00     3749     6309
UI2Agriculture_Minimal:Quants2     1.95      0.17     1.61     2.30 1.00     3700     6197
UI2Agriculture_Light:Quants2       1.50      0.16     1.18     1.82 1.00     3498     5653
UI2Agriculture_Intense:Quants2     1.66      0.16     1.34     1.98 1.00     3529     5571

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.88      0.01     0.86     0.91 1.00    14456     7432

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.693 (95% CI [0.683, 0.704])
     Marginal R2: 0.126 (95% CI [0.114, 0.138])
```

Figure M34: Posterior summary of the model of total abundance for North America (Fig. M32).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Quants + (1 | SS/SSB)
   Data: model_data (Number of observations: 585)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 18)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.48      0.32     0.96     2.22 1.00     4449     5656

~SS:SSB (Number of levels: 75)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.57      0.10     0.39     0.78 1.00     3372     5937

Regression Coefficients:
                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                          3.63      0.41     2.82     4.45 1.00     4221     5356
UI2Secondaryvegetation             0.13      0.24    -0.33     0.60 1.00    10628     7513
UI2Agriculture_Minimal             0.32      0.48    -0.63     1.26 1.00    12634     7358
UI2Agriculture_Light              -1.03      0.32    -1.66    -0.41 1.00    11549     7636
UI2Agriculture_Intense            -1.68      0.43    -2.52    -0.86 1.00    12092     8025
Quants2                            0.37      0.19     0.01     0.73 1.00     8829     7665
UI2Secondaryvegetation:Quants2    -0.70      0.23    -1.14    -0.25 1.00     9704     8146
UI2Agriculture_Minimal:Quants2    -0.65      0.47    -1.58     0.27 1.00    11400     7260
UI2Agriculture_Light:Quants2       0.22      0.36    -0.48     0.92 1.00    11246     8224
UI2Agriculture_Intense:Quants2     1.64      0.51     0.66     2.65 1.00    12925     8343
```

```
Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.98      0.03     0.92     1.04 1.00    12818     7423

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.630 (95% CI [0.595, 0.663])
     Marginal R2: 0.061 (95% CI [0.032, 0.101])
```

D.3 Non-native species proportion

The following model diagnostic plots refer to the comparison of the proportions of non-native species in primary vegetation, secondary vegetation and agricultural land use in Europe and North America (Fig. 5).

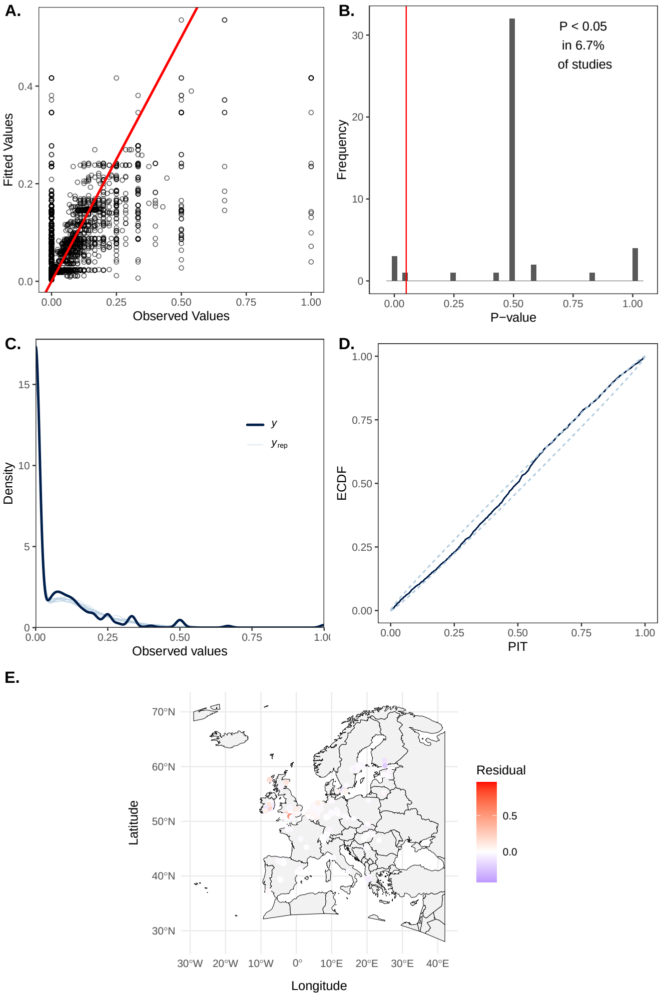


Figure M35: Model diagnostic plots for the zero-and-one inflated beta model of non-native species proportions of richness P_{SR} in Europe: $P_{SR} \sim \text{LandUse} + (1|\text{SS/SSB})$. Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals. Due to the zero-and-one inflated structure of the data, deviations of PIT values from uniformity are to be expected and do not necessarily indicate poor model fit.

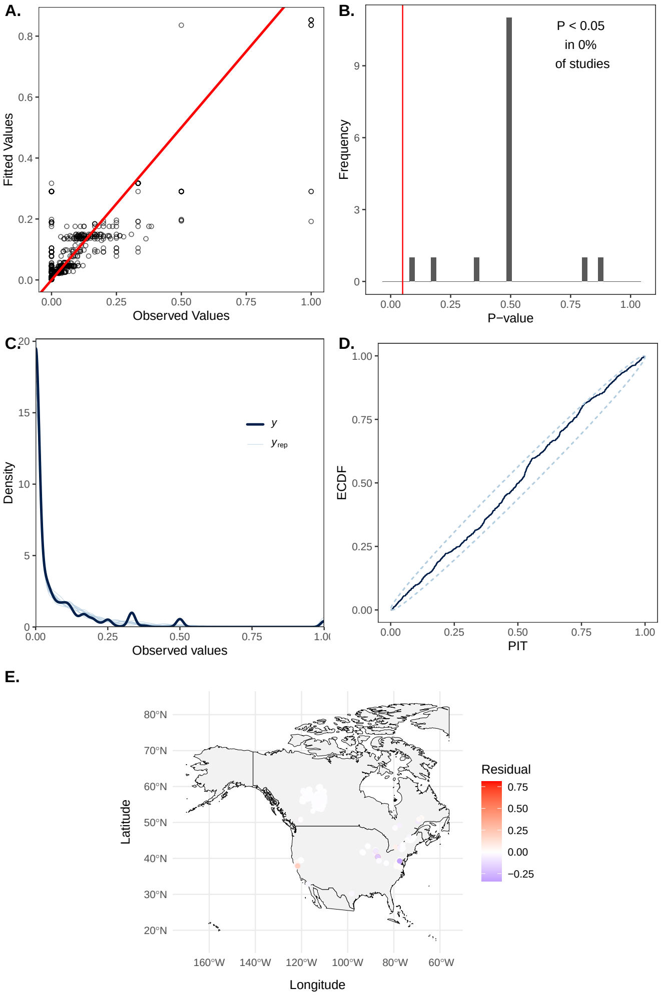


Figure M36: Model diagnostic plots for the zero-and-one-inflated beta model of non-native proportions of species richness P_{SR} in North America: $P_{SR} \sim \text{LandUse} + (1|\text{SS}/\text{SSB})$. Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals. Due to the zero-and-one inflated structure of the data, deviations of PIT values from uniformity are to be expected and do not necessarily indicate poor model fit.

Table M25: Posterior summary of the model of species richness for Europe (Fig. M35).

```
BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit; phi = log; zoi = logit; coi = logit
Formula: SiteSpeciesProps ~ UI2 + (1 | SS/SSB)
         phi ~ 1
         zoi ~ 1 + (1 | SS)
         coi ~ 1 + (1 | SS)
   Data: model_data (Number of observations: 2837)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 99)
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         0.86      0.08     0.73     1.02 1.00     3693     7103
sd(zoi_Intercept)     3.66      0.47     2.86     4.70 1.00     5324     9853
sd(coi_Intercept)     2.37      0.59     1.43     3.75 1.00    10014    12712

~SS:SSB (Number of levels: 823)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.08      0.04     0.01     0.14 1.00     3649     4537

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                 -1.82      0.16    -2.14    -1.52 1.00     3927     7542
phi_Intercept              3.44      0.05     3.35     3.53 1.00    20882    15297
zoi_Intercept             -0.61      0.40    -1.42     0.18 1.00     1819     3867
coi_Intercept             -6.22      0.80    -8.01    -4.90 1.00    14550    13338
UI2Secondaryvegetation    -0.05      0.13    -0.31     0.22 1.00     9089    12602
UI2Agriculture_Minimal    -0.00      0.14    -0.27     0.28 1.00     8772    12633
UI2Agriculture_Light       0.17      0.14    -0.11     0.45 1.00     8197    12246
UI2Agriculture_Intense     0.11      0.15    -0.17     0.40 1.00     8079    11756

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.353 (95% CI [0.309, 0.402])
     Marginal R2: 0.003 (95% CI [2.961e-04, 0.008])
```

Table M26: Posterior summary of the model of species richness for North America (Fig. **??**).

```
BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit; phi = log; zoi = logit; coi = logit
Formula: SiteSpeciesProps ~ UI2 + (1 | SS/SSB)
         phi ~ 1
         zoi ~ 1 + (1 | SS)
         coi ~ 1 + (1 | SS)
   Data: model_data (Number of observations: 832)
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 35)
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         1.06      0.19     0.77     1.51 1.00     2071     3682
sd(zoi_Intercept)     5.19      1.14     3.42     7.83 1.00     2794     4846
sd(coi_Intercept)     3.81      1.26     2.05     6.81 1.00     5529     6003

~SS:SSB (Number of levels: 119)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.08      0.05     0.00     0.19 1.00     2601     2917

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                 -2.31      0.25    -2.82    -1.82 1.00      996     2041
phi_Intercept              4.00      0.08     3.85     4.16 1.00    10248     7498
zoi_Intercept              1.01      0.85    -0.61     2.80 1.00     1244     2462
coi_Intercept             -6.23      1.36    -9.37    -3.99 1.00     6056     5299
UI2Secondaryvegetation     0.30      0.12     0.07     0.54 1.00     6543     7357
UI2Agriculture_Minimal     0.48      0.20     0.08     0.86 1.00     4748     7035
UI2Agriculture_Light       0.53      0.22     0.10     0.95 1.00     3773     5904
```

```
UI2Agriculture_Intense     0.53      0.27    -0.00     1.04 1.00     4984     6886

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.658 (95% CI [0.552, 0.715])
     Marginal R2: 0.002 (95% CI [7.614e-08, 0.012])
```

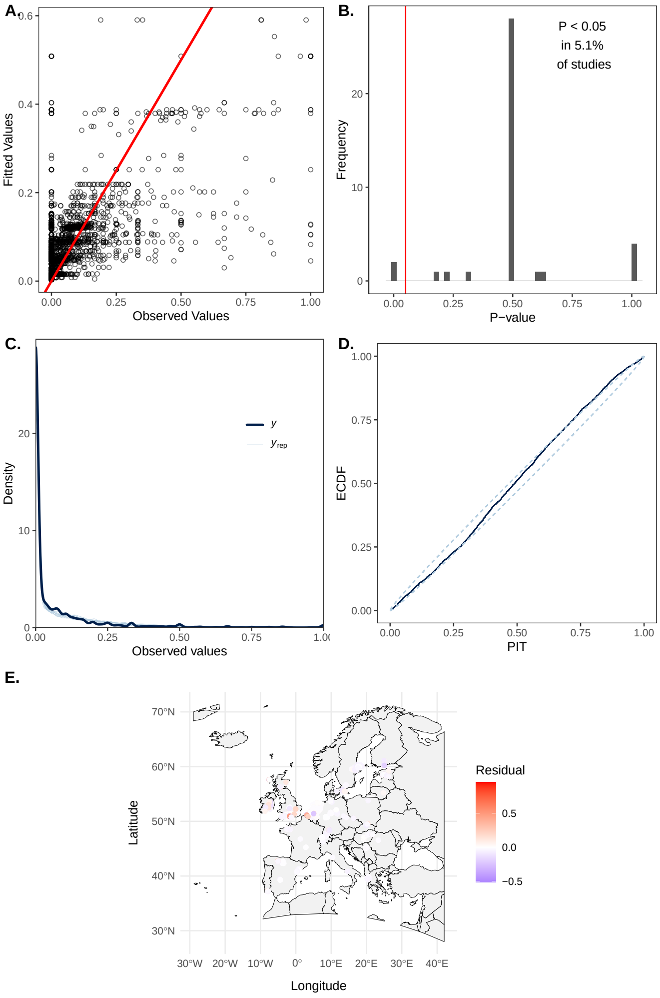


Figure M37: Model diagnostic plots for the zero-and-one-inflated beta model of non-native proportions of total abundance P_{TA} in Europe: $P_{TA} \sim \text{LandUse} + (1|\text{SS/SSB})$. Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals. Due to the zero-and-one inflated structure of the data, deviations of PIT values from uniformity are to be expected and do not necessarily indicate poor model fit.

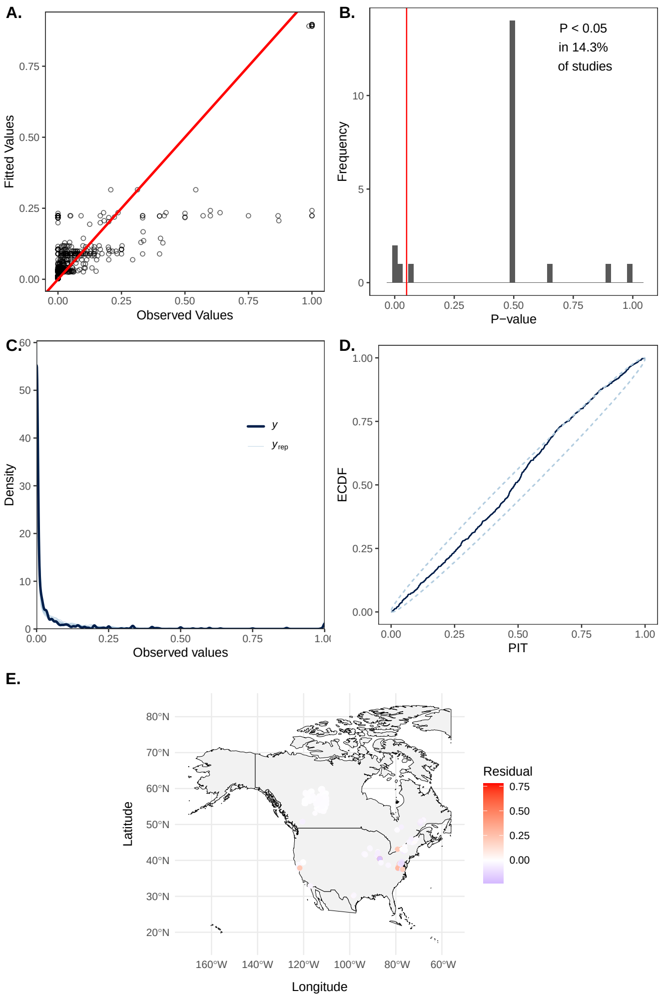


Figure M38: Model diagnostic plots for the zero-and-one-inflated beta model of non-native proportions of total abundance P_{TA} in North America: $P_{TA} \sim$ LandUse + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals. Due to the zero-and-one inflated structure of the data, deviations of PIT values from uniformity are to be expected and do not necessarily indicate poor model fit.

Table M27: Posterior summary of the model of total abundance for Europe (Fig. M37).

BRMS Summary

```
 Family: zero_one_inflated_beta 
  Links: mu = logit; phi = log; zoi = logit; coi = logit 
Formula: SiteTotAbunProps ~ UI2 + (1 | SS/SSB) 
         phi ~ 1
         zoi ~ (1 | SS)
         coi ~ (1 | SS)
   Data: model_data (Number of observations: 2837) 
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 99) 
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         1.02      0.10     0.85     1.23 1.00     6129    11007
sd(zoi_Intercept)     3.66      0.47     2.86     4.71 1.00     5835    10593
sd(coi_Intercept)     2.36      0.59     1.42     3.72 1.00    10034    13639

~SS:SSB (Number of levels: 823) 
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.18      0.06     0.05     0.29 1.00     3358     4339

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                 -1.88      0.23    -2.33    -1.43 1.00     6490    10653
phi_Intercept              2.35      0.05     2.26     2.45 1.00    13682    14449
zoi_Intercept             -0.62      0.41    -1.45     0.15 1.00     2006     4348
coi_Intercept             -6.22      0.80    -8.05    -4.91 1.00    15486    13607
UI2Secondaryvegetation    -0.09      0.21    -0.51     0.33 1.00     9832    13033
UI2Agriculture_Minimal    -0.14      0.22    -0.57     0.30 1.00     9582    12465
UI2Agriculture_Light       0.12      0.23    -0.32     0.56 1.00     8993    11493
UI2Agriculture_Intense     0.07      0.23    -0.37     0.53 1.00     8918    12233

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.364 (95% CI [0.313, 0.412])
     Marginal R2: 0.004 (95% CI [1.334e-04, 0.010])
```

Table M28: Posterior summary of the model of total abundance for North America (Fig. M38).

BRMS Summary

```
 Family: zero_one_inflated_beta 
  Links: mu = logit; phi = log; zoi = logit; coi = logit 
Formula: SiteTotAbunProps ~ UI2 + (1 | SS/SSB) 
         phi ~ 1
         zoi ~ 1 + (1 | SS)
         coi ~ 1 + (1 | SS)
   Data: model_data (Number of observations: 832) 
  Draws: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
         total post-warmup draws = 10000

Multilevel Hyperparameters:
~SS (Number of levels: 35) 
                  Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)         1.50      0.29     1.04     2.17 1.00     2935     5413
sd(zoi_Intercept)     5.14      1.13     3.40     7.78 1.00     2627     5391
sd(coi_Intercept)     3.75      1.18     2.01     6.55 1.00     6608     6724

~SS:SSB (Number of levels: 119) 
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.25      0.16     0.01     0.56 1.00     1010     3282

Regression Coefficients:
                       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                 -2.29      0.39    -3.06    -1.53 1.00     1712     3326
phi_Intercept              2.61      0.10     2.41     2.82 1.00     2468     4435
zoi_Intercept              0.98      0.85    -0.66     2.72 1.00     1435     2792
coi_Intercept             -6.22      1.34    -9.24    -4.01 1.00     7007     7286
UI2Secondaryvegetation     0.10      0.23    -0.36     0.57 1.00     7274     6367
UI2Agriculture_Minimal    -0.15      0.40    -0.94     0.63 1.00     4981     7290
UI2Agriculture_Light       0.68      0.43    -0.14     1.55 1.00     3742     5370
```

```
UI2Agriculture_Intense     0.37      0.58    -0.80     1.49 1.00     4899     6503

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.576 (95% CI [0.440, 0.648])
     Marginal R2: 0.003 (95% CI [2.082e-06, 0.027])
```

E Abundance model comparison

The following model diagnostic plots refer to the comparison of four possible models of total abundance: The Gaussian model of log(total abundance+1), the Gaussian model of log(rescaled abundance+0.01), the zero-and-one-inflated beta model of rescaled abundance, and the zero-inflated negative binomial model of (rounded) total abundance (Fig. S20).

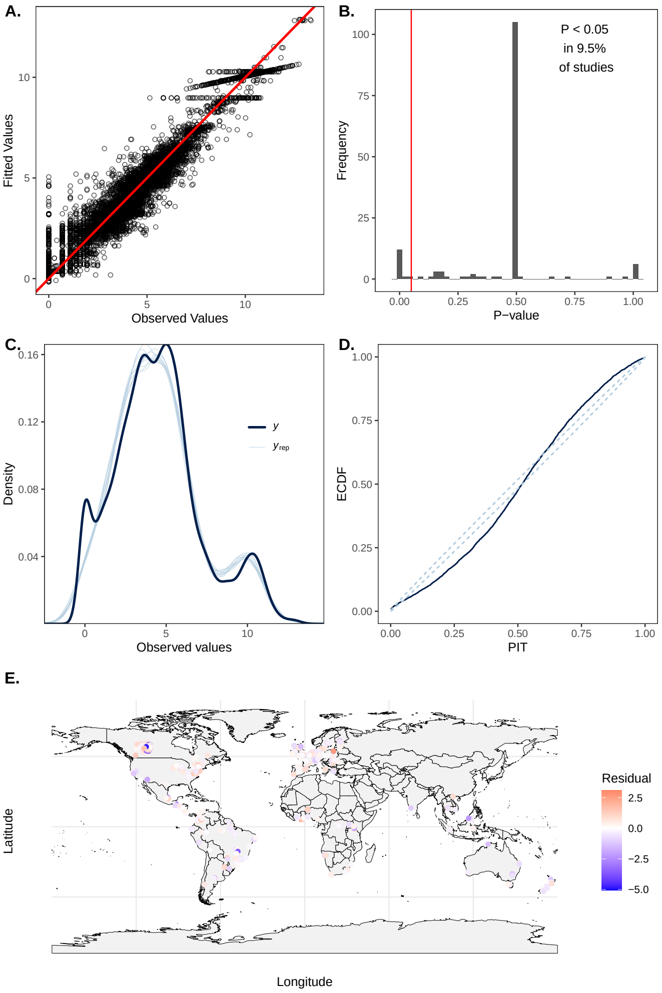


Figure M39: Model diagnostic plots for the Gaussian model of log(total abundance+1) $\sim$ LandUse $\times$ Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

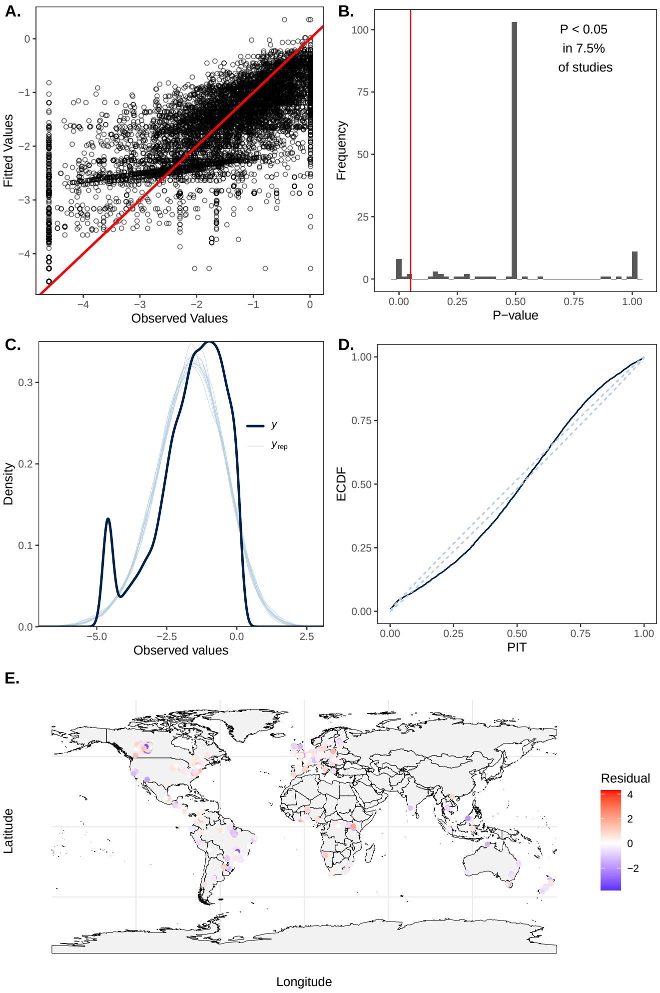


Figure M40: Model diagnostic plots for the Gaussian model of log(rescaled total abundance+0.01) $\sim$ LandUse $\times$ Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

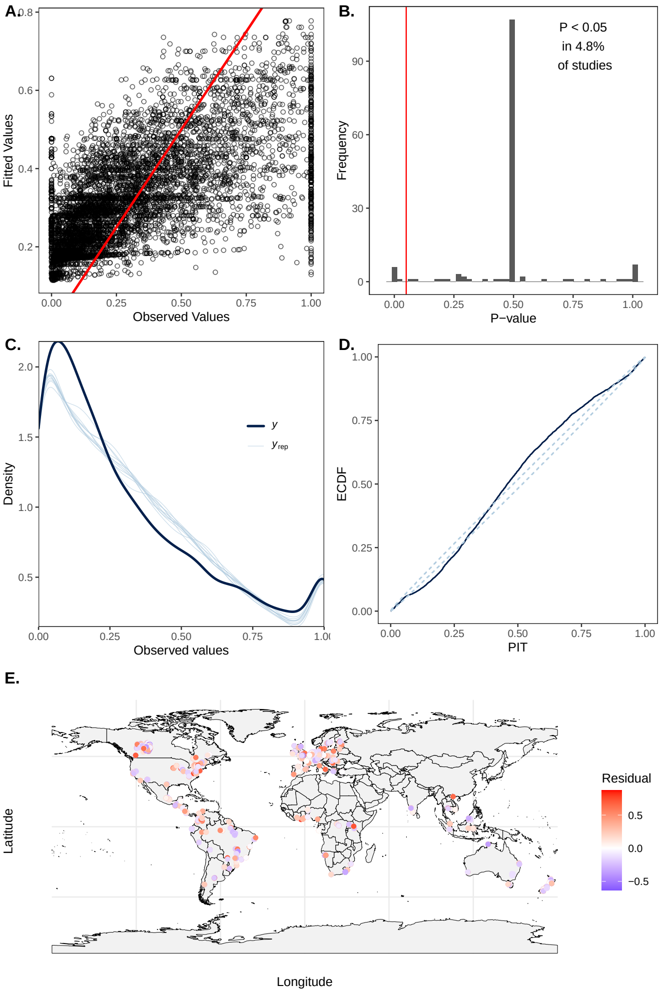


Figure M41: Model diagnostic plots for the beta distributed model of rescaled total abundance $\sim$ LandUse $\times$ Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

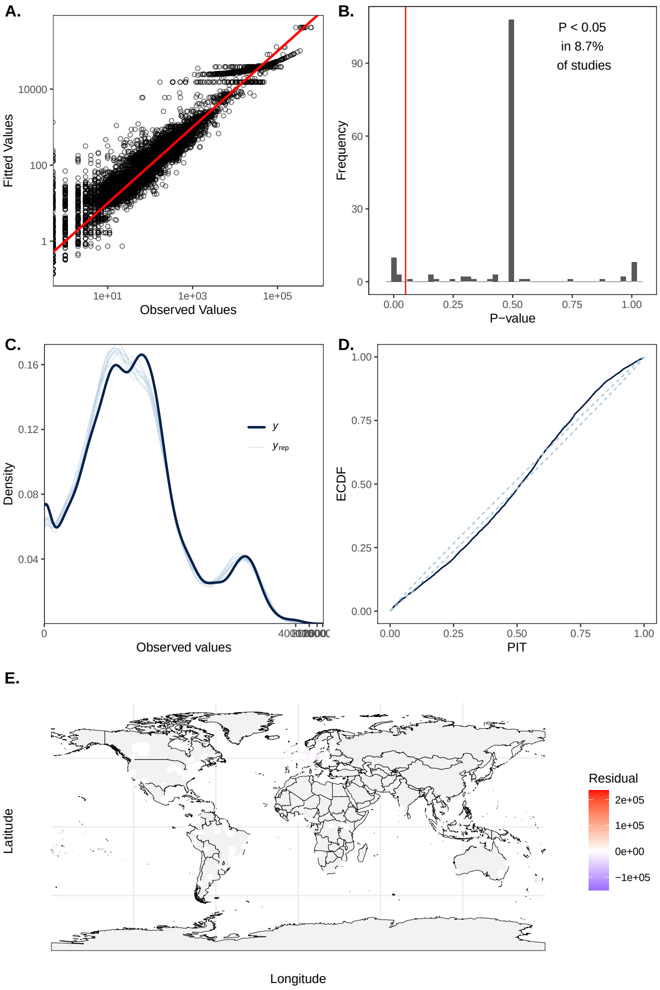


Figure M42: Model diagnostic plots for the zero-inflated negative binomial model of total abundance ∼ LandUse × Region + (1|SS/SSB). Model diagnostics show (a) fitted versus observed values, (b) spatial autocorrelation test results, (c) density plot of predictions and observed values, (d) ECDF of PIT values, and (e) spatial plot of model residuals.

Table M29: Posterior summary of the Gaussian model of log(total abundance+1) (Fig. M39).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund ~ UI2 * Region + (1 | SS/SSB)
   Data: model_data (Number of observations: 6751)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.11      0.09     1.93     2.29 1.00     2233     4433

~SS:SSB (Number of levels: 1561)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.42      0.02     0.38     0.47 1.00     5133     9603

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                               4.52      0.24     4.06     4.99 1.01      966     2347
UI2Secondaryvegetation                                  0.06      0.12    -0.19     0.30 1.00     2496     5894
UI2Agriculture_Minimal                                  0.32      0.14     0.05     0.58 1.00     2570     5728
UI2Agriculture_Light                                   -0.03      0.13    -0.29     0.23 1.00     2325     4971
UI2Agriculture_Intense                                 -0.01      0.14    -0.28     0.26 1.00     2398     4976
RegionNorthAmerica                                      0.44      0.41    -0.36     1.24 1.00     1343     3448
RegionSouthandSoutheastAsia                             1.77      0.52     0.76     2.79 1.00     1781     4232
RegionSouthandCentralAmerica                            0.97      0.34     0.32     1.64 1.00     1185     2812
RegionSubsaharanAfrica                                  0.65      0.54    -0.43     1.72 1.00     1690     3616
RegionAustralasia                                       2.02      0.51     1.03     3.01 1.00     1869     3936
UI2Secondaryvegetation:RegionNorthAmerica              -0.05      0.17    -0.38     0.29 1.00     3651     7859
UI2Agriculture_Minimal:RegionNorthAmerica              -0.50      0.23    -0.96    -0.04 1.00     4489    10349
UI2Agriculture_Light:RegionNorthAmerica                -0.61      0.20    -1.00    -0.21 1.00     3960     8045
UI2Agriculture_Intense:RegionNorthAmerica              -0.54      0.23    -0.99    -0.09 1.00     4577     9581
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.56      0.46    -1.45     0.34 1.00    14235    14128
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.57      0.28    -1.13    -0.01 1.00     7906    11350
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.91      0.17    -1.24    -0.57 1.00     3462     7930
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.60      0.27    -1.13    -0.07 1.00     7160    12236
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.30      0.15    -0.60    -0.01 1.00     3134     7552
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.53      0.16    -0.84    -0.21 1.00     3191     6550
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.45      0.17    -0.78    -0.11 1.00     3014     6697
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.27      0.22    -0.70     0.16 1.00     4503     9359
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.52      0.21    -0.92    -0.11 1.00     5173    10073
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -1.31      0.20    -1.70    -0.93 1.00     4194     8757
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.83      0.21    -1.24    -0.43 1.00     4461     9178
UI2Agriculture_Intense:RegionSubsaharanAfrica          -1.84      0.26    -2.35    -1.32 1.00     6165    10745
UI2Secondaryvegetation:RegionAustralasia               -0.18      0.25    -0.67     0.31 1.00     6298    11106
UI2Agriculture_Minimal:RegionAustralasia               -1.04      0.17    -1.38    -0.70 1.00     3667     7811
UI2Agriculture_Light:RegionAustralasia                 -0.23      0.21    -0.64     0.20 1.00     4588     9173
UI2Agriculture_Intense:RegionAustralasia               -0.20      0.18    -0.55     0.16 1.00     3443     7870

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.81      0.01     0.80     0.83 1.00    14469    15031

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.910 (95% CI [0.908, 0.912])
     Marginal R2: 0.053 (95% CI [0.023, 0.086])
```

Table M30: Posterior summary of the Gaussian model of log(rescaled total abundance+0.01) (Fig. M40).

BRMS Summary

```
 Family: gaussian
  Links: mu = identity
Formula: LogAbund_RS ~ UI2 * Region + (1 | SS/SSB)
   Data: model_data (Number of observations: 6751)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
```

```
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.68      0.04     0.61     0.76 1.00     5181     9106

~SS:SSB (Number of levels: 1561)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.35      0.02     0.31     0.40 1.00     5112     9455

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                              -1.18      0.13    -1.45    -0.92 1.00     2258     3108
UI2Secondaryvegetation                                  0.02      0.12    -0.22     0.27 1.00     2563     5095
UI2Agriculture_Minimal                                  0.19      0.13    -0.07     0.46 1.00     2434     4905
UI2Agriculture_Light                                   -0.11      0.13    -0.36     0.14 1.00     2262     4034
UI2Agriculture_Intense                                 -0.03      0.13    -0.29     0.23 1.00     2309     4754
RegionNorthAmerica                                      0.24      0.19    -0.13     0.62 1.00     3095     5839
RegionSouthandSoutheastAsia                             0.50      0.23     0.05     0.95 1.00     3685     6731
RegionSouthandCentralAmerica                            0.48      0.17     0.14     0.82 1.00     2797     4730
RegionSubsaharanAfrica                                  0.24      0.23    -0.21     0.69 1.00     3778     6672
RegionAustralasia                                       0.27      0.23    -0.20     0.72 1.00     3278     6084
UI2Secondaryvegetation:RegionNorthAmerica              -0.00      0.17    -0.33     0.33 1.00     3634     7799
UI2Agriculture_Minimal:RegionNorthAmerica              -0.23      0.23    -0.68     0.23 1.00     4786     9142
UI2Agriculture_Light:RegionNorthAmerica                -0.42      0.20    -0.81    -0.03 1.00     3715     8045
UI2Agriculture_Intense:RegionNorthAmerica              -0.41      0.22    -0.85     0.03 1.00     4336     8467
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.28      0.46    -1.18     0.61 1.00    13505    14160
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.40      0.29    -0.97     0.17 1.00     6874    10764
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.79      0.17    -1.11    -0.46 1.00     3361     7216
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.53      0.28    -1.08     0.02 1.00     6186    11951
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.28      0.15    -0.58     0.02 1.00     3229     6762
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.50      0.16    -0.81    -0.18 1.00     3013     6357
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.35      0.16    -0.68    -0.03 1.00     3048     5583
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.19      0.22    -0.62     0.24 1.00     4697    10107
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.43      0.21    -0.85    -0.02 1.00     5188     9537
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -1.26      0.20    -1.65    -0.87 1.00     4095     9015
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.69      0.21    -1.09    -0.28 1.00     4415     8407
UI2Agriculture_Intense:RegionSubsaharanAfrica          -1.62      0.27    -2.14    -1.10 1.00     6054    10261
UI2Secondaryvegetation:RegionAustralasia               -0.13      0.24    -0.60     0.33 1.00     5677    10170
UI2Agriculture_Minimal:RegionAustralasia               -0.89      0.18    -1.24    -0.55 1.00     3557     7447
UI2Agriculture_Light:RegionAustralasia                 -0.34      0.22    -0.77     0.08 1.00     4575     7755
UI2Agriculture_Intense:RegionAustralasia               -0.26      0.18    -0.61     0.09 1.00     3559     8249

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.86      0.01     0.85     0.88 1.00    14528    15033

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.501 (95% CI [0.487, 0.515])
     Marginal R2: 0.049 (95% CI [0.035, 0.066])
```

Table M31: Posterior summary of the zero-and-one-inflated beta model of rescaled total abundance (Fig. M41).

```
                                                      BRMS Summary
 Family: zero_one_inflated_beta
  Links: mu = logit
Formula: Total_abundance_RS ~ UI2 * Region + (1 | SS/SSB)
   Data: model_data (Number of observations: 6751)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.75      0.04     0.67     0.84 1.00     4549     9393

~SS:SSB (Number of levels: 1561)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.27      0.03     0.22     0.32 1.00     3996     7372

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                              -0.47      0.13    -0.73    -0.21 1.00     1688     3468
UI2Secondaryvegetation                                  0.11      0.12    -0.13     0.35 1.00     2066     5330
UI2Agriculture_Minimal                                  0.32      0.13     0.06     0.59 1.00     1922     4727
UI2Agriculture_Light                                   -0.07      0.13    -0.32     0.18 1.00     1710     4437
```

```
UI2Agriculture_Intense                                 -0.05      0.13    -0.31     0.22 1.00     1897     4840
RegionNorthAmerica                                      0.37      0.20    -0.02     0.75 1.00     2349     4799
RegionSouthandSoutheastAsia                             0.48      0.24     0.02     0.95 1.00     3261     7079
RegionSouthandCentralAmerica                            0.37      0.18     0.02     0.72 1.00     2206     4742
RegionSubsaharanAfrica                                  0.32      0.24    -0.15     0.81 1.00     3285     6285
RegionAustralasia                                       0.11      0.24    -0.37     0.59 1.00     2518     5593
UI2Secondaryvegetation:RegionNorthAmerica              -0.35      0.17    -0.68    -0.02 1.00     2903     6589
UI2Agriculture_Minimal:RegionNorthAmerica              -0.50      0.23    -0.94    -0.05 1.00     3311     7741
UI2Agriculture_Light:RegionNorthAmerica                -0.61      0.20    -1.00    -0.22 1.00     3093     6468
UI2Agriculture_Intense:RegionNorthAmerica              -0.70      0.22    -1.15    -0.27 1.00     3553     8131
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.36      0.61    -1.54     0.84 1.00    12235    13832
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.55      0.29    -1.12     0.01 1.00     5523    12328
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.70      0.17    -1.02    -0.38 1.00     2749     7334
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.39      0.28    -0.95     0.15 1.00     5791    11955
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.34      0.16    -0.65    -0.04 1.00     2633     6429
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.44      0.17    -0.77    -0.11 1.00     2558     6418
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.25      0.17    -0.58     0.08 1.00     2382     6235
UI2Agriculture_Intense:RegionSouthandCentralAmerica     0.04      0.22    -0.39     0.46 1.00     3855     8212
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.21      0.21    -0.62     0.19 1.00     4585    11349
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -0.83      0.22    -1.26    -0.41 1.00     3989     8197
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.48      0.22    -0.92    -0.06 1.00     3917     8852
UI2Agriculture_Intense:RegionSubsaharanAfrica          -1.33      0.28    -1.89    -0.80 1.00     5693    11814
UI2Secondaryvegetation:RegionAustralasia               -0.17      0.24    -0.66     0.31 1.00     4408     9969
UI2Agriculture_Minimal:RegionAustralasia               -1.01      0.18    -1.36    -0.67 1.00     3076     7756
UI2Agriculture_Light:RegionAustralasia                 -0.11      0.23    -0.55     0.34 1.00     3946    10268
UI2Agriculture_Intense:RegionAustralasia               -0.10      0.19    -0.47     0.27 1.00     2968     8007

Further Distributional Parameters:
    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
phi     5.30      0.10     5.10     5.51 1.00    12121    13779
zoi     0.10      0.00     0.10     0.11 1.00    28769    13844
coi     0.44      0.02     0.40     0.47 1.00    29953    14009

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.276 (95% CI [0.261, 0.291])
     Marginal R2: 0.037 (95% CI [0.024, 0.053])
```

Table M32: Posterior summary of the zero-inflated negative binomial model of total abundance (Fig. M42).

```
BRMS Summary
 Family: zero_inflated_negbinomial
  Links: mu = log; zi = logit
Formula: Total_abundance ~ UI2 * Region + (1 | SS/SSB)
         zi ~ 1
   Data: model_data (Number of observations: 6751)
  Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup draws = 20000

Multilevel Hyperparameters:
~SS (Number of levels: 297)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     2.22      0.10     2.03     2.42 1.00     4298     8353

~SS:SSB (Number of levels: 1561)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.46      0.02     0.41     0.50 1.00     5834    11529

Regression Coefficients:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                                               4.69      0.24     4.22     5.16 1.00     2112     4289
zi_Intercept                                           -5.01      0.20    -5.44    -4.65 1.00    42844    14598
UI2Secondaryvegetation                                  0.05      0.11    -0.17     0.26 1.00     5945    10031
UI2Agriculture_Minimal                                  0.36      0.12     0.12     0.61 1.00     5853    10513
UI2Agriculture_Light                                   -0.02      0.12    -0.26     0.21 1.00     5263     9737
UI2Agriculture_Intense                                  0.03      0.13    -0.23     0.28 1.00     5501     9538
RegionNorthAmerica                                      0.43      0.43    -0.42     1.28 1.00     2397     4680
RegionSouthandSoutheastAsia                             1.81      0.54     0.73     2.86 1.00     3775     7503
RegionSouthandCentralAmerica                            0.92      0.35     0.23     1.63 1.00     2409     4666
RegionSubsaharanAfrica                                  0.39      0.57    -0.70     1.51 1.00     3323     6706
RegionAustralasia                                       2.18      0.53     1.13     3.23 1.00     3323     6724
UI2Secondaryvegetation:RegionNorthAmerica              -0.15      0.15    -0.44     0.15 1.00     8749    12652
UI2Agriculture_Minimal:RegionNorthAmerica              -0.42      0.23    -0.87     0.03 1.00    10964    14597
UI2Agriculture_Light:RegionNorthAmerica                -0.29      0.20    -0.69     0.11 1.00     9436    14590
UI2Agriculture_Intense:RegionNorthAmerica              -0.29      0.23    -0.75     0.16 1.00    10962    14894
```

```
UI2Secondaryvegetation:RegionSouthandSoutheastAsia     -0.44      0.43    -1.26     0.42 1.00    30970    14724
UI2Agriculture_Minimal:RegionSouthandSoutheastAsia     -0.60      0.25    -1.10    -0.10 1.00    14664    14294
UI2Agriculture_Light:RegionSouthandSoutheastAsia       -0.79      0.16    -1.10    -0.48 1.00     7728    13338
UI2Agriculture_Intense:RegionSouthandSoutheastAsia     -0.60      0.25    -1.08    -0.11 1.00    12850    14578
UI2Secondaryvegetation:RegionSouthandCentralAmerica    -0.21      0.14    -0.47     0.06 1.00     7210    12627
UI2Agriculture_Minimal:RegionSouthandCentralAmerica    -0.42      0.15    -0.72    -0.12 1.00     6972    11225
UI2Agriculture_Light:RegionSouthandCentralAmerica      -0.25      0.15    -0.55     0.06 1.00     6940    12150
UI2Agriculture_Intense:RegionSouthandCentralAmerica    -0.21      0.20    -0.61     0.18 1.00     9453    13869
UI2Secondaryvegetation:RegionSubsaharanAfrica          -0.39      0.20    -0.77    -0.00 1.00    11222    14507
UI2Agriculture_Minimal:RegionSubsaharanAfrica          -1.06      0.20    -1.44    -0.67 1.00     9881    14039
UI2Agriculture_Light:RegionSubsaharanAfrica            -0.51      0.20    -0.91    -0.11 1.00     9719    14239
UI2Agriculture_Intense:RegionSubsaharanAfrica          -1.52      0.25    -2.00    -1.03 1.00    11939    14456
UI2Secondaryvegetation:RegionAustralasia               -0.25      0.26    -0.76     0.28 1.00    17905    14256
UI2Agriculture_Minimal:RegionAustralasia               -1.06      0.16    -1.37    -0.74 1.00     8043    12915
UI2Agriculture_Light:RegionAustralasia                 -0.25      0.21    -0.65     0.15 1.00    10260    14579
UI2Agriculture_Intense:RegionAustralasia               -0.29      0.18    -0.64     0.05 1.00     7916    12310

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
shape     2.03      0.04     1.94     2.11 1.00    19526    15571

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).

# Bayesian R2 with Compatibility Interval

  Conditional R2: 0.790 (95% CI [0.673, 0.839])
     Marginal R2: 0.000 (95% CI [7.755e-06, 4.241e-04])
```