# Supplementary material - Tables

### Table S1: Summary measures of species richness and abundance per plot, for the main dataset of bees caught in along transects. The first two columns provide information from the main dataset and second column only for the common species that were present in more than 4 plots (“common species”)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Exploratory | Plot | Bee Total Abundance | Bee Species Richness | Common species - Bee Abundance | Commons species - Bee Richness |
| Alb | AEG01 | 31 | 11 | 8 | 28 |
| AEG03 | 97 | 19 | 13 | 86 |
| AEG04 | 46 | 14 | 12 | 44 |
| AEG06 | 13 | 5 | 4 | 12 |
| AEG07 | 41 | 12 | 10 | 39 |
| AEG09 | 54 | 19 | 11 | 40 |
| AEG12 | 31 | 7 | 5 | 29 |
| AEG17 | 40 | 13 | 11 | 37 |
| AEG24 | 60 | 13 | 12 | 59 |
| AEG46 | 55 | 14 | 11 | 52 |
| Belgium | BELAS | 136 | 26 | 22 | 131 |
| BELDB | 88 | 17 | 15 | 86 |
| BELDBE | 123 | 27 | 22 | 111 |
| BELHB | 42 | 16 | 15 | 41 |
| BELKH | 63 | 24 | 12 | 49 |
| BELMJ | 103 | 29 | 24 | 97 |
| BELOP | 103 | 24 | 21 | 100 |
| BELRD | 87 | 21 | 16 | 81 |
| BELSG | 101 | 21 | 19 | 99 |
| Hainich | HEG02 | 29 | 14 | 11 | 22 |
| HEG03 | 9 | 7 | 7 | 9 |
| HEG07 | 44 | 14 | 13 | 43 |
| HEG08 | 14 | 9 | 8 | 12 |
| HEG09 | 21 | 9 | 8 | 20 |
| HEG17 | 51 | 12 | 10 | 49 |
| HEG42 | 17 | 9 | 8 | 16 |
| Schorfheide | SEG01 | 9 | 7 | 6 | 8 |
| SEG02 | 11 | 7 | 7 | 11 |
| SEG03 | 17 | 5 | 5 | 17 |
| SEG04 | 54 | 10 | 8 | 52 |
| SEG16 | 56 | 15 | 12 | 47 |
| SEG35 | 26 | 7 | 6 | 25 |
| SEG42 | 38 | 14 | 10 | 30 |
| SEG43 | 10 | 5 | 4 | 9 |
| SEG44 | 36 | 14 | 10 | 31 |
| SEG46 | 65 | 18 | 14 | 58 |

## Table S2: List of species in the main dataset and in the subset of species found in 4 or more plots. IUCN Red list status 2015 in parenthesis: Data Deficient (DD), Least Concern (LC), Near Threatened (NT), Vulnerable (VU)

|  |  |
| --- | --- |
| **Present in 4 or more plots (common)** | **Present in less than 4 plots (rare)** |
| ***Andrena sp.*** | |
| *Andrena\_bicolor (LC)* | *Andrena\_alfkenella (DD)* |
| *Andrena\_cineraria (LC)* | *Andrena\_angustior (DD)* |
| *Andrena\_dorsata (DD)* | *Andrena\_barbilabris (DD)* |
| *Andrena\_flavipes (LC)* | *Andrena\_chrysosceles (DD)* |
| *Andrena\_fulvago (DD)* | *Andrena\_florea (DD)* |
| *Andrena\_gravida (DD)* | *Andrena\_florivaga (LC)* |
| *Andrena\_haemorrhoa (LC)* | *Andrena\_fulva (DD)* |
| *Andrena\_labialis (DD)* | *Andrena\_fulvata (DD)* |
| *Andrena\_nigroaenea (LC)* | *Andrena\_helvola (DD)* |
| *Andrena\_nitida (LC)* | *Andrena\_labiata (DD)* |
| *Andrena\_ovatula (NT)* | *Andrena\_minutula (DD)* |
| *Andrena\_wilkella (DD)* | *Andrena\_minutuloides (DD)* |
|  | *Andrena\_nitidiuscula (LC)* |
|  | *Andrena\_proxima (DD)* |
|  | *Andrena\_scotica (DD)* |
|  | *Andrena\_semilaevis (DD)* |
|  | *Andrena\_subopaca (LC)* |
|  | *Andrena\_tibialis (LC)* |
|  | *Andrena\_vaga (LC)* |
|  | *Andrena\_viridescens (DD)* |
|  | *Anthophora\_aestivalis (LC)* |
|  | *Anthophora\_plumipes (LC)* |
| ***Apis sp.*** | |
| *Apis\_mellifera (wild) (DD)* |  |
| ***Bombus sp.*** | |
| *Bombus\_hortorum (LC)* | *Bombus\_jonellus (LC)* |
| *Bombus\_humilis (LC)* | *Bombus\_muscorum (VU)* |
| *Bombus\_hypnorum (LC)* | *Bombus\_ruderarius (LC)* |
| *Bombus\_lapidarius (LC)* | *Bombus\_subterraneus (LC)* |
| *Bombus\_lucorum (LC)* | *Bombus\_wurflenii (LC)* |
| *Bombus\_pascuorum (LC)* |  |
| *Bombus\_pratorum (LC)* |  |
| *Bombus\_soroeensis (LC)* |  |
| *Bombus\_sylvarum (LC)* |  |
| *Bombus\_terrestris (LC)* |  |
| ***Ceratina sp.*** | |
|  | *Ceratina\_cyanea (LC)* |
| ***Chelostoma sp.*** | |
| *Chelostoma\_florisomne (LC)* | *Chelostoma\_campanularum (LC)* |
|  | *Chelostoma\_distinctum (LC)* |
|  | *Chelostoma\_rapunculi (LC)* |
| ***Dasypoda sp.*** | |
| *Dasypoda\_hirtipes (LC)* |  |
| ***Colletes sp.*** | |
|  | *Colletes\_cunicularius (LC)* |
| ***Eucera sp.*** | |
|  | *Eucera\_longicornis (LC)* |
| ***Halictus sp.*** | |
| *Halictus\_scabiosae (LC)* | *Halictus\_eurygnathus (LC)* |
| *Halictus\_tumulorum (LC)* | *Halictus\_maculatus (LC)* |
|  | *Halictus\_rubicundus (LC)* |
|  | *Halictus\_simplex (LC)* |
|  | *Halictus\_subauratus (LC)* |
| ***Hoplitis sp.*** | |
|  | *Hoplitis\_leucomelana (LC)* |
| ***Hylaeus sp.*** | |
|  | *Hylaeus\_confusus (LC)* |
|  | *Hylaeus\_gibbus (NA)* |
|  | *Hylaeus\_hyalinatus (LC)* |
|  | *Hylaeus\_variegatus (LC)* |
| ***Lasioglossum sp.*** | |
| *Lasioglossum\_calceatum (LC)* | *Lasioglossum\_albipes (LC)* |
| *Lasioglossum\_lativentre (LC)* | *Lasioglossum\_fulvicorne (LC)* |
| *Lasioglossum\_leucozonium (LC)* | *Lasioglossum\_glabriusculum (LC)* |
| *Lasioglossum\_malachurum (LC)* | *Lasioglossum\_laevigatum (NT)* |
| *Lasioglossum\_pauxillum (LC)* | *Lasioglossum\_laticeps (LC)* |
| *Lasioglossum\_sexnotatum (NT)* | *Lasioglossum\_leucopus (LC)* |
| *Lasioglossum\_villosulum (LC)* | *Lasioglossum\_majus (NT)* |
| *Lasioglossum\_zonulum (LC)* | *Lasioglossum\_minutissimum (LC)* |
|  | *Lasioglossum\_morio (LC)* |
|  | *Lasioglossum\_parvulum (LC)* |
|  | *Lasioglossum\_punctatissimum (LC)* |
|  | *Lasioglossum\_puncticolle (LC)* |
|  | *Lasioglossum\_setulosum (NT)* |
|  | *Lasioglossum\_xanthopus (NT)* |
| ***Megachile sp.*** | |
|  | *Megachile\_circumcincta (LC)* |
|  | *Megachile\_versicolor (DD)* |
|  | *Megachile\_willughbiella (LC)* |
| ***Osmia sp.*** | |
| *Osmia\_bicornis (LC)* | *Osmia\_bicolor (LC)* |
|  | *Osmia\_niveata (LC)* |
| ***Panurgus sp.*** | |
|  | *Panurgus\_calcaratus (LC)* |
| ***Trachusa sp.*** | |
|  | *Trachusa\_byssina (LC)* |

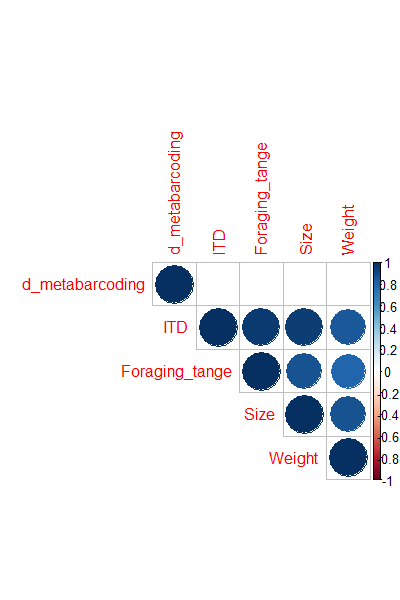
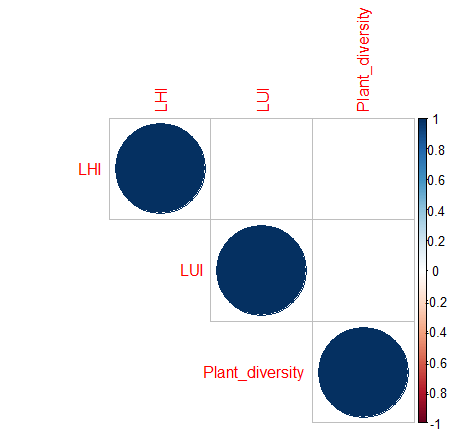
### Table S3: Linear mixed effects model between pollen diversity from individual bee species (response variable) and environmental variables (explanatory). Only tested for species sufficiently abundant in numerous plots. Significance codes: \*\*\* 0,001; \*\* 0,01; \* 0,05; ns >0.05.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Pollen Diversity from *Apis mellifera*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | -0.007 | 0.193 | -0.038 | 0.970 | Ns |
| Land use index (LUI) | -0.396 | 0.781 | -0.507 | 0.618 | Ns |
| Land heterogeneity index (LHI) | 0.572 | 0.897 | 0.638 | 0.531 | Ns |
|  |  |  |  |  |  |
| **Pollen Diversity from *Bombus lapidarius*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | 0.421 | 0.110 | 14.296 | 0.001 | \*\*\* |
| Land use index (LUI) | 0.313 | 0.431 | 0.507 | 0.485 | Ns |
| Land heterogeneity index (LHI) | -0.109 | 0.557 | 0.038 | 0.848 | Ns |
|  |  |  |  |  |  |
| **Pollen Diversity from *Bombus pascuorum*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | -0.043 | 0.184 | 0.536 | 0.476 | Ns |
| Land use index (LUI) | 0.107 | 0.648 | 0.027 | 0.871 | Ns |
| Land heterogeneity index (LHI) | 2.874 | 1.087 | 6.990 | 0.018 | \* |
|  |  |  |  |  |  |
| **Pollen Diversity from *Andrena haemorrhoa*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | 0.028 | 0.253 | 0.002 | 0.968 | Ns |
| Land use index (LUI) | 1.419 | 0.838 | 2.716 | 0.128 | Ns |
| Land heterogeneity index (LHI) | 0.508 | 1.210 | 0.176 | 0.683 | Ns |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| **Pollen Diversity from *Lasioglossum pauxilum*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | 0.017 | 0.109 | 0.022 | 0.887 | Ns |
| Land use index (LUI) | 0.572 | 0.531 | 0.738 | 0.419 | Ns |
| Land heterogeneity index (LHI) | 0.874 | 0.797 | 1.203 | 0.309 | Ns |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| **Pollen Diversity from *Bombus terrestris*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | -0.282 | 0.785 | 0.041 | 0.844 | Ns |
| Land use index (LUI) | -0.560 | 0.590 | 0.259 | 0.623 | Ns |
| Land heterogeneity index (LHI) | 0.859 | 0.413 | 0.738 | 0.413 | Ns |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| **Pollen Diversity from *Andrena nitida*** | **Estimate** | **St. Error** | **F** | **Pr(>F)** | **sign.** |
| Plant Diversity | 0.277 | 0.229 | 2.550 | 0.161 | Ns |
| Land use index (LUI) | -0.929 | 0.704 | 1.701 | 0.240 | Ns |
| Land heterogeneity index (LHI) | 0.446 | 1.100 | 0.165 | 0.699 | Ns |

# Supplementary material - Figures

### Figure S2: Correlation matrices only showing significant correlations p<0.05 a) between environmental variables, b) between numerical traits from species. Land use heterogeneity (LHI), Land use intensity index (LUI), Plant diversity (Plant\_diversity), Specialization level index d´ (d\_metabarcoding), Intertegular distance (ITD),

a)

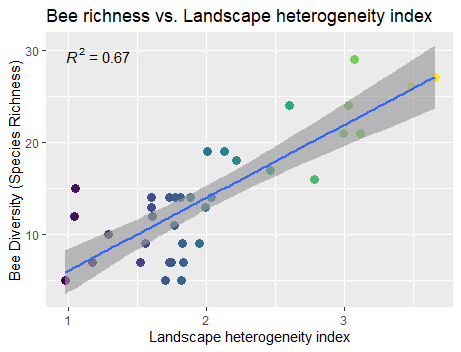
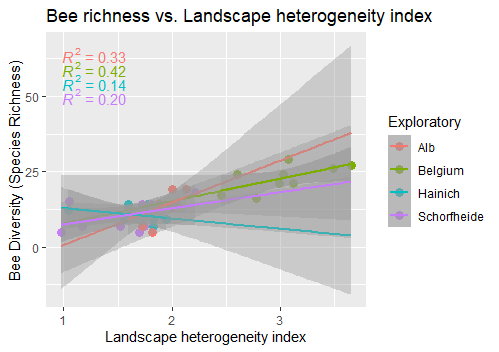


b)

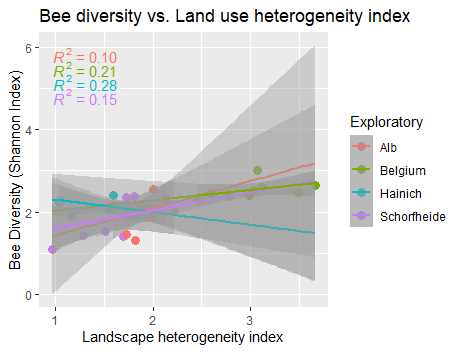
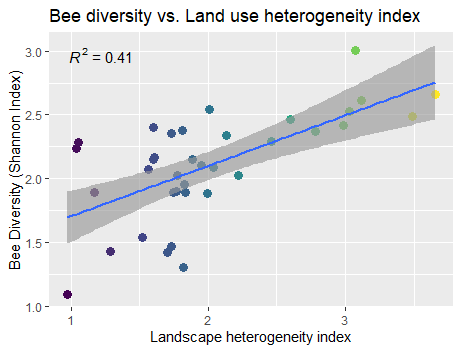
### Figure S3: Visualization of correlation between bee species richness, bee diversity and landscape heterogeneity (LHI), pollen diversity and local plant diversity, also separate for each region (Alb, Hainich, Schorfheide and Belgium).

### Landscape heterogeneity index (LHI) (blue, green, yellow, from less to more diverse landscape); Exploratories: Alb (red), Belgium (green), Hainich (blue), Schorfheide (violet).

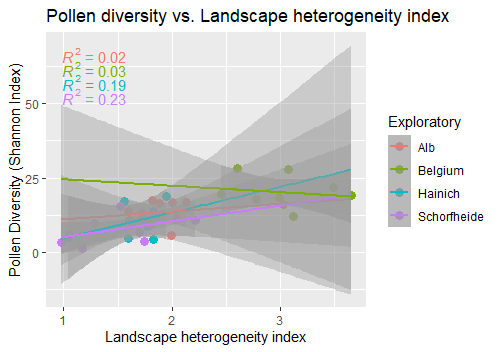
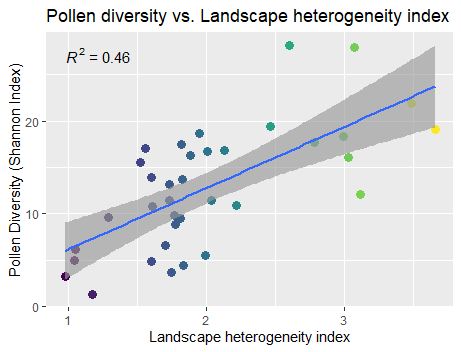
### a) Bee species richness vs. LHI



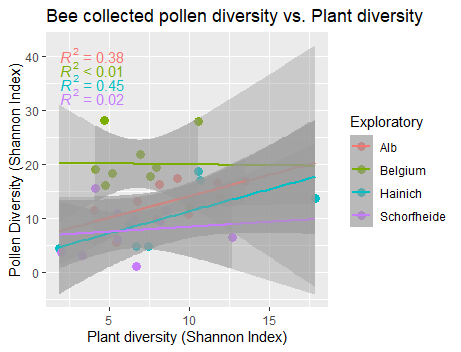
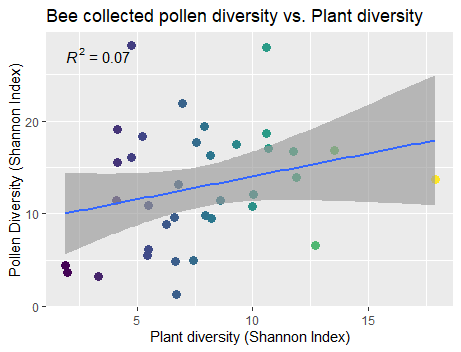
### b) Bee diversity (Shannon) vs. LHI



### c) Pollen diversity vs. LHI



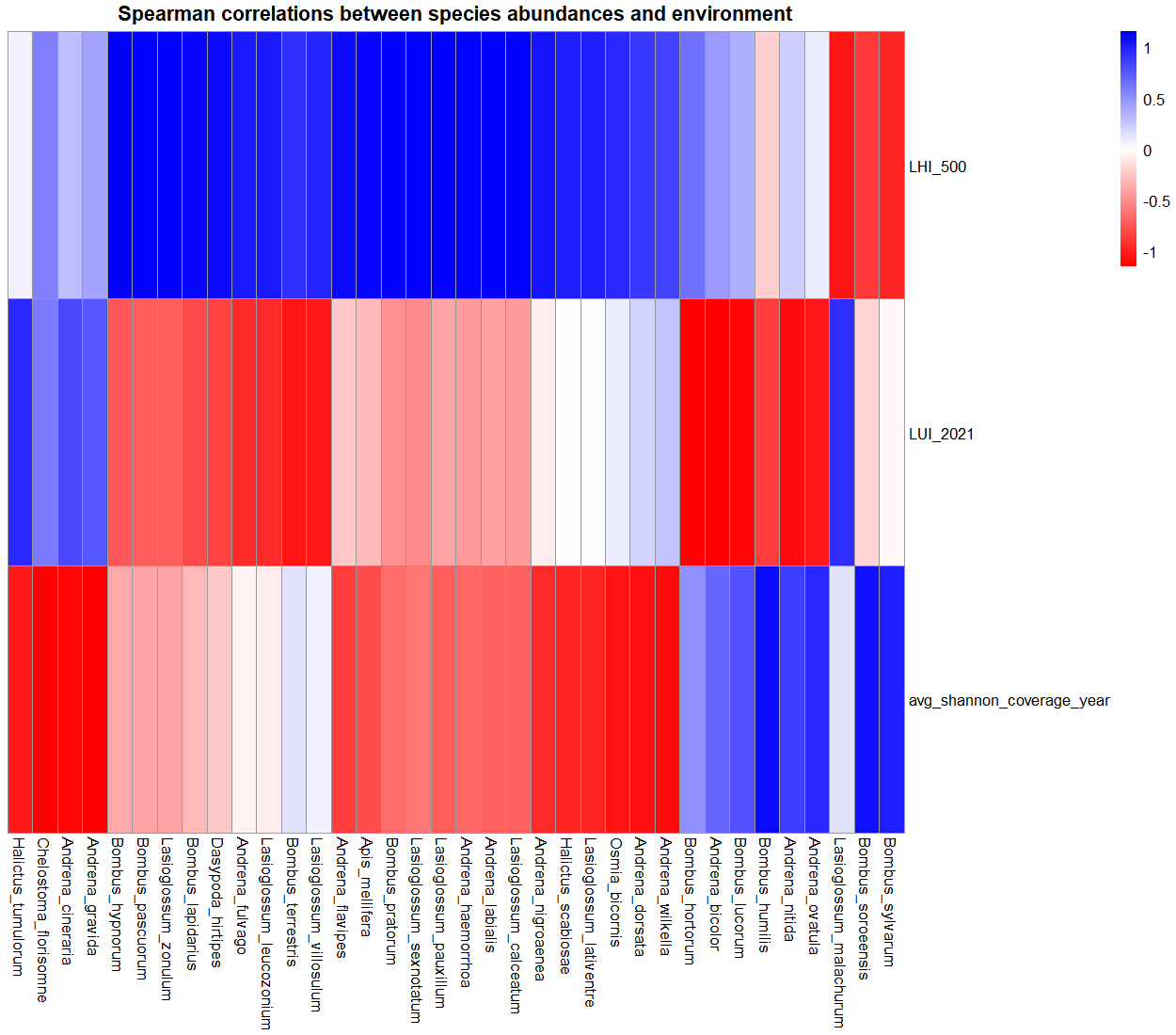
### d) Pollen diversity vs. plant diversity

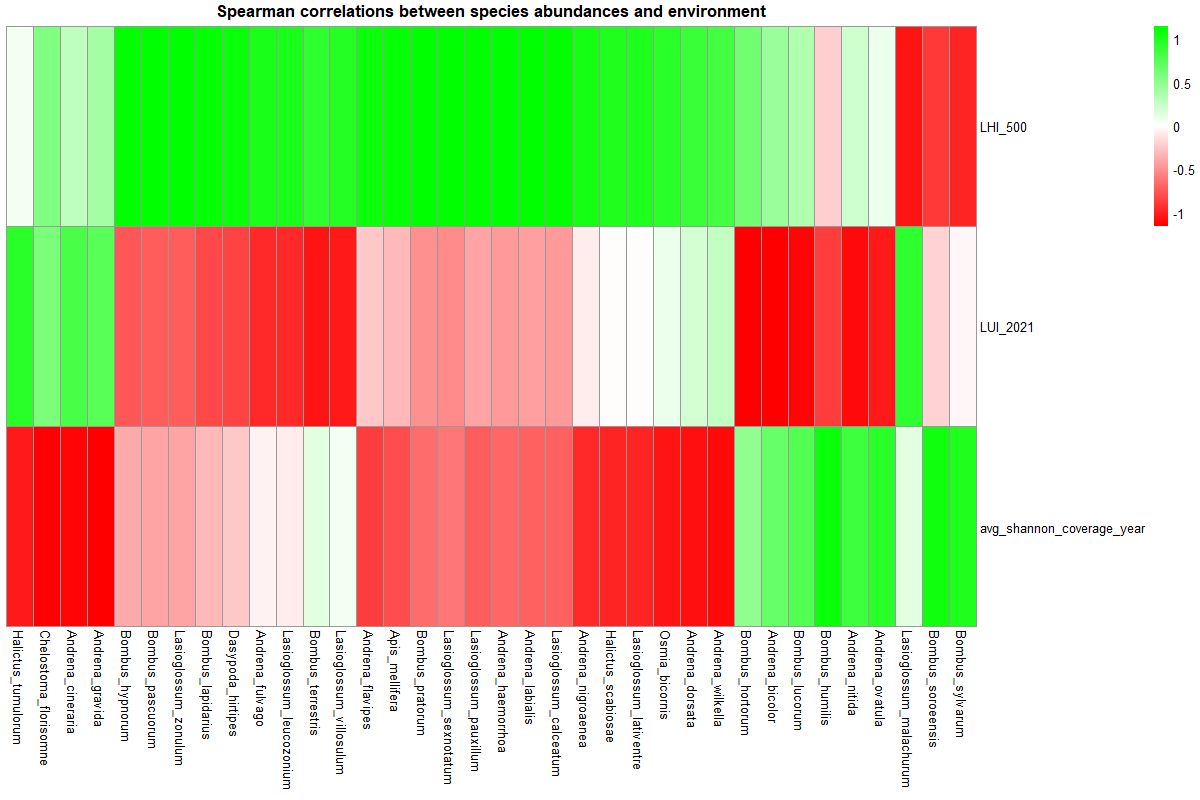


## Figure S4: Heatmap of Spearman correlations between abundance of species and different environmental variables. Landscape heterogeneity index (LHI), Land use intensity index (LUI).

Red: negative correlation, White: no correlation, Blue: positive correlation. Species names not in italic so as not to alter original graph (R Software).

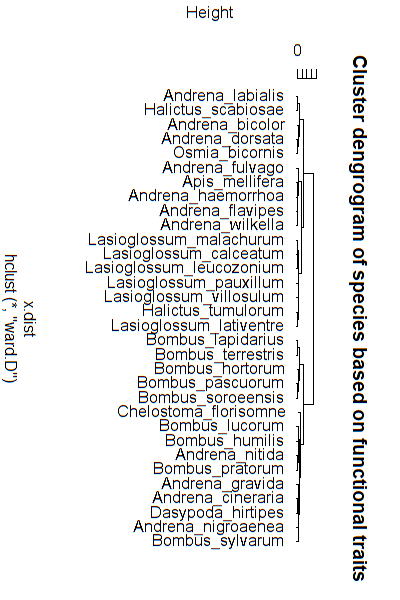
LHI LUI Plant diversity



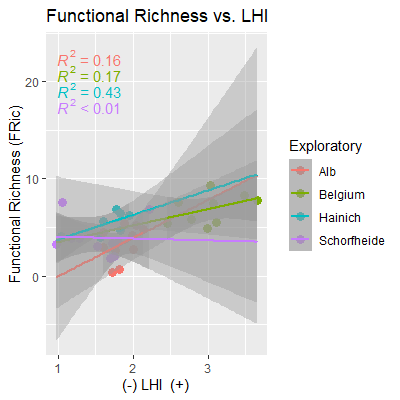
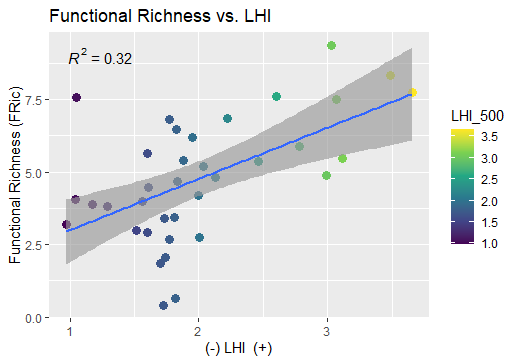


### Figure S5: Cluster dendogram of species based on functional traits (average female size and specialization level d´).

Species names not in italic so as not to alter original graph (R Software).



### Figure S6: Visualization of significant correlations for functional indices (functional Richness vs landscape heterogeneity (LHI)), also separate for each region (Alb, Hainich, Schorfheide and Belgium). Landscape heterogeneity index (LHI) (blue, green, yellow, from less to more diverse landscape); Exploratories: Alb (red), Belgium (green), Hainich (blue), Schorfheide (violet).



# Supplementary material – Details on protocols and methods

### Protocol 1: Additional information about sites

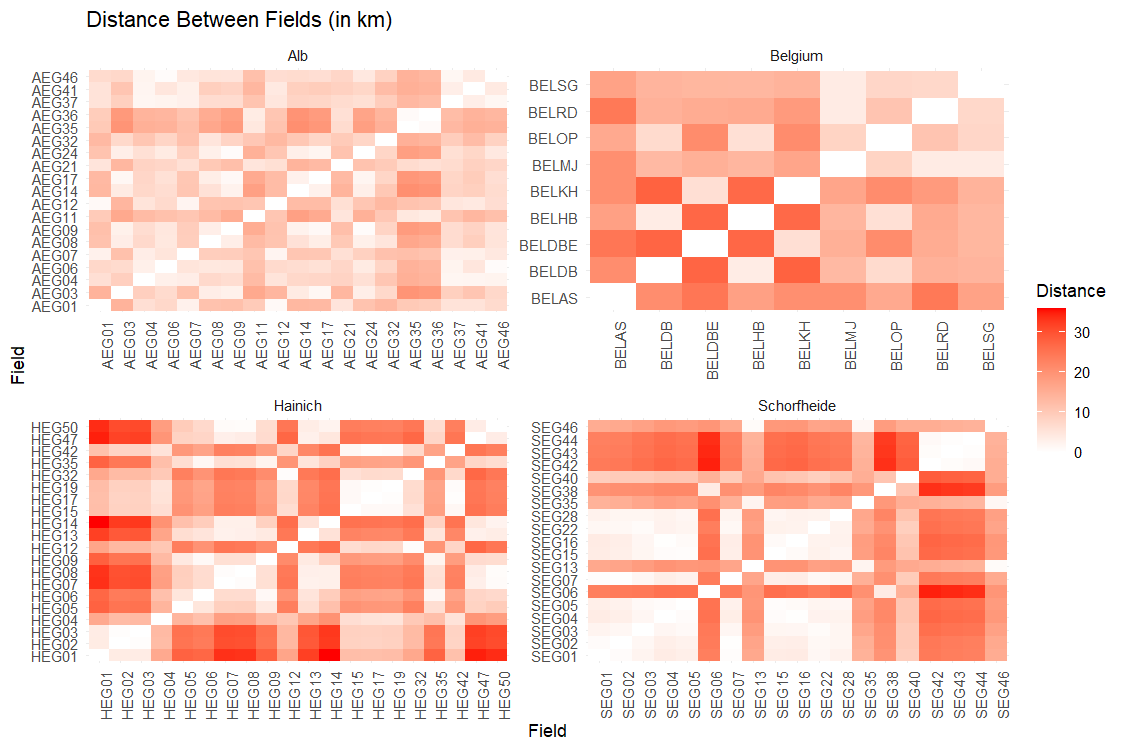
The plots are located in areas with a mix use of nature conservation, agriculture and urban areas. Figure P1.1 and P1.2 shows a heatmap representing the distance between plots, and the subset of plots with less than 1 km in between fields. Figure P1.3 shows the diversity of sizes within the units of management grassland (meadows) between plots.

Figure P1.1: Distance between fields (in kilometers), per site. The stronger the orange color, the higher the distance.

### 

Figure P1.2: Subset of plots with less than 1 km in between them. Distance between fields (in kilometers), per site. The stronger the orange color, the higher the distance.

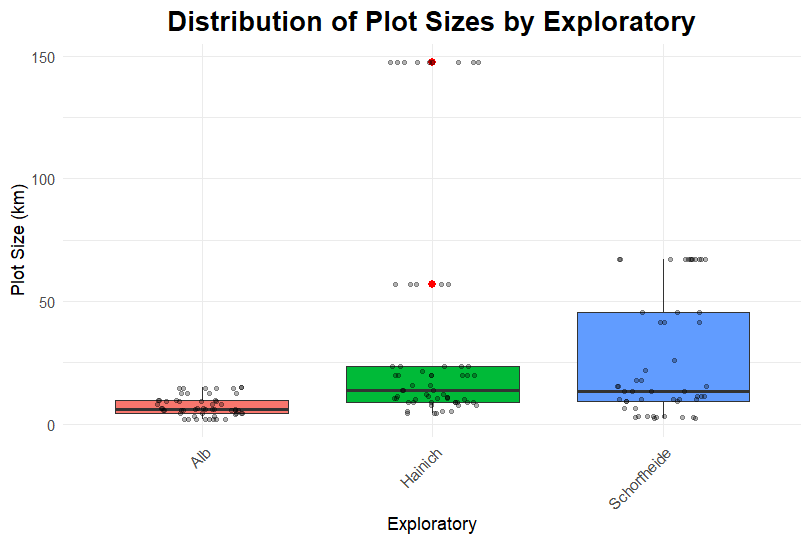


Figure P1.3: Distribution of plot sizes (managed are for agriculture) per exploratory

### Spatial autocorrelation test

Given the closeness of some of our plots with each other, we performed a spatial autocorrelation test on our variables of interest, to evaluate whether they whether there was a spatial dependence of the data (Table P1). Results suggest all variables except Plant diversity have an effect of spatial autocorrelation, suggesting the data in plots closer together may be associated. Based on these results we included in our models a spatial autocorrelation term. Results in the main text of this manuscript reflect significances including the autocorrelation term.

Table P1: Spatial autocorrelation Moran I test over environmental and community variables of interest.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variable tested** | **Moran I statistic** | **Moran I statistic standard deviate** | **p-value** | **Spatial autocorrelation effect** |
| Test for Land use intensity | 0,264 | 2,794 | 0,003 | Yes |
| Test for Plant diversity | 0,087 | 1,127 | 0,130 | No |
| Test for Landscape heterogeneity | 0,807 | 8,004 | 0,000 | Yes |
| Test for Bee Richness | 0,585 | 5,837 | 0,000 | Yes |
| Test for Bee diversity | 0,361 | 3,737 | 0,093 | Yes |

### Protocol 2: Barcoding and Metabarcoding Protocol

We used VSEARCH v2.14.2 (Rognes et al., 2016) to join paired ends of forward and reverse reads. We also used VSEARCH to remove reads shorter than 150bp, quality filtering (EE < 1) (Edgar & Flyvbjerg, 2015), *de-novo* chimera filtering (following UCHIME3) (Edgar, 2016b) and determination of amplicon sequence variants (ASVs) as previously done for pollen metabarcoding networks (Martins et al., 2023). Reads were first directly mapped iteratively with global alignments using VSEARCH against a floral ITS2 reference databases for the study region an identity cut-off threshold of 97%. This database was created with BCdatabaser (Keller et al., 2020) and a species list of Central Europe and curated (Quaresma et al., 2024). For species that could not be assigned to species level with this procedure, a hierarchical classification with the SINTAX (Edgar, 2016a) in VSEARCH was performed using a curated global database on genus level (Quaresma et al., 2023).

### Protocol 3: Details on environmental and bee foraging trait variables

### Plant diversity

For the plots in Germany, the plant diversity was measured as the percentage cover of all plant species within 16m2 per plot in the flowering season from 2020 and 2021. The percentage of cover from each plant species was taken from field assessments carried out by the Core Botany team of the Biodiversity Exploratories and included all plant species (Hinderling et al., 2022). We used a subset of the original dataset by selecting those plants that flowered between April and July and hence were of relevance for pollen and nectar collecting bees; we excluded non-flowering plants. For the plots in Belgium, respective field measurements were carried out by our team by placing 30 quadrats of 1 m² at the ends and in the middle of each 25 m transect line during every plot visit. We identified all flowering plants and counted the number of flowering stems available for bees within quadrants. We calculated the approximate cover of each plant species based on their size using mean leaf length (or leaf stalk + leaf length) from databases as a proxy for plant radius. We then intrapolated our measurements to 16 m2, in order to match the area of the measurements in Germany. Finally we calculated the Shannon diversity of plants per plot and the exponential of this index (Hill index) (Chao et al., 2014; Roswell et al., 2021), which were the values used as plant diversity.

### Pollen sources

Figures P3 (1-4) shows the composition of the pollen found in bees in each plot, for plants with 10 or more occurrences in each site, for further reference on the plant community in the plots and surroundings. There is a predominance of herbaceous so also woody sources (eg., *Acer pseudoplatanus*).

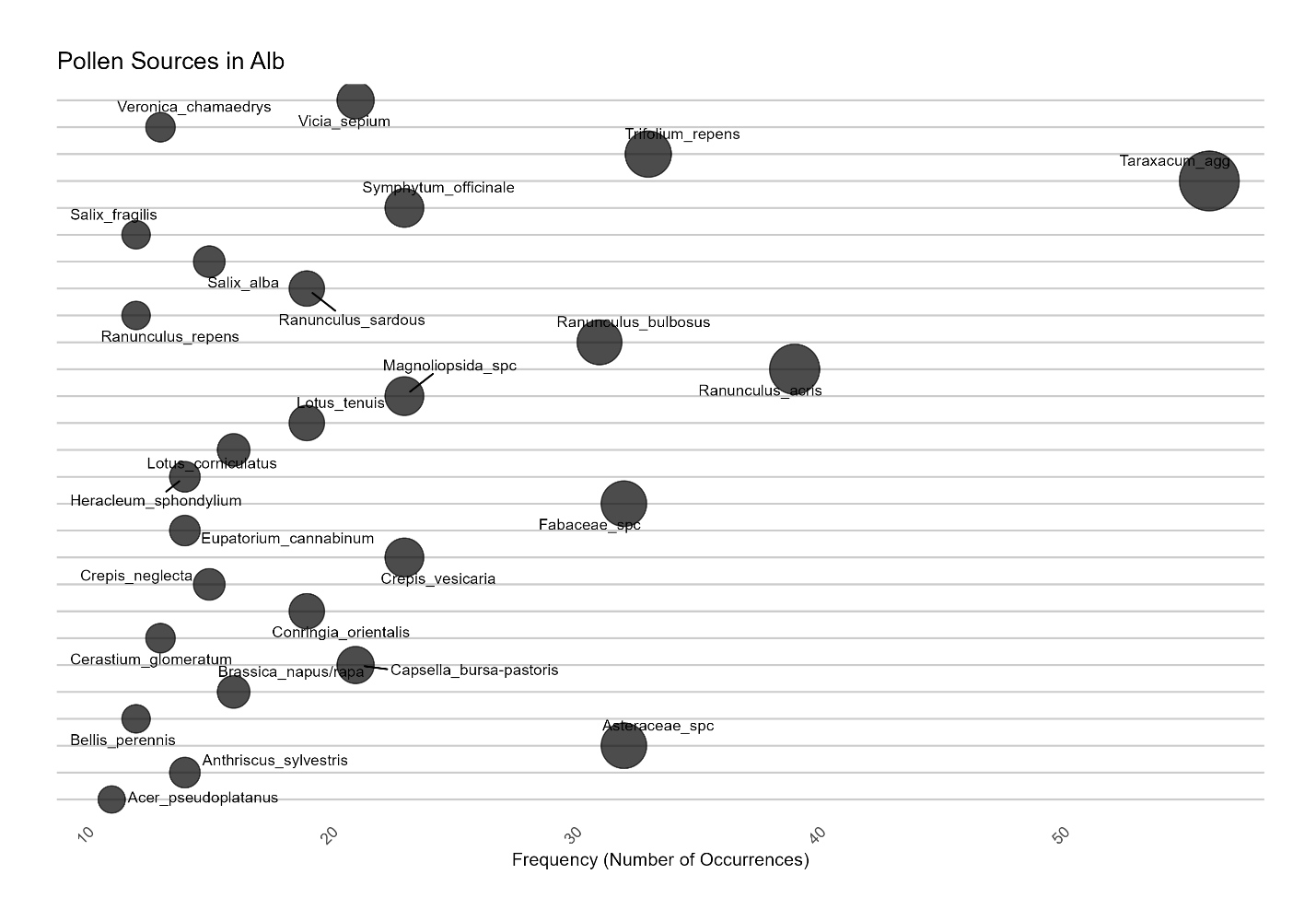


Figure P3.1: Main sources of pollen. Frequency of plant species in the metabarcoding records of the site Alb (for plants with more than 10 occurrences).

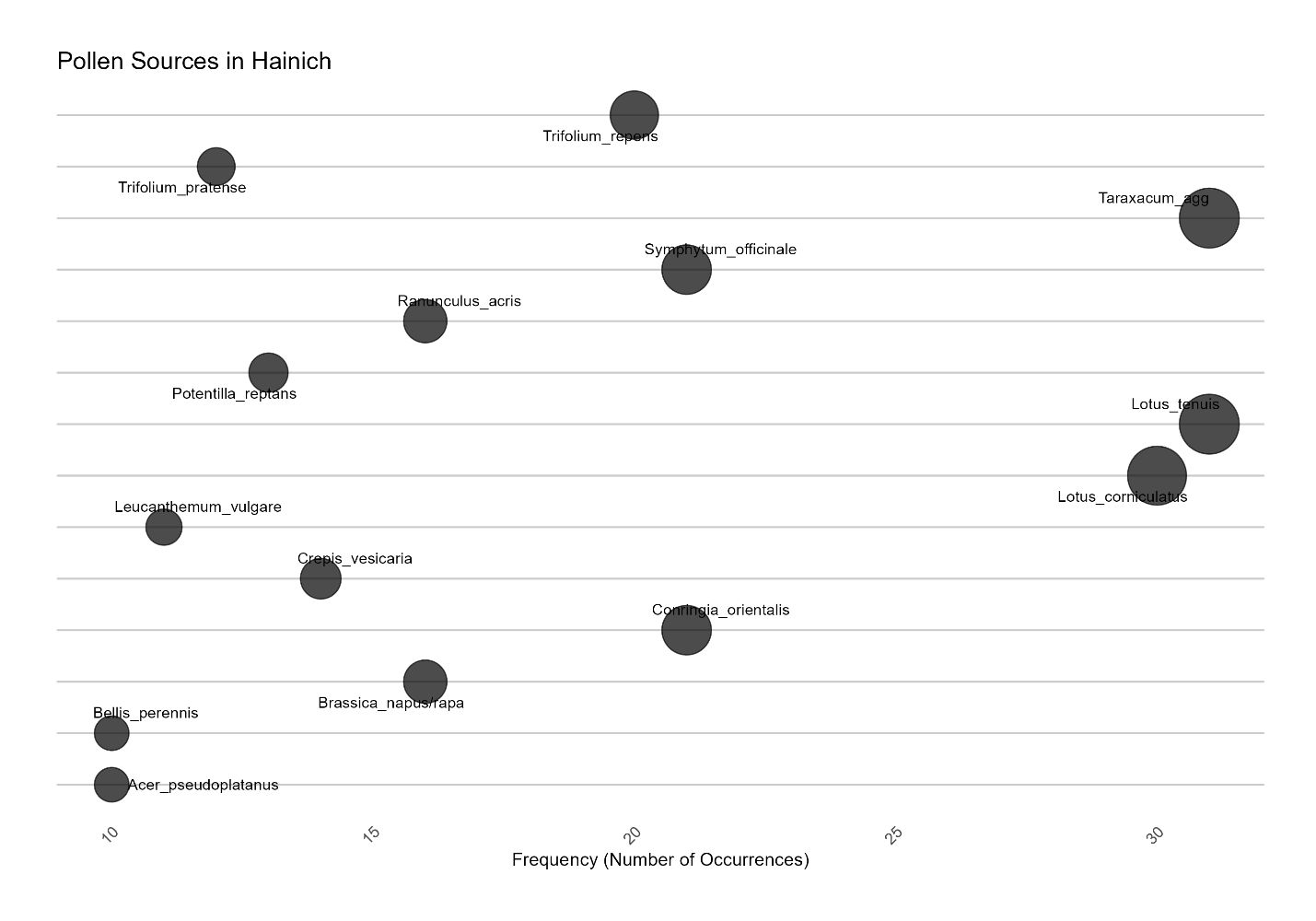


Figure P3.2: Main sources of pollen. Frequency of plant species in the metabarcoding records of the site Hainich (for plants with more than 10 occurrences).

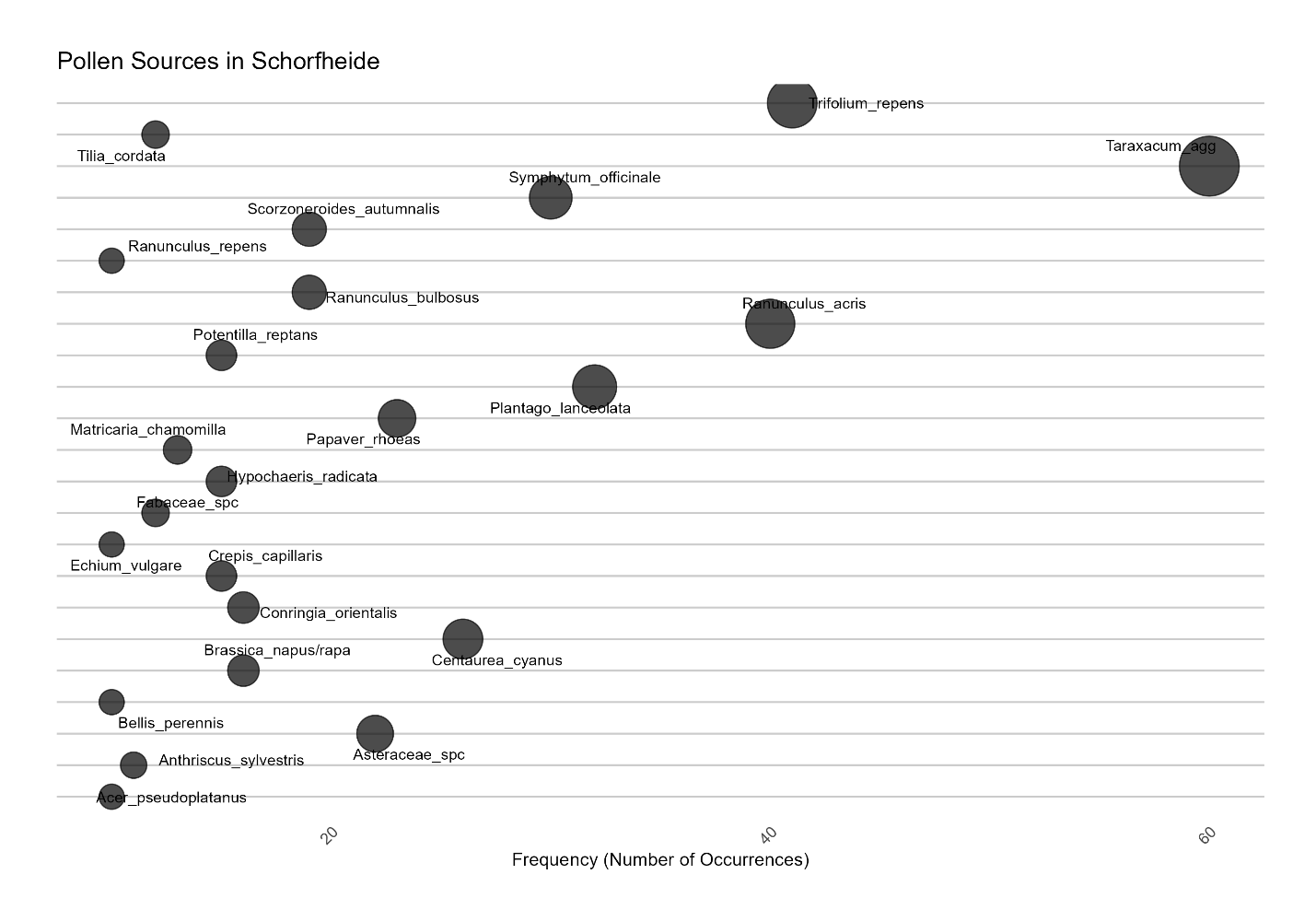


Figure P3.3: Main sources of pollen. Frequency of plant species in the metabarcoding records of the site Schorfheide (for plants with more than 10 occurrences).

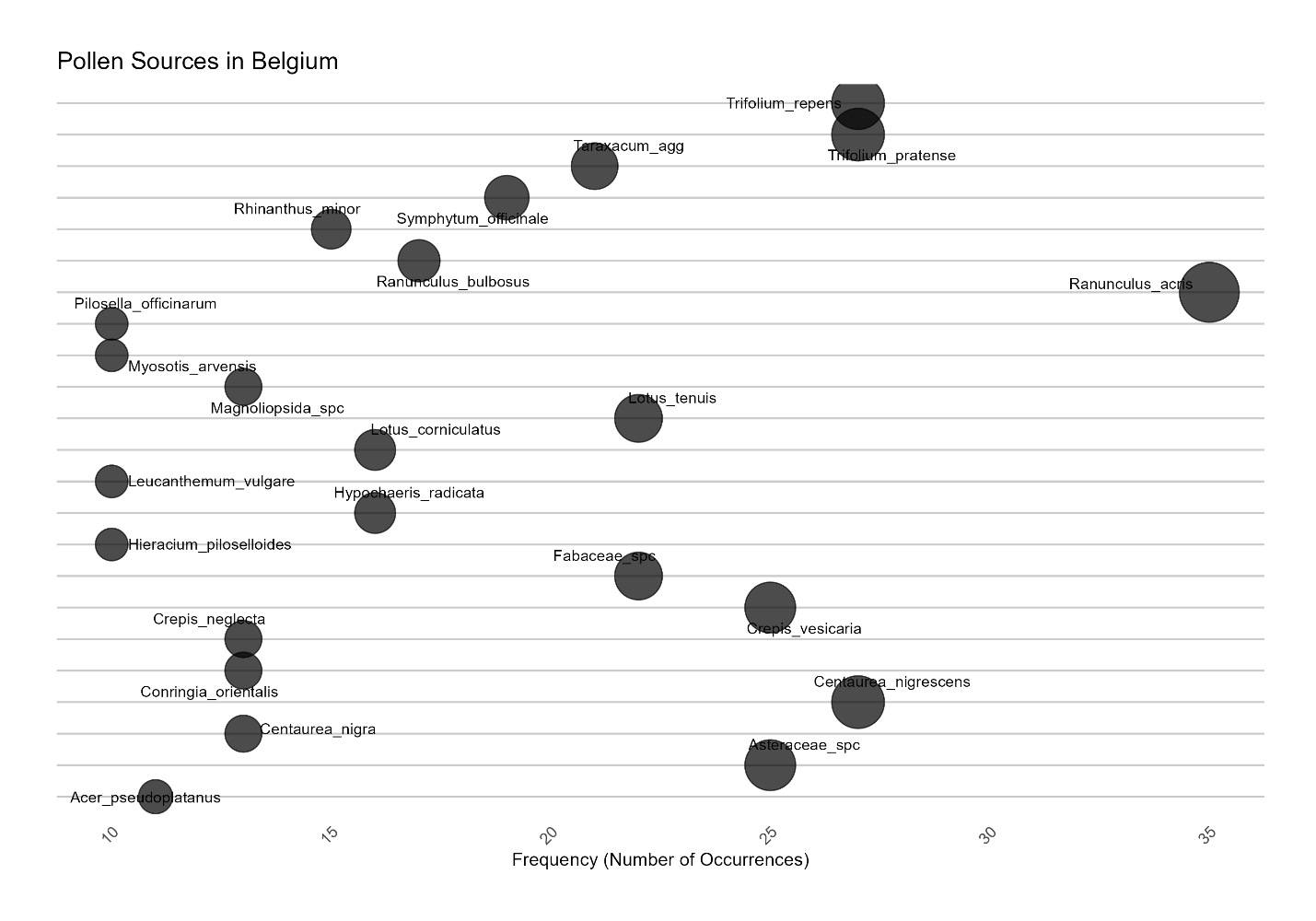


Figure P3.4: Main sources of pollen. Frequency of plant species in the metabarcoding records of the site Belgium (for plants with more than 10 occurrences).

### Land-use intensity index (LUI)

Our plots were located along a land-use intensity (LUI) gradient, which can be measured as a continuous variable following (Blüthgen et al., 2012) and based on the frequency of mowing, the frequency and amount of grazing animals (livestock units days of grazing ha−1 year−1) and the amount of fertilizer used in the field (kg nitrogen ha−1 year−1 ) (Blüthgen et al., 2012; Ostrowski et al., 2020; Vogt et al., 2019). To help interpret this index for our study plots, we explored a priori which LUI components contributed the most to the general index in our subset of plots in 2021 (Figure P3.5). Mowing and grazing were rarely performed at the same plot, but alternated, and only 6 out of our 26 plots were fertilized. Consequently, high intensity land-use at our plots were driven mainly by a combination of high fertilization and strong grazing activity.

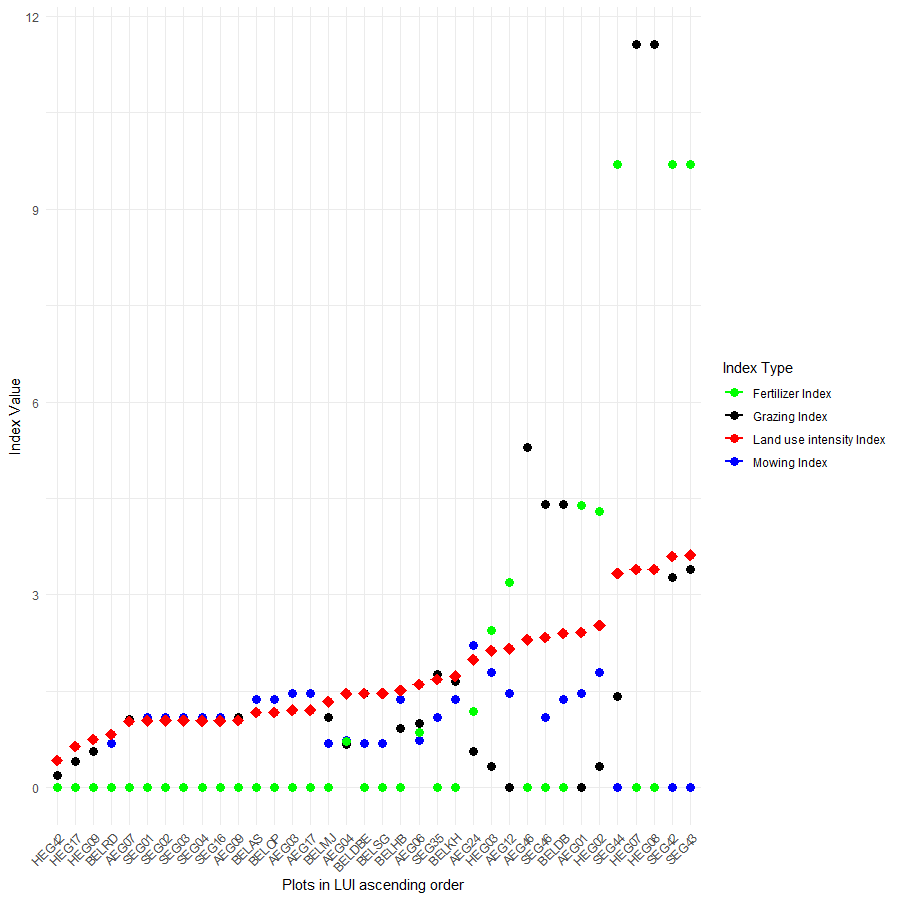


Figure P3.5: Index values of the three individual land-use intensity (LUI) components (grazing (black), mowing (blue) and fertilization (green)) for a better interpretation of the mechanisms behind the general LUI Index.

### Land-use heterogeneity index (LHI)

To capture diversity of habitats and land-uses in the surrounding landscape we calculated a land-use heterogeneity index (LHI). We defined land-use classes based on ATKIS classifications as the dominant habitats (i.e. agricultural land, forest, woods, mire, heath, bare land, water, roads, settlements) and subtypes based on intrinsic characteristics and human modifications (i.e. agricultural land into cropland, orchard, vineyard, etc., forest into deciduous or perennial, roads into natural or paved). Single trees and forest or hedges at the border of farms were also accounted for as part of woods. We used existing image databases to classify the surrounding landscape into different land-uses and to quantify the area of each land-use. For plots in Belgium, we used the Biological Valuation Map (BVM) which surveys biologically relevant habitats in the Flemish Region of Belgium in the flowering season of the main dominant plant species once a decade (De Saeger et al., 2017). For plots in Germany, we used the database a remote sensing open access platform from the Biodiversity Exploratories that integrates data collected from drone images, LIDAR (light detection and ranging) and sensors to monitor biodiversity in the experimental plots, updated lastly in 2022 (Magdon et al., 2023; Wöllauer et al., 2021). To quantify the diversity in land-use types around the plots we extracted the percentage of area that each land-use type occupied in a 500 m radius around the plot center (Parreño et al., 2023). The value of 500 m was selected based on the approximate foraging range of most solitary species, estimated to be 150-600 m (Gathmann & Tscharntke, 2002). We then calculated a Shannon diversity index per plot (called SHDI in the literature, LHI in our study), using the proportions of each land-use type, following the formula:

where Pi = proportion of the landscape occupied by patch land cover type (class) i

LHI is a landscape metric widely used in biodiversity science that takes both the number of classes and the abundance of each class into account (McGarigal & Cushman, 2002). All analyses were carried out in ArcGIS Software and Python. For the plots in Belgium, the land cover dataset encompasses spatial location properties and description as code in an attribute, covering the entire country. The data was projected using the Belge lambert 1972 coordinate system, based on the Lambert Conformal conic projection system, and adhering to the D-Belge 1972 datum. Class descriptions were provided in separate fields labeled from EENH1 to EENH7, which were consolidated into a single field to generate final description codes. For the plots in Germany, we used the RSBD database in which the data were projected in the ETRS 1989 UTM Zone 32N coordinate system using the Transverse Mercator projection. The GCS ETRS 1989 datum was prescribed for the data. The land cover data in Germany were classified into two schemes (geometric property and attribute property). The attribute property contained unique plot numbers and corresponding class descriptions, while three fields in the data represented feature descriptions using code numbers. Programming scripts in Python used to extract the areas of lands use and calculate the landscape heterogeneity index can be found on Github (Sumeers, 2023/2023)

### Information on trait database for Intertegular distance, female bee size and foraging range

The trait database was constructed as part of the EU FP6 project ALARM (2004-2009), and developed further under the FP7 programme STEP (2010-2015). Since 2014 all development and maintenance has been done independently by the author (SR). Data has been gathered from published peer reviewed papers and books, from the grey literature and from personal communication from a host of observers. Data sources include taxonomic revisionary and descriptive texts, treatments of national apifaunas and other faunistic studies, red lists, short notes, the pollination and diversity literature along with verifiable postings on various social media outlets. In addition to this, measurements of Inter-tegular distance (ITD) have been provided by over 60 scientists and private individuals based on material in museums and other academic institutions and personal collections. The literature set is absolutely large and cannot be cited in the current paper. However, the database is in an advanced state of preparation for publication on a publicly available website (publication due Autumn 2024).

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