**Supplementary Material for the study:** ‘Disentangling direct and indirect effects of forest structure on biodiversity: Bat responses to forest structure, management and insect prey’ by Hendel et al. (2024)

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## S1) Methodological details

### S1.1) Number of sampling locations

Originally data were collected on 66 plots. Due to missing data for one plot (CFB094) and a visual outlier (CFB034, see A1.1), data from 64 plots (n=64) were used for this study.

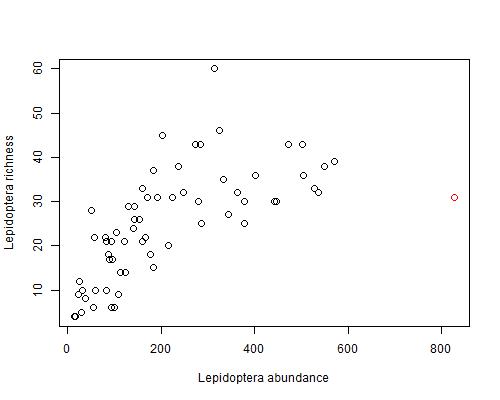
**

Figure S1.1) *Outlier in the Lepidoptera abundance visualized within the abundance-richness relationship. The red dot highlights the outlier (CFB034), which we excluded from the analysis.*

### S1.2) Sampling dates overview

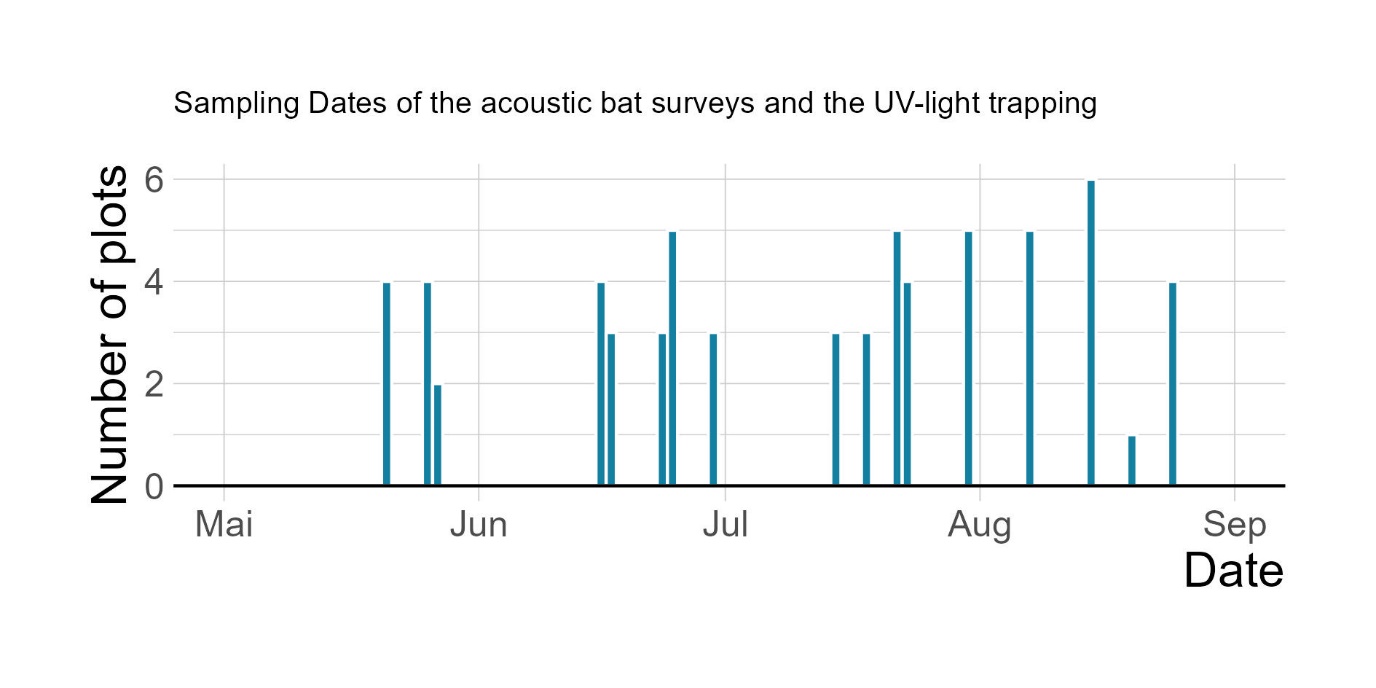


Figure S1.2*: Overview of the sampling Dates for the acoustic bat surveys and the UV-light trapping, indicating how many plots were sampled in parallel. In total, 64 plots were included in this study. Sampling Dates represent the date when the UV-light traps were active, but bat loggers were also active the night before and after.*

### S1.3) Vegetation data imputation

The vegetation surveys that were used to impute the 12 missing values in the understory dataset, were carried out between 2016 and 2018 on the same plots (Helbach et al., 2022). Instead of 18 one square meter plots, 6 plots of 5 x 5 meters were used in this survey. Due to the larger spatial scale of the survey, this prior survey included on average 3 species more than the survey in 2020. In order to account for the differences in spatial scale and time, we used regression imputation to predict understory richness and cover values for the 12 missing plots. First, we created linear models with the 2020 survey of species richness and cover respectively as a response and the prior surveys as predictor. The model for species richness was significant (F= 86.36 on 1 and 57 DF, p-value: 5.144e-13) as was the model for cover (F = 82.62 on 1 and 54 DF, p-value: 1.795e-12). We then predicted species richness and cover for the missing values of 2020 by extracting the respective model values based on the known species richness and cover from the prior surveys.

### S1.4) Metabarcoding

We use bulk sample metabarcoding to identify moth species from the UV-light traps. The retrieved barcodes were blasted against the Barcode of Life databank (BOLD, Ratnasingham & Hebert, 2007). Assignments with a sequence similarity of 97% or higher were considered reliable identifications. The number of reads was transformed into presence-absence records per species and plot. Species with less than 10 reads across all plots were excluded from the dataset and species with less than two reads per plot were treated as absence record.

## S2) Details for the collected data

### S2.1) Correlation amongst variables

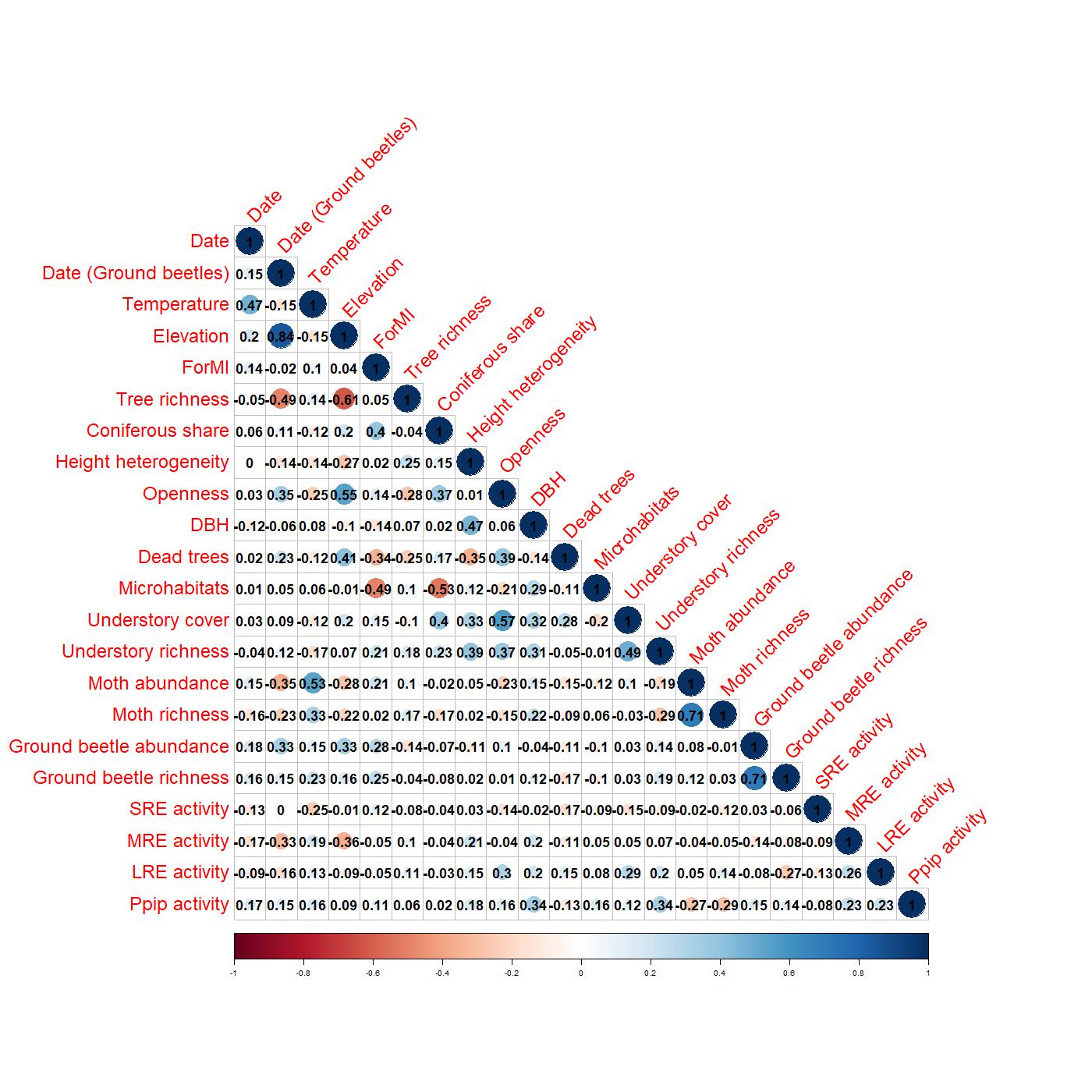


Figure S2.1) *Pearson correlation coefficients for predictor variables. Date information refers to the day of the year when bat loggers and UV traps where placed.*

### S2.2) Microhabitat availability per type and plot

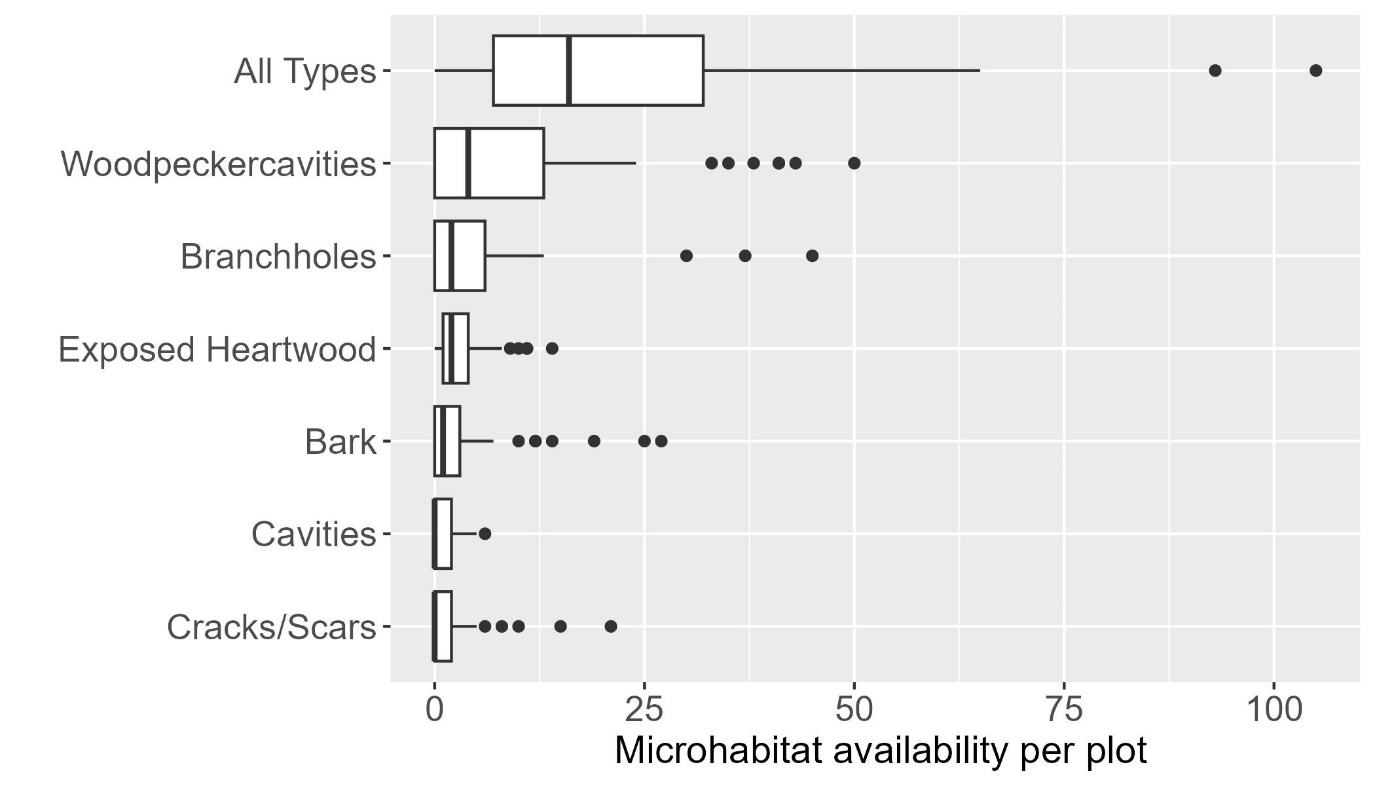


Figure S.2.2) *Microhabitat availability by type and plot (N=64). Included are only microhabitat types that are potentially suitable as bat roosts. Microhabitat inventories were conducted on the largest 15 living trees and 15 dead trees per plot (for details see Spînu et al. (2022).*

### S2.3) Moths occurrences by species



Figure S2.3) *Moth species occurrence probabilities across plots (N=64). Occurrence probabilities refer to the proportion of plots in which the species was detected. Species with an occurrence probability* < *0.15 are not shown.*

### S2.4) Ground beetle occurrences by species

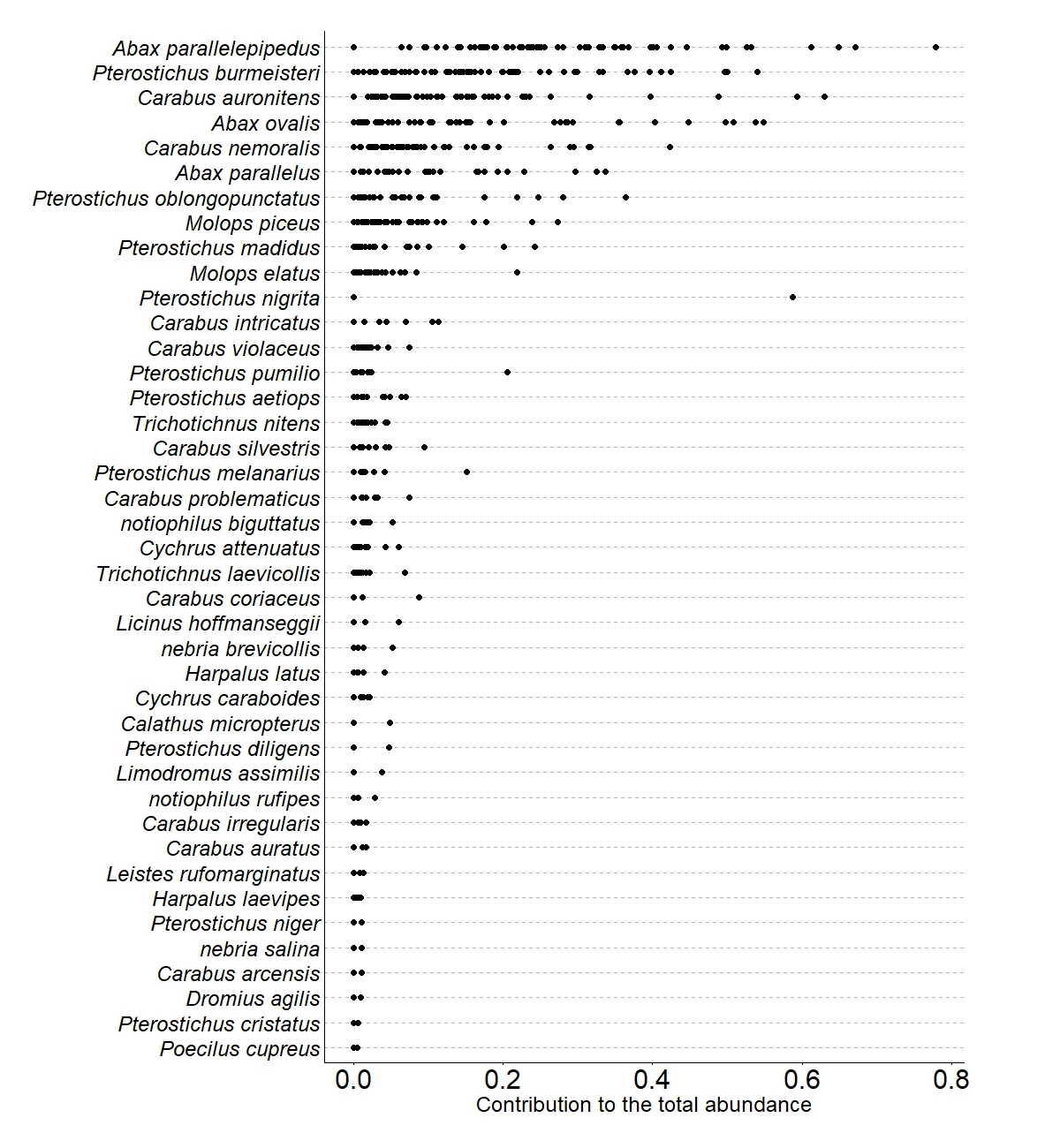


Figure S2.4) *Mean contribution of the individual carabid species abundances to the total abundance per plot (N=64). Species are sorted by their mean contribution across plots.*

### S2.5) Bat activities by guild and bat species groups

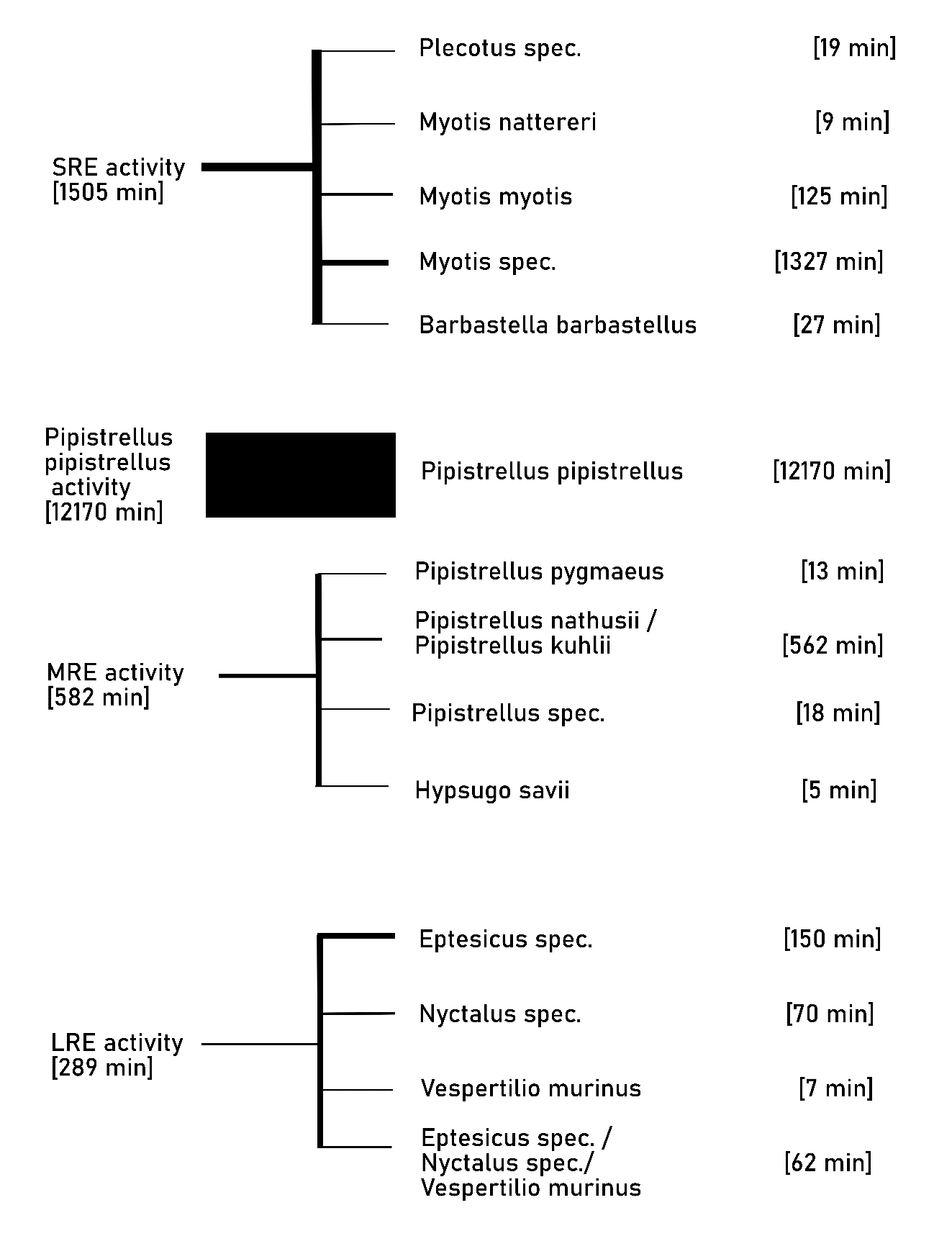


Figure S2.5) *Total bat guild and bat species-group activities across plots (N=64). 1-min activities of each group are given in brackets. Line thickness roughly correspond to the observed species- group activities. The guild grouping from Frey-Ehrenbold et. al (2013) was used.*

## S3) Details on the model building

### S3.1) Model formula for full- and variable-selected and modified gam models

Table S3.1: List of all model formula for full- and variable-selected gam models.

|  |  |  |  |
| --- | --- | --- | --- |
| Response variables | Model | Model formula | family |
| Understory Cover | Full | s(ForMI, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Standing dead trees, k=3) + Elevation | neg. bin. |
| Selected | s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) | neg. bin. |
| Understory Richness | Full | s(Understory cover, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(ForMI, k=3) + Elevation | gaussian |
| Selected | s(Understory cover, k = 3) + s(Coniferous share, k = 3) + s(Tree richness, k = 3) + s(Height heterogeneity, k = 3) + s(Openness, k = 3) + s(DBH, k=3) | gaussian |
| Moth abundance | Full | (Understory cover, k=3) + s(Understory richness, k=3) + s(ForMI, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(Standing dead trees, k=3) + s(DBH, k=3) + s(Date, k=3) + Elevation + Temperature | neg. bin. |
| Selected | s(Understory cover, k=3) + s(Understory richness, k=3) + s(Standing dead trees, k=3) +Temperature+ s(Date, k=3) +Elevation | neg. bin. |
| Modified | s(MRE, k = 3) + s(P.pipistrellus, k = 3) + s(Understory cover, k=3) + s(Understory richness, k=3) + s(Standing dead trees, k=3) +Temperature+ s(Date, k=3) +Elevation | neg. bin. |
| Moth richness | Full | s(Moth abundance, k=3) + s(Understory cover, k=3) + s(Understory richness, k=3) + s(ForMI, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(Standing dead trees, k=3) + s(DBH, k=3) + s(Date, k=3) + Elevation + Temperature | gaussian |
| Selected | s(Moth abundance, k=3) + s(Coniferous share, k=3) + s(Tree richness, k=3) + s(Height heterogeneity, k=3) + s(Date, k=3) +Elevation | gaussian |
| Ground beetle abundance | Full | s(Understory cover, k=3) + s(Understory richness, k=3) + s(ForMI, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Standing dead trees, k=3) + s(Date ground beetle sampling, k=3) + Elevation | neg. bin. |
| Selected | s(Understory richness, k=3) + s(ForMI, k=3) + s(Coniferous share, k=3) + s(DBH, k=3) + s(Date ground beetle sampling, k = 3) +Elevation | neg. bin. |
| Ground beetle richness | Full | s(Ground beetle abundance, k=3) + s(Understory cover, k=3) + s(Understory richness, k=3) + s(ForMI, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(Standing dead trees, k=3) + s(DBH, k=3) + s(Date ground beetle sampling, k=3) + Elevation | gaussian |
| Selected | s(Ground beetle abundance, k=3) + s(ForMI, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Date ground beetle sampling, k = 3) | gaussian |
| Microhabitats | Full | s(ForMI, k=3) + s(Coniferous share, k=3) + s(Tree richness, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(Standing dead trees, k=3) + s(DBH, k=3) + Elevation | neg. bin. |

|  |  |  |  |
| --- | --- | --- | --- |
| Table S3.1 Continued | | | |
| Response variables | Model | Model formula | family |
| SRE Bats | Full | s(Understory cover, k=3) + s(Moth abundance, k=3) + s(Moth richness, k=3) + s(Ground beetle abundance, k=3) + s(Ground beetle richness, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Standing dead trees, k=3) + s(ForMI, k=3) + s(Microhabitats, k=3) + s(Date, k=3) + Temperature +Elevation | neg. bin. |
| Selected | s(Understory cover, k = 3) + s(Moth abundance, k=3) + s(Moth richness, k = 3) + s(Standing dead trees, k=3) + s(DBH, k = 3) + Temperature | neg. bin. |
| MRE Bats | Full | s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Standing dead trees, k=3) + s(ForMI, k=3) + s(Microhabitats, k=3) + s(Date, k=3) + Temperature + Elevation | neg. bin. |
| Selected | s(Openness, k=3) + s(ForMI, k=3) + s(Tree richness, k=3) + s(Microhabitats, k = 3) + Elevation + Temperature | neg. bin. |
| P. pipistrellus | Full | s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + Standing dead trees + s(ForMI, k=3) + s(Microhabitats, k=3) + s(Date, k=3) + Temperature + Elevation | neg. bin. |
| Selected | s(Openness, k = 3) + s(DBH,k = 3) + s(ForMI, k = 3) + s(Coniferous share, k = 3) + s(Date, k = 3) + Temperature | neg. bin. |
| LRE Bats | Full | s(Moth abundance, k=3) + s(Moth richness, k=3) + s(Ground beetle abundance , k=3) + s(Ground beetle richness, k=3) + s(Tree richness, k=3) + s(Coniferous share, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + s(DBH, k=3) + s(Standing dead trees, k=3) + s(ForMI, k=3) + s(Microhabitats, k=3) + s(Date, k=3) + Temperature + Elevation, | neg. bin. |
| Selected | s(Ground beetle abundance, k=3) + s(Ground beetle richness, k=3) + s(Openness, k=3) + s(Height heterogeneity, k=3) + Temperature + s(Date, k=3) | neg. bin. |

### S3.2) Automatic variable selection results

Table S3.2 – Part I) *Results of the variable selection process. The numbers represent how many times each variable was selected into the top ranked models with a delta AICc <= 2. Each model was allowed to contain 6 variables only. When two or more variables were included the same number of times, the variable in the model with the lower AICc was chosen.*

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Total number of models with delta AICC** <= 2 | **Elevation** | **ForMI** | **Tree richness** | **Coniferous share** | **Openness** | **Height heterogeneity** | **DBH** | **Dead trees** | **Microhabitats** | **Date** | **Temperature** | **Understory cover** | **Understory richness** | **Moth abundance** | **Moth richness** | **Ground beetle abundance** | **Ground beetle richness** |
| **Understory cover** | **3** | **0** | **2** | **0** | **2** | **3** | **3** | **0** | **2** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** |
| **Understory richness** | **8** | **2** | **2** | **3** | **8** | **4** | **4** | **4** | **0** | **X** | **X** | **X** | **8** | **X** | **X** | **X** | **X** | **X** |
| **Moth abundance** | **4** | **2** | **0** | **0** | **0** | **0** | **1** | **0** | **3** | **X** | **3** | **4** | **4** | **4** | **X** | **X** | **X** | **X** |
| **Moth richness** | **9** | **4** | **1** | **5** | **9** | **0** | **3** | **2** | **1** | **X** | **9** | **0** | **0** | **0** | **9** | **X** | **X** | **X** |
| **Ground beetle abundance** | **4** | **3** | **4** | **0** | **4** | **0** | **0** | **1** | **0** | **X** | **1** | **X** | **0** | **1** | **X** | **X** | **X** | **X** |
| **Ground beetle richness** | **16** | **2** | **9** | **0** | **1** | **2** | **2** | **3** | **1** | **X** | **3** | **X** | **0** | **1** | **X** | **X** | **16** | **X** |
| **SRE** | **5** | **0** | **1** | **0** | **0** | **0** | **0** | **1** | **2** | **0** | **0** | **5** | **5** | **X** | **5** | **4** | **0** | **0** |
| **MRE** | **6** | **6** | **6** | **6** | **0** | **6** | **1** | **0** | **1** | **3** | **1** | **4** | **X** | **X** | **X** | **X** | **X** | **X** |
| **P. pipistrellus** | **15** | **1** | **9** | **3** | **4** | **12** | **0** | **15** | **0** | **4** | **15** | **8** | **X** | **X** | **X** | **X** | **X** | **X** |
| **LRE** | **1** | **0** | **0** | **0** | **0** | **1** | **1** | **0** | **0** | **0** | **1** | **1** | **X** | **X** | **X** | **X** | **1** | **1** |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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### S3.3) Results overview table

Table S3.3 – Part I*: Results of the generalised additive models (gams). Table contains results of the variable selected models (selected) and where gams where change based on the suggestions of the SEM modified gam results are reported in addition. For all variables the directionality of the effect is indicated with symbols: / and \ indicating positive or negative relationships* *(linear or asymptotic), ‘n’ unimodal and ‘u’ to inverse unimodal relationships and ‘\_‘ for relationships without direction, while ‘X’ means that the relationship was not considered. Significance effects with p < 0.05 are indicated with \*, n=64*

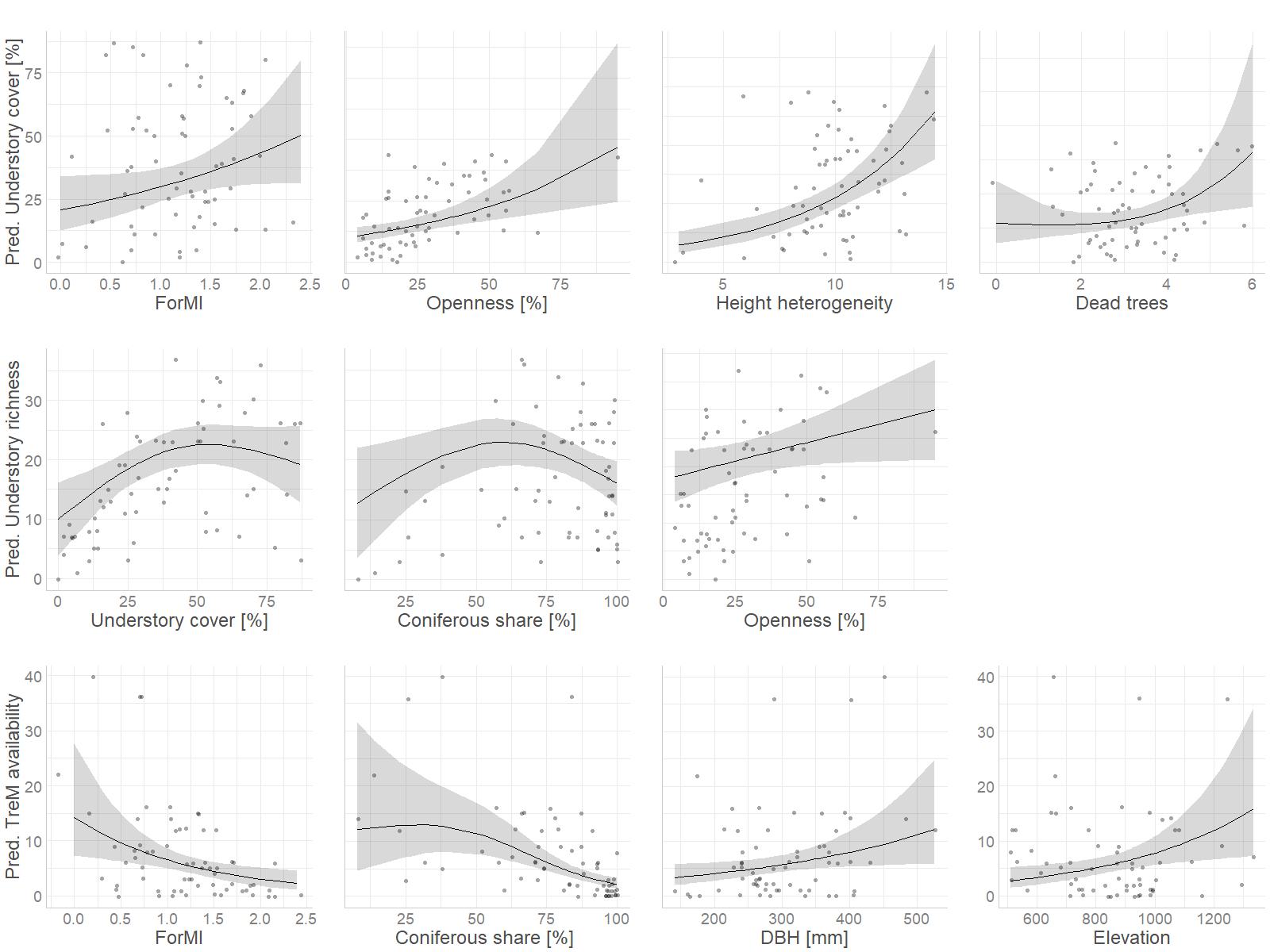
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model | **Elevation** | **ForMI** | **Tree richness** | **Coniferous share** | **Openness** | **Height heterogeneity** | **DBH** | **Dead trees** | **Microhabitats** | **Date** | **Temperature** | **Understory cover** | **Understory richness** | **Moth abundance** | **Moth richness** | **Ground beetle abundance** | **Ground beetle richness** | **MRE** | **Pipistrellus pipistrellus** | **Deviance explained** |
| **Understory cover** | selected |  | **/\*** |  | **/** | **/\*** | **/\*** |  | **/\*** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **0.50** |
| **Understory richness** | selected |  |  | **/** | **n\*** | **/\*** | **/** | **/** |  | **X** | **X** | **X** | **n\*** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **0.56** |
| **Moth abundance** | selected | **\** |  |  |  |  |  |  | **\\*** | **X** | **n\*** | **/\*** | **/\*** | **\\*** | **X** | **X** | **X** | **X** | **X** | **X** | **53.4** |
| modified | **\** |  |  |  |  |  |  | **\\*** |  | **n** | **/\*** | **\*/** | **\\*** |  |  |  |  | **\*\** | **\*\** | **61.3** |
| **Moth richness** | selected | **/** |  | **/\*** | **\\*** |  | **/** |  |  | **X** | **\\*** |  |  |  | **/\*** | **X** | **X** | **X** | **X** | **X** | **78.5** |
| **Ground beetle abundance** | selected | **/** | **/\*** |  | **n\*** |  |  | **/** |  | **X** | **/** | **X** |  | **n** | **X** | **X** | **X** | **X** | **X** | **X** | **39.8** |
| **Ground beetle richness** | selected |  | **n\*** |  |  | **-** | **-** | **/** |  | **X** | **-** | **X** |  |  | **X** | **X** | **/\*** | **X** | **X** | **X** | **60.5** |

Table S3.3 – Part II*:*

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Elevation** | **ForMI** | **Tree richness** | **Coniferous share** | **Openness** | **Height heterogeneity** | **DBH** | **Dead trees** | **Date** | **Temperature** | **Microhabitats** | **Understory cover** | **Understory richness** | **Moth abundance** | **Moth richness** | **Ground beetle abundance** | **Ground beetle richness** | **Deviance explained** |
| **Microhabitats** |  | **/\*** | **\\*** | **/** | **\\*** | **\** | **/** | **/\*** | **-** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **56.3** |
| **SRE** | selected |  |  |  |  |  |  | **/** | **\** |  | **\\*** |  | **\\*** | **X** | **/\*** | **\\*** |  |  | **34.1** |
| **MRE** | selected | **\\*** | **n\*** | **n\*** |  | **/\*** |  |  |  |  | **/** | **\** | **X** | **X** | **X** | **X** | **X** | **X** | **61.6** |
| **Pipistrellus pipistrellus** | selected |  | **n\*** |  |  | **/\*** |  | **/\*** |  | **u\*** | **/** | **/** | **X** | **X** | **X** | **X** | **X** | **X** | **41.9** |
| **LRE** | selected |  |  |  |  | **/\*** | **/\*** |  |  | **\\*** | **/\*** |  | **X** | **X** | **X** | **X** | **n\*** | **\\*** | **66.8** |

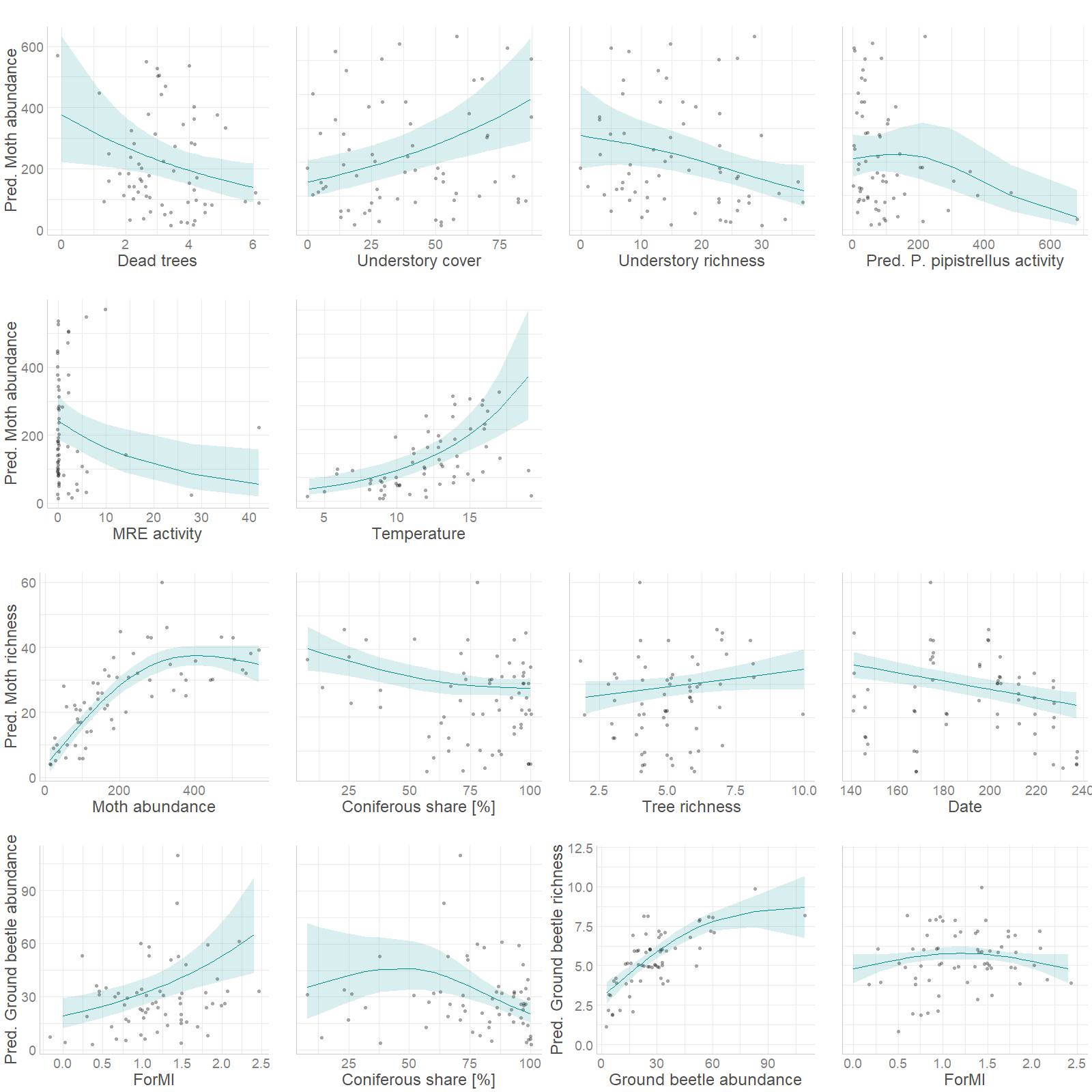
## S4) Visualization of the model responses

### S.4.1) Microhabitat and understory response graphs



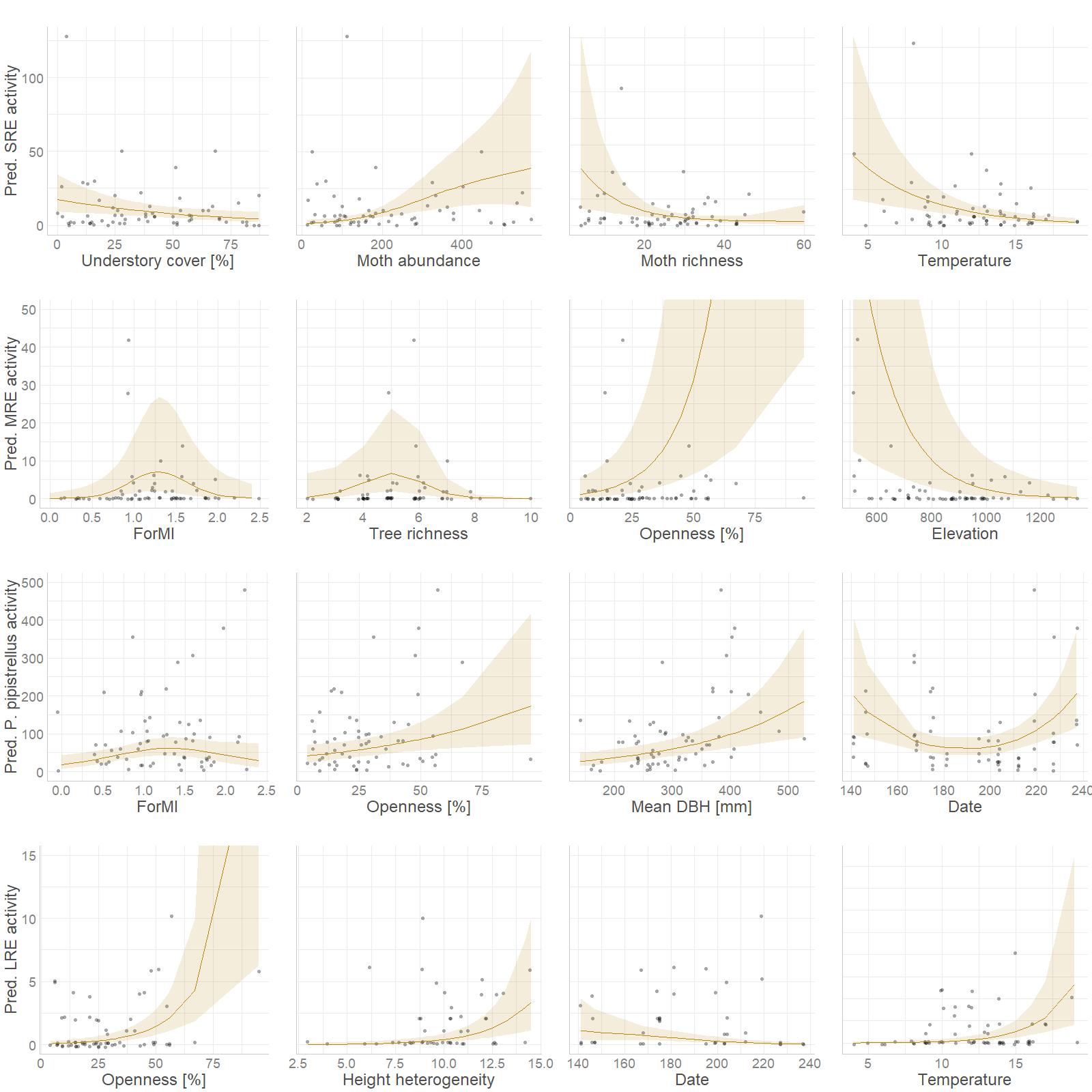
*Figure S4.1) All significant responses of microhabitats and understory characteristics*

### S4.2) Insect response graphs



*Figure S10. All significant responses of insect groups*

### S4.3) Bat activity response graphs



*Figure S11. Significant bat activity responses. Bat guild abbreviations: short- (SRE), mid- (MRE) and long-range- (LRE) echolocating bats. P. pipistrellus activities were evaluated separately from MRE activities.*