Supplementary material

Appendix S1: tree-related microhabitat occurrences

Table S1. Summary table of the occurrence (and % of occurrence) of each tree-related microhabitat surveyed at each tree.

Tree-related microhabitats	Fruit trees (N = 16)	Oak trees (N = 21)	Other trees (N = 20)	Total (N = 57)
Foliose and fruticose lichens	16 (100%)	21 (100%)	19 (95%)	56 (98%)
Bark loss	16 (100%)	21 (100%)	17 (85%)	54 (95%)
Bark shelter*	12 (75%)	15 (71%)	5 (25%)	32 (56%)
Crack and lightning scar*	7 (44%)	13 (62%)	5 (25%)	25 (44%)
Burr and decayed canker	7 (44%)	10 (48%)	6 (30%)	23 (40%)
Other cavity (rot hole and hollow branch) *	9 (56%)	8 (38%)	3 (15%)	20 (35%)
Witch boom and epicormic shoots	2 (13%)	10 (48%)	5 (25%)	17 (30%)
Dendrotelm (phytotelmata and water-filled hole)	7 (44%)	4 (19%)	6 (30%)	17 (30%)
Ivy and lianas	1 (6%)	3 (14%)	3 (15%)	7 (12%)
Bryophytes	1 (6%)	2 (10%)	2 (10%)	5 (9%)
Woodpecker breeding cavity*	1 (6%)	1 (5%)	0 (0%)	2 (4%)
Fungi (polypore and pulpy agaric)	0 (0%)	2 (10%)	0 (0%)	2 (4%)

* TreM-roost: TreM type that can be used as roosting sites.
Note: all TreM types were considered as TreM-prey (TreM that can enhance prey abundance).

Appendix S2: Bat echolocation call identification

We used BatScope 3.2 (Obrist & Boesch, 2018) for processing the bat calls. BatScope cuts recordings into single echolocation calls, extracts relevant numeric variables from call spectrograms measure, statistically classifies each call to genus and species, and assigns each recording to a species with an associated classification probability. While we did not use the species identification proposed by BatScope to avoid errors due to machine misclassification (Russo et al., 2018), instead we used this software to (i) detect recordings containing bat calls, (ii) automatically extract several call parameters (e.g. echolocation call peak frequency), and (iii) sort bat recordings thanks to a user-friendly interface. We then manually identified each bat pass contained in each recording to best taxonomic level possible following Obrist et al., (2004) and Barataud (2015). Thus, bat passes having ambiguous calls somewhat difficult to identify at species level were either assigned to species complex (e.g. *Pipistrellus nathusii/kuhlii*), genus (e.g. *Plecotus* spp.) or genus complex (e.g. nyctaloid group: *Eptesicus/Nyctalus/Vespertilio* spp.). For *Myotis* species, we could distinguish calls of *Myotis myotis* (i.e. species level) from small *Myotis* species (hereafter referred to as "*Myotis* spp."), *Myotis blythii* being absent in the study area.

References

Barataud, M. (2015) *Acoustic ecology of European bats, species identification, study of their habitat and foraging behavior*. Paris: Muséum national d'histoire naturelle; Biotope: Mèze.

Obrist, M.K., Boesch, R. & Flückiger, P.F. (2004) Variability in echolocation call design of 26 Swiss bat species: consequences, limits and options for automated field identification with a synergetic pattern recognition approach. *Mammalia,* **68,** 307-322.

Obrist, M.K. & Boesch, R. (2018) BatScope manages acoustic recordings, analyses calls, and classifies bat species automatically. *Canadian Journal of Zoology*, **96**, 939-954.

Russo, D, Ancillotto, L. & Jones, G. (2018). Bats are still not birds in the digital era: echolocation call variation and why it matters for bat species identification. *Canadian Journal of Zoology*, **96**, 63-78.

Appendix S3: land-use types

Table S3. Details on the reclassification of land use types from Tournant et al. (2013) used to compute at multiple spatial scales (i) a standard Shannon diversity index of habitats and (ii) an edge density index (i.e. total length of all edge segments between multiple habitat patches in the buffer divided by the buffer area); both in the surrounding landscapes around the 57 studied trees.

Original land cover classes (n=14)	Re-classification for the Shannon diversity index and edge density calculation (n = 10)
Old buildings (<1930)	
Recent buildings (>= 1930)	Built-up areas
Built-up areas	
Forest edges	Forest edges
Hedgerows and orchards	Hedgerows and orchards
Grasslands	Grasslands
Crop and bare lands	Crop and bare lands
Forests	Forests
Marshes and bogs	Marshes and bogs
Water bodies	Water bodies
Streams	Streams
Minor roads	
Major roads	Roads
Motorway bridges	

Appendix S4: landscape metrics

Table S4. Summary table of the landscape variables calculated at five spatial scales around the trees. The median and range (in brackets) are provided.

Landscape variables	Buffer size (radius)				
	100 m	250 m	500 m	1000 m	2000 m
% of forest	0.64 (0-31)	11.22 (0-59)	22.43 (0-76)	27.69 (0-80)	31.36 (4-53)
Edge density	121.79 (6-406)	140.67 (41-336)	159.39 (30-288)	148.24 (36-272)	145.30 (93-215)
SHDI	0.63 (0.02-1.42)	1.03 (0.29-1.46)	1.14 (0.25-1.47)	1.23 (0.45-1.54)	1.33 (0.95-1.50)

SHDI: Shannon's diversity index calculated across all the reclassified habitat types.

Appendix S5: reference list of R packages used

"glmmTMB" package: Brooks et al. (2017)

"landscapemetrics" package: Hesselbarth et al. (2019)

"MuMIn" package: Bartoń (2020)

'emmeans' package: Lenth (2020)

"spdep" package: Bivand (2020)

"DHARMa" package: Hartig (2017)

"performance" package: Lüdecke et al. (2021)

References

Bartoń, K. (2020) MuMIn: Multi-model inference. R package version 1.43.17. Available at https://cran.r-project.org/web/packages/MuMIn/index.html.

Bivand, R. (2020) spdep: Spatial Dependence: Weighting Schemes, Statistics. R package version 1.1-5. Available at https://cran.r-project.org/web/packages/spdep/index.html.

Brooks, M.E., Kristensen, K., van Benthem, K.J., Magnusson, A., Berg, C.W., Nielsen, A., Skaug, H.J., Machler, M. & Bolker, B.M. (2017) glmmTMB balances speed and flexibility among packages for zero-inflated generalized linear mixed modeling. *The R journal,* **9,** 378-400.

Hartig, F. (2017) DHARMa: residual diagnostics for hierarchical (multi-level/mixed) regression models. R package version 0.3.2.0. Available at https://cran.r-project.org/web/packages/DHARMa/index.html.

Hesselbarth, M.H., Sciaini, M., With, K.A., Wiegand, K. & Nowosad, J. (2019) landscapemetrics: an open-source R tool to calculate landscape metrics. *Ecography,* **42,** 1648-1657.

Lenth, R. (2020) emmeans: Estimated Marginal Means, aka Least-Squares Means. R package version 1.5.0. Available at https://cran.r-project.org/web/packages/emmeans/index.html.

Lüdecke, D., Ben-Shachar, M.S., Patil, I., Waggoner, P. & Makowski D. (2021). performance: An R package for assessment, comparison and testing of statistical models. *Journal of Open Source Software*, 6, 3139. Available at https://cran.r-project.org/web/packages/performance/index.html.

Appendix S6: statistical analysis – description of the multi-step approach

We performed a multi-step approach before building our final full models. A summary of this approach is presented in Figure S5.

Step 1- Given that our three variables depicting tree size were highly correlated (Spearman's correlation coefficient $|r| > 0.7$), we undertook a Principal Component Analysis (PCA) on log-transformed values of DBH, tree height, and tree crown area. The first PCA axis accounted for 82% of the variance and was retained to summarize information on tree size. High values of the PCA axis indicated tall trees with large DBH and crown area (Table S6).

Step 2- To reduce the number of landscape variables and avoid multicollinearity among predictors, we independently assessed the relationships between bat activity and each landscape variable measured at the five spatial scales. We fitted a series univariate GLMMs using the same distribution and random structure as previously described and selected the most relevant scales using the second order Akaike Information Criterion (*AICc*). For each pair of bat activity/landscape variable, we selected the best "scale of effect" (Martin, 2018) by choosing the scale in which the landscape variable led to the smallest *AICc*.

Step 3- As we were interested to unravel the effects of tree-related microhabitat diversity of isolated trees and their interactive effects with the landscape on bats, we built eight separate models to test each interaction between TreM diversity (either TreM-prey or TreM-roost) and the three landscape variables retained at the most relevant spatial scale (step 2), as well as with the distance between trees and the nearest woody habitat. To avoid model overfitting, we selected the most relevant interaction by following the same procedure as described in step 2.

Reference

Martin, A.E. (2018) The spatial scale of a species' response to the landscape context depends on which biological response you measure. *Current Landscape Ecology Reports,* **3,** 23-33.
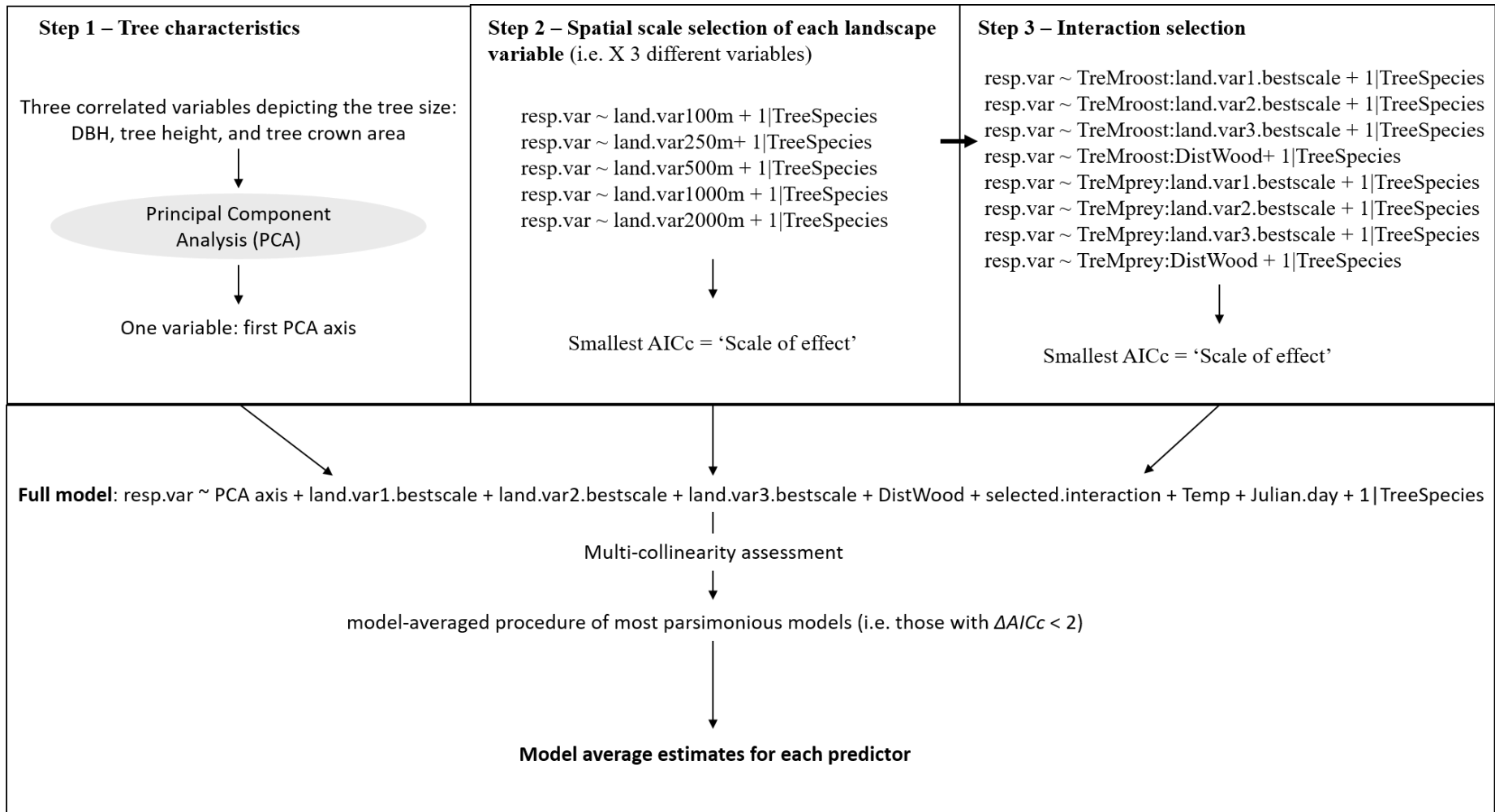
Figure S6. Schemes summarizing all the procedure of the statistical analysis following a multi-step approach and performed for each species and group of species activity.

Table S6. Results from (a) the Principal component analysis (PCA) of variables describing tree characteristics (only the first PC axis (PC1) was retained for inclusion in the models), and (b) the Spearman's correlation test between PC1 and variables describing tree characteristics (step 1).

(a)

Tree characteristics	PC1	PC2	PC3
Crown area	0.59	-0.19	0.79
Height	0.46	0.79	-0.24
DBH	0.58	-0.59	-0.57
Variation explained (%)	0.82	0.11	0.07
Eigenvalue	2.45	0.32	0.23

(b)

	PC1	DBH	Height	Crown area
PC1				
DBH	0.87			
Height	0.89	0.67		
Crown area	0.91	0.70	0.75	

Appendix S7: statistical analysis – model validation

Because sites were relatively close to each other (median = 1532 m, range 1050-2924), we assessed spatial autocorrelation of model residuals with Moran's I test. We only found significant spatial autocorrelation for the activity of species complex *Pipistrellus nathusii/kuhlii* (*p-value* = 0.002). In this case, we included an extra parameter in the best model known as the 'autocovariate'; this is a distance-weighted function of neighbouring response values to the model's explanatory variables, using the *autocov_dist* function ("spdep" package). By capturing the spatial autocorrelation, the Moran's I test was no longer significant. We then compared estimates between the best model and the autocovariate model (Table S6).

Overall model validation was then performed with the "DHARMa" package. Model overdispersion was checked with the "performance" package. When screening diagnostic plots for model validation, we detected one outlier in *Barbastella barbastellus* activity. We conducted dusk survey one month following the data collection and confirmed the presence of a roost (unpublished data). Thus, this site was disregarded when calculated *B. barbastellus* activity.

We finally examined the goodness-of-fit for each best model using the marginal R^2 (variance explained by the fixed effects) (Nakagawa & Schielzeth, 2013).

Reference

Nakagawa, S. & Schielzeth, H. (2013) A general and simple method for obtaining R2 from generalized linear mixed-effects models. *Methods in Ecology and Evolution,* **4,** 133-142.

Table S7. Results of the comparison between the best model and the autocovariate model for the activity of species complex *Pipistrellus nathusii/kuhlii.*

Variables	Best model			Autocovariate model		
	Estimates	SE	*P-value*	Estimates	SE	*P-value*
TreM_roost	0.208	0.190	0.274	0.193	0.192	0.306
SHDI100	0.358	0.183	0.051	0.365	0.184	0.047
SHDI100:TreM_Roost	0.659	0.209	0.002	0.670	0.211	0.001
AutocovDist	-	-	-	0.110	0.178	0.537
AICc		250.7			252.9	
I Moran test (*P-value*)		0.002			0.055	

Appendix S8: bat occurrence and activity data

Table S8. Summary table of occurrence and activity (number of bat passes per night) of each bat taxon recorded around trees.

Bat taxon	Fruit trees (N = 16)		Oak trees (N = 21)		Other trees (N = 20)		Total (N = 57)	
	Occ.	Act.	Occ.	Act.	Occ.	Act.	Occ.	Act.
*Barbastella barbastellus**	5	25	10	27	7	155	22	207
Eptesicus/Nyctalus/Vespertilio spp.*	15	186	21	176	18	110	54	472
Miniopterus schreibersii	4	5	6	12	6	8	16	25
*Myotis myotis**	10	44	9	28	10	17	29	89
Myotis spp.*	15	136	20	169	18	190	53	495
*Pipistrellus nathusii/kuhlii**	12	66	11	52	6	65	29	183
*Pipistrellus pipistrellus**	16	436	21	1219	20	650	57	2305
Plecotus spp.*	8	25	7	15	9	18	24	58
Rhinolophus ferrumequinum	2	2	0	0	0	0	2	2
*Rhinolophus hipposideros**	6	8	15	59	10	22	31	89

* taxon included in the statistical analyses.