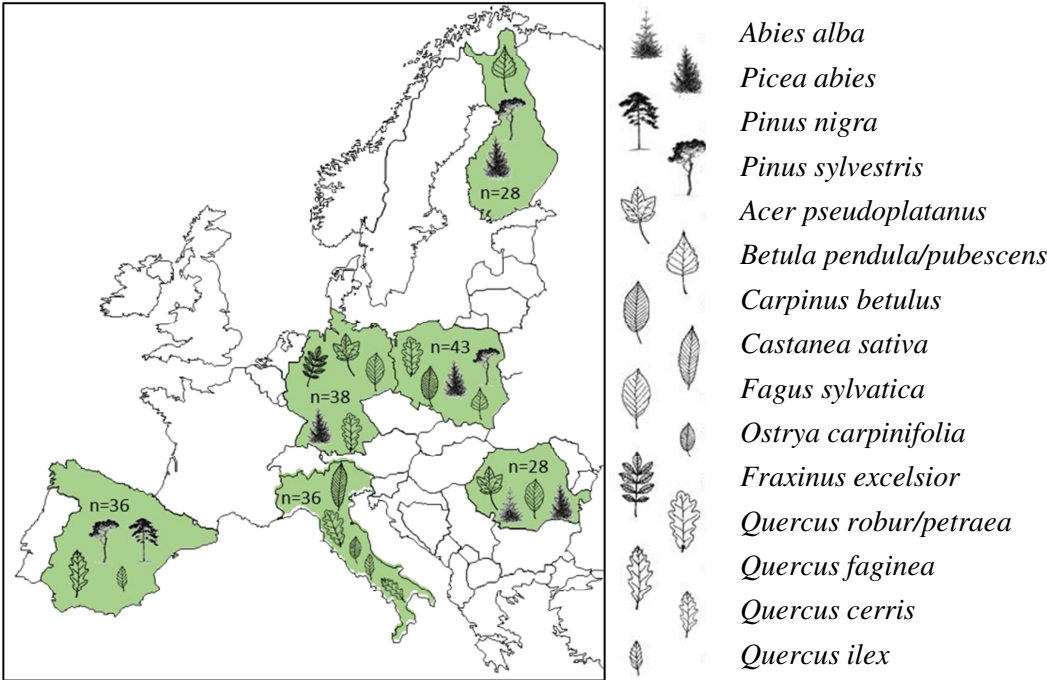Barbaro L, Allan E, Ampoorter E, Castagneyrol B, Charbonnier Y, De Wandeler H, Kerbiriou C., Milligan HT, Vialatte A, Carnol M, Deconchat M, De Smedt P, Jactel H, Koricheva J, Le Viol I, Muys B, Scherer-Lorenzen M, Verheyen K, van der Plas F. 2019 Biotic predictors complement models of bat and bird responses to climate and tree diversity in European forests. *Proc. R. Soc. B*

http://dx.doi.org/10.1098/rspb.2019.

Supplement S1. Location map of sampled forest plots of the FunDivEurope exploratory platform in Europe, spread across Spain, Italy, Romania, Germany, Poland and Finland (N = 209). The regional pool of tree species sampled and the number of plots per country are indicated.

Abies alba
Picea abies
Pinus nigra
Pinus sylvestris
Acer pseudoplatanus
Betula pendula/pubescens
Carpinus betulus
Castanea sativa
Fagus sylvatica
Ostrya carpinifolia
Fraxinus excelsior
Quercus robur/petraea
Quercus faginea
Quercus cerris
Quercus ilex

Supplement S2. Calculating species diversity rarefaction curves using Hill number

We performed rarefaction and extrapolation curves for bird species diversity, in order to insure that the observed patterns were not only due to the lower species pool with increasing latitude (Chao et al. 2014a) using R-package iNEXT (Hsieh et al. 2016). The Hill number of order 1 allows calculating the effective number of species and is equivalent to the exponential of Shannon entropy (Chao et al. 2014b, Morante-Filho et al. 2018). It is not sensible to changes in sample coverage since each species is weighted according to its abundance in the community, and can be seen as the number of common or typical species in a given community (Jost 2007). We found that there was overall a rather good estimation of species diversity and sample coverage (figures 1 and 2) except for bats in Finland where regional species pool fall to N = 3 species due to bioclimatic limitations (Charbonnier et al. 2016).
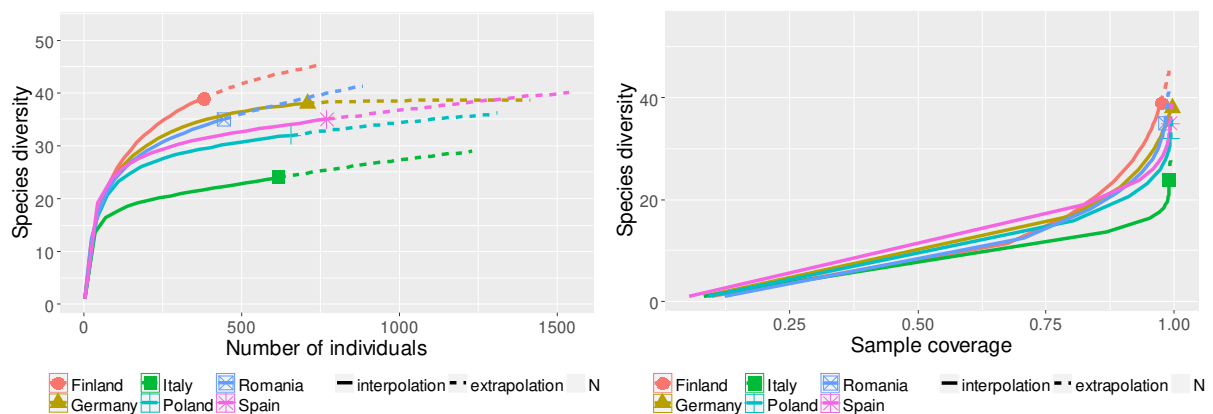

Fig. S2a Bird species diversity rarefaction and extrapolation curves using Hill number of order 1
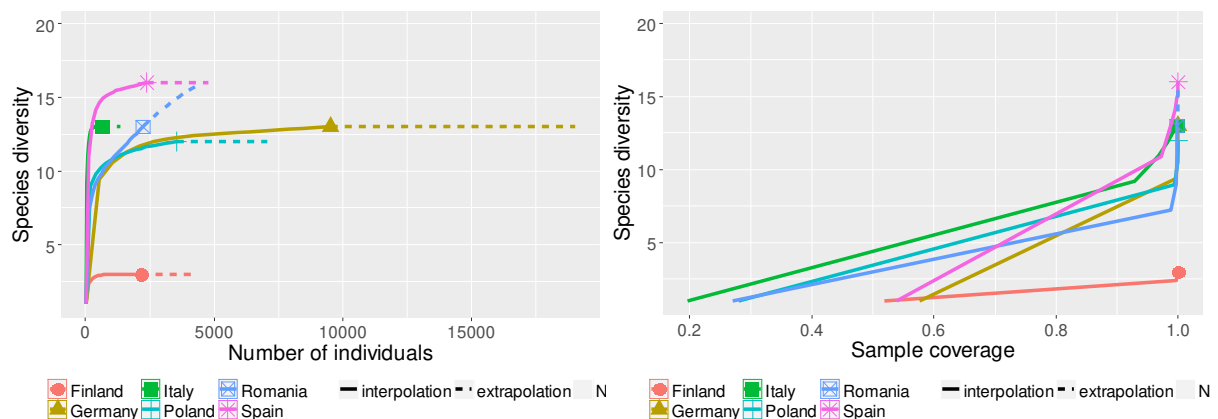

Fig. S2b Bat species diversity rarefaction and extrapolation curves using Hill number of order 1

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Supplement S3. Bat and bird species categorical traits

Species	forag	diet	nurse	migr	date	home
BARBAR	edge	spec	tree	resid	may	small
EPTNIL	open	interm	build	short	july	large
EPTSER	edge	gener	build	resid	july	large
HYPSAV	open	gener	cave	short	july	large
MINSCH	open	interm	cave	short	june	very large
MYOBEC	glean	interm	tree	resid	may	small
MYOBRA	edge	gener	tree	resid	june	small
MYODAU	open	gener	tree	resid	june	mid
MYOEMA	glean	spec	build	resid	july	small
MYOBLY	mixed	interm	build	resid	july	large
MYOMYO	mixed	interm	build	short	july	large
MYONAT	glean	gener	tree	resid	july	mid
MYOESC	glean	gener	tree	resid	july	mid
NYCLAS	open	gener	tree	long	june	very large
NYCLEI	open	gener	tree	long	june	large
NYCNOC	open	gener	tree	long	july	very large
PIPKUH	edge	gener	build	resid	may	mid
PIPNAT	edge	interm	tree	long	may	mid
PIPPIP	edge	gener	build	resid	june	mid
PIPPYG	edge	gener	build	short	june	mid
PLEAUR	glean	spec	tree	resid	july	small
PLEAUS	mixed	spec	build	resid	june	small
RHIEUR	mixed	spec	cave	resid	july	very large
RHIFER	mixed	interm	build	resid	july	very large
RHIHIP	mixed	gener	build	resid	july	mid
TADTEN	open	interm	cave	resid	july	small
VESMUR	open	interm	build	long	may	large

Table S3a. Bat categorical traits used for computing FDiv metrics (species codes use first three letters of genus and species scientific names). Trait codes and categories are listed in table S2b.

Trait	Category	Reference
Foraging methods (forag)	Gleaning	Dietz et al. (2009)
	Edge foragers	
	Open foragers	
Diet specialization (diet)	Generalist	Dietz et al. (2009)
	Intermediate	
	Specialist	
Nursery site (nurse)	Building	Dietz et al. (2009)
	Cave and rock	
	Tree	
Migration (migr)	Resident	Dietz et al. (2009)
	Short-distance migrant	
	Long-distance migrant	
Average birth date (date)	May	Dietz et al. (2009)
	June	
	July	
Home-range size (home)	Small <100 ha	Dietz et al. (2009)
	Mid 101-500 ha	
	Large 501-2000 ha	
	Very large >2000 ha	

Table S3b. Codes for categories of bat species categorical traits.

References

Dietz, C et al. 2009 Bats of Britain, Europe and Northwest Africa. A & C Black.

Species	forag	diet	nest	migr	date	home
AEGCAU	under	insect	shrub	resid	march	small
ALAARV	ground	mixed	ground	short	earlapr	small
ALERUF	ground	mixed	ground	resid	may	large
ANTTRI	ground	insect	ground	long	lateapr	mid
BONBON	ground	mixed	ground	resid	earlapr	large
CARCAR	under	seeds	shrub	short	lateapr	small
CARCHL	under	seeds	shrub	resid	earlapr	mid
CARSPI	canopy	seeds	tree	short	lateapr	mid
CERBRA	bark	insect	cavity	resid	earlapr	small
CERFAM	bark	insect	cavity	resid	lateapr	small
COCCOC	canopy	mixed	tree	short	lateapr	large
COLOEN	ground	seeds	cavity	short	lateapr	large
COLPAL	ground	seeds	tree	short	lateapr	large
CORONE	ground	mixed	tree	resid	earlapr	large
CORRAX	ground	mixed	tree	resid	march	large
CUCCAN	canopy	insect	ground	long	june	large
DENLEU	bark	insect	cavity	resid	lateapr	large
DENMAJ	bark	insect	cavity	resid	earlapr	large
DENMED	bark	insect	cavity	resid	lateapr	large
DRYMAR	bark	insect	cavity	resid	lateapr	large
EMBCIA	ground	mixed	ground	resid	lateapr	small
EMBCIR	ground	mixed	ground	resid	may	small
EMBCIT	ground	mixed	ground	resid	may	small
ERIRUB	under	mixed	ground	short	lateapr	mid
FICALB	canopy	insect	cavity	long	may	small
FICHYP	canopy	insect	cavity	long	may	small
FICPAR	canopy	insect	cavity	long	june	small
FRICOE	canopy	mixed	tree	short	earlapr	small
GALGAL	prober	mixed	ground	short	lateapr	large
GARGLA	under	mixed	tree	resid	earlapr	large
JYNTOR	prober	insect	cavity	long	earlapr	mid
LOXCUR	canopy	seeds	tree	short	march	large
LULARB	ground	insect	ground	resid	march	mid
LUSMEG	under	insect	ground	long	lateapr	mid
LYRTET	ground	mixed	ground	resid	june	large
MUSSTR	canopy	insect	cavity	long	june	small
ORIORI	canopy	insect	tree	long	june	large
PARATE	canopy	insect	cavity	short	may	small
PARCAE	canopy	insect	cavity	short	earlapr	small
PARCRI	canopy	mixed	cavity	resid	earlapr	mid
PARMAJ	canopy	insect	cavity	resid	earlapr	small
PARMON	canopy	mixed	cavity	resid	may	small
PARPAL	canopy	mixed	cavity	resid	may	small
PHOPHO	canopy	insect	cavity	long	may	mid
PHYBON	canopy	insect	ground	long	may	small
PHYCOL	canopy	insect	ground	short	lateapr	small
PHYDES	canopy	insect	ground	long	june	small
PHYLUS	canopy	insect	ground	long	june	small
PHYSIB	canopy	insect	ground	long	june	small
PICCAN	prober	insect	cavity	resid	june	large
PICVIR	prober	insect	cavity	resid	lateapr	large
PRUMOD	ground	insect	ground	short	lateapr	small
PYRPYR	under	seeds	tree	resid	may	mid
PYRRAX	prober	mixed	cavity	resid	lateapr	large
REGIGN	canopy	insect	tree	resid	may	small
REGREG	canopy	insect	tree	short	may	small
SERCIT	ground	seeds	tree	short	lateapr	mid
SERSER	ground	seeds	tree	short	may	small
SITEUR	bark	insect	cavity	resid	lateapr	mid
STUVUL	prober	mixed	cavity	short	earlapr	mid
SYLATR	under	mixed	shrub	short	lateapr	small
SYLBOR	under	mixed	shrub	long	june	small
SYLCAN	under	insect	shrub	long	may	small
SYLCUR	under	insect	shrub	long	june	small
TRINEB	prober	insect	ground	short	may	large
TRIOCH	prober	insect	tree	short	may	large
TROTRO	ground	insect	ground	resid	may	small
TURILI	prober	mixed	shrub	short	lateapr	mid
TURMER	prober	mixed	shrub	short	march	mid
TURPHI	prober	mixed	tree	short	march	mid
TURPIL	prober	mixed	tree	short	earlapr	mid
TURVIS	prober	mixed	tree	short	march	mid
UPUEPO	prober	insect	cavity	long	lateapr	large

Table S3c. Bird species categorical traits used for computing FDiv metrics (species codes use first three letters of genus and species scientific names). Trait codes and categories are listed in table S2d.

Trait	Category	Reference
Foraging methods (forag)	Ground prober	Barbaro and van Halder (2009)
	Ground gleaner	
	Understory gleaner	
	Canopy foliage gleaner or hawker	
	Bark forager	
Diet (diet)	Insectivore	Cramp et al. (1994)
	Mixed diet	
	Granivore	
Nest site location (nest)	Cavity	Cramp et al. (1994)
	Open, in tree	
	Open, in shrub	
	Open, on ground	
Migration (migr)	Resident	Cramp et al. (1994)
	Short-distance migrant	
	Long-distance migrant	
Average laying date (date)	March	Barbaro and van Halder (2009)
	Early April	
	Late April	
	Early May	
	Late May and June	
Home-range size (home)	< 1 ha	Barbaro and van Halder (2009)
	1-4 ha	
	> 4 ha	

Table S3d. Codes for categories of bird species categorical traits.

References

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Cramp, S. et al. 1994 Handbook of the birds of Europe, the Middle East and North Africa: the birds of the Western Palearctic. Oxford University Press.

Supplement S4. Species Thermal Indices for European bats

The distribution maps of European bats were obtained from the Atlas of European Mammals (Mitchell-Jones et al. 1999; accessed from the European Environment Agency at http://eunis.eea.europa.eu), using grid cells of 50 × 50 km. According to recent changes in the knowledge of bat distribution, including taxonomic changes (i.e., *Myotis* spp, *Eptesicus* spp, *Plecotus* spp), we updated these distribution maps using a set of recent publications (Evin et al. 2009, Garcia-Mudarra et al. 2009, Ibáñez et al. 2006, Juste et al. 2012, Puechmaille et al. 2012, Rebelo et al. 2010, Salicini et al. 2011, 2013, Santos et al. 2014).

Species	Number of cells	Thermal range	Thermal centroid
Barbastella barbastellus	588	14.88	9.07
Eptesicus nilssonii	665	13.31	4.34
*Eptesicus serotinus**	883	16.27	9.43
Hypsugo savii	244	15.82	11.76
Miniopterus schreibersii	442	13.23	12.30
Myotis bechsteinii	436	12.99	9.37
Myotis blythii	346	16.92	11.10
Myotis brandtii	464	10.88	6.67
Myotis daubentonii	1127	17.85	8.30
Myotis emarginatus	412	14.62	10.69
Myotis escalerai	78	8.80	13.40
Myotis myotis	873	16.66	10.01
*Myotis nattereri**	777	15.23	8.49
*Myotis (nattereri) sp A***	216	12.48	12.47
Nyctalus lasiopterus	61	9.95	12.30
Nyctalus leisleri	479	16.24	9.23
Nyctalus noctula	906	15.99	8.45
Pipistrellus kuhlii	394	16.57	12.28
Pipistrellus nathusii	585	15.36	8.65
Pipistrellus pipistrellus	1279	18.30	9.36
Pipistrellus pygmaeus	1740	18.69	9.75
Plecotus auritus	1119	15.54	8.08
Plecotus austriacus	679	15.84	10.00
Rhinolophus euryale	272	12.07	12.22
Rhinolophus ferrumequinum	698	16.96	11.24
Rhinolophus hipposideros	715	16.73	10.62
Tadarida teniotis	216	15.75	13.12
Vespertilio murinus	437	12.51	3.13

* sensu stricto ; **sensu Salicini et al. (2013)

Table S4. Bat Species Thermal Indices (STIs)

We further extracted the mean annual temperature from WorldClim (Hijmans *et al.,* 2005; http://www.worldclim.org) within a similar grid than the one used in the Atlas of European Mammals. The total cover of distribution maps for European bats varied between 61 cells for *Nyctalus lasiopterus* and 1740 cells for *Pipistrellus pygmaeus,* while bat thermal ranges ranged from 8.80 in *Myotis escalerai* to 18.69 in *Pipistrellus pygmaeus* (table S3).

References

Evin, A. et al. 2009 A new species for the French bat list: *Myotis escalerai* (Chiroptera: Vespertilionidae). Mammalia 73: 142–144.

García-Mudarra, JL. et al. 2009 The Straits of Gibraltar: barrier or bridge to Ibero-Moroccan bat diversity? Biological Journal of the Linnean Society 96: 434-450.

Hijmans, RJ et al. 2005 Very high resolution interpolated climate surfaces for global land areas. International Journal of Climatology 25: 1965–1978.

Ibáñez, C et al. 2006 The Iberian contribution to cryptic diversity in European bats. - Acta Chiropterologica 8: 277-297.

Juste, J et al. 2012 Phylogeny and systematics of Old World serotine bats (genus *Eptesicus*, Vespertilionidae, Chiroptera). Zoologica Scripta 42: 441–457.

Mitchell-Jones, AJ et al. 1999 The Atlas of European mammals. Poyser, London.

Puechmaille, SJ et al. 2012 Genetic analyses reveal further cryptic lineages within the *Myotis nattereri* species complex. Mammalian Biology 77: 224-228.

Salicini, I et al. 2011 Multilocus phylogeny and species delimitation within the Natterer's bat species complex in the Western Palearctic. Molecular Phylogenetics and Evolution 61: 888-898.

Salicini, I et al. 2013 Deep differentiation between and within Mediterranean glacial refugia in a flying mammal, the *Myotis nattereri* bat complex. Journal of Biogeography 40: 1182–1193.

Santos, H et al. 2014 Influences of ecology and biogeography on shaping the distributions of cryptic species: three bat tales in Iberia. Biological Journal of the Linnean Society of London 112: 150–162.

Supplement S5. Species Specialization Indices for European bats

Bat species specialization to habitat indices (SSI) were assessed using an independent dataset from the French National Bat Survey (http://vigienature.mnhn.fr/page/vigie-chiro)

French National Bat Survey

Volunteer-based standardized monitoring schemes have been widely implemented in Europe and North America (Jiguet et al. 2012, Barlow et al. 2015, Newson et al. 2015). In France, the National Museum of Natural History (MNHN) initiated the French National Bat Survey (BS) in 2006 (Azam et al. 2016). This scheme provides a dataset of 6774 sites distributed across the country with both habitat features and bat call identifications (28 species and 960 500 bat calls).

Sampling methods

The French National BS asks keen volunteers to count bats twice a year using point-counts or road surveys: once during the period 15th June to 31st July, and a second time between 15th August and 31st September. We used data from the road survey protocol to assess the species specialization index (SSI). The choice of the road survey is delegated to the volunteers for safety reasons. The circuit must be covered at night at low speed (recording at constant speed: 30 ± 5 km.h^{-1}), excluding non-paved roads, roads with a lot of traffic and high-speed roads. All roads selected must be of similar width, ca 10 m. Observers were asked to select a road circuit of at least 30 km and located in a 10 km radius around their home, and not overlapping itself. The second requirement was to design a circuit crossing, as much as possible, the different habitats occurring in the sampled area proportionally to their total area. To avoid biases in habitat sampling (i.e., sampling preferentially the most species-rich habitats), we validated each circuit and defined randomly a starting point on the circuit. Starting from this

point, the circuit was divided into ten 2-km road segments, separated by 1-km road segments in which no recording was performed. Such a sampling design allowed obtaining the best possible correlation between the proportion of each habitat sampled and the proportion of each habitat at the national scale ($R^2 = 0.94$), except for urban areas which were slightly overrepresented in the dataset.

Assessing bat habitat specialization

In the French National Bat Survey, volunteers were involved in collecting habitat variables on a detailed and adapted basis. Habitat features were recorded during the first visit to the circuit. The appropriate habitat codes were chosen from an established hierarchical system that allows describing more than 950 habitat types, as widely used in breeding bird surveys (see Crick 1992 for the UK, and Barnagaud et al. 2012, for the French breeding bird surveys). However, these codes were adapted to take into account bat foraging specifics and particularly the linear landscape elements where bats tend to forage preferentially (for more details about the French National Bat Survey, see http://vigienature.mnhn.fr/page/releves-d-habitats). Habitat classes were collected within a radius of 100m around the sampled points and grouped into 18 classes in order to obtain a sufficient number of samples per habitat class (for more methodological informations, see Julliard et al. 2006, Devictor et al. 2008, Kerbiriou et al. 2010).

Bat species specialization index (SSI)

We quantified bat species specialization index (SSI, table S5) as the level of habitat specialization for a given bat species, as the coefficient of variation (SD/mean) of its densities across habitats following Julliard et al. (2006). SSI is thus independent from species habitat preferences. However, we also assessed bat species specialization to forest habitats only, by

calculating a ratio of the mean density of a given species in forest habitats only on the mean density in non-forest habitats.

Bat species	Habitat Specialization Index	Specialization to forest
Tadarida teniotis	1.941	0.007
Barbastella barbastellus	1.438	0.309
Eptesicus serotinus	1.499	0.586
Myotis daubentonii	2.023	0.053
Myotis spp.	1.739	0.156
Nyctalus leisleri	1.166	0.442
Nyctalus noctula	1.723	0.137
Hypsugo_savi	1.794	0.011
Pipistrellus kuhlii	0.697	0.164
Pipistrellus nathusii	1.676	0.011
Pipistrellus pipistrellus	0.702	0.179
Pipistrellus pygmaeus	2.247	0.072
Plecotus spp.	1.717	0.527
Nyctalus lasiopterus	2.517	0.893

Table S5. Bat Species Specialization Indices (SSIs)

References

Azam, C et al. 2016 Disentangling the relative effect of light pollution, impervious surfaces and intensive agriculture on bat activity with a national-scale monitoring program. Landscape Ecology 31: 2471–2483.

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Jiguet, F et al. 2012 French citizens monitoring ordinary birds provide tools for conservation and ecological sciences. Acta Oecologica 44: 58–66.

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Kerbiriou, C et al. 2010 Long term trends monitoring of bats, from biodiversity indicator production to species specialization assessment. Society for Conservation Biology, 24th Annual Meeting, 3 - 7 July, 2010, Edmonton, Alberta, Canada.

Newson, SE et al. 2015 A novel citizen science approach for large-scale standardised monitoring of bat activity and distribution, evaluated in eastern England. Biological Conservation 191: 38–49.

Rebelo, H et al. 2010 Predicted impact of climate change on European bats in relation to their biogeographic patterns. Global Change Biology 16: 561–576.

Supplement S6. Null models for functional diversity metrics

We used a null model approach to correct functional diversity metrics for species richness levels and disentangle the drivers of trait diversity from those of taxonomic diversity (Calba et al. 2014, Pellissier et al. 2018). We recalculated 1000 times FD metrics for simulated communities with randomized trait values that were equally species-rich as the observed communities to calculate the standardized deviation of FD (FD_{dev}) values as follows:

$$FD_{dev} = \frac{FD_{obs} - \overline{FD_{exp}}}{sd(FD_{exp})} \;,$$

where FD_{obs} is the observed FD value, $\overline{FD_{exp}}$ is the average of the 1000 randomized (i.e., expected) FD values and $sd(FD_{exp})$ is the standard deviation of the 1000 randomized (i.e., expected) FD values.

We found that observed values and simulated values for FD metrics were overall highly correlated, with R = 0.77 for bird functional richness (FRic); R = 0.81 for bird functional evenness (FEve) and R = 0.77 for bat functional evenness; R = 0.78 for bird functional entropy (Rao's Q) and R = 0.71 for bat functional entropy; R = 0.96 for bird mean body mass and R = 0.80 for bat mean body mass. Only simulated bat functional richness was less correlated to observed values, with R = 0.50.

After analyzing FD_{dev} using the same modelling procedure than for observed FD values (see table S6), we found consistencies in model selection with the same predictors being significant for bird functional entropy (mean precipitation and ungulate browsing), bat functional evenness (insect herbivory), bird mean body mass (mean temperature, mean precipitation and spider abundance) and bat mean body mass (deciduous tree cover, earthworm abundance and ungulate browsing).

On the other hand, we found discrepancies in predictor selection for bird and bat functional richness, bird functional evenness and bat functional entropy. However, as functional richness depends on taxonomic diversity (Laliberté & Legendre 2010), it is not surprising that the pure effect of trait diversity is no more consistent when considered independently from taxonomic

species richness. Moreover, for bat functional richness, the correlation between observed and simulated values was low. Finally, the two poorly-performing models (bird FEve and batRao) were not including biotic predictors in initial models fitted for observed values, but respectively climatic and habitat variables, while in the simulated values, the predictors were instead habitat-related for bird FEve (deciduous tree cover) and biotic-related for bat Rao's Q (earthworm abundance, see table S6).

	Significant predictors in best models for observed *FD* values	Model performance and significant predictors for FD_{dev}		
Birds		estimates	R^{2}m	*P*
FRic	+ Temp + Insect + Spider	ns	-	-	-
FEve	- Prec	- Decid	-0.158	0.026	0.05
Rao	**- Prec** + Spider **+ Brows**	**- Prec**	- 0.289	0.183	0.001
		- Insect	- 0.140		0.004
		+ Brows	0.089		0.05
CWM mass	**+ Temp - Prec + Spider**	**+ Temp**	0.126	0.115	0.05
		- Prec	-0.128		0.02
		- Treerao	-0.061		0.05
		+ Spider	0.066		0.05
Bats				
FRic	- Stratif	- Earth	-0.258	0.097	0.005
FEve	+ Undric **+ Insect**	**+ Insect**	0.304	0.069	0.006
Rao	- Stratif	- Earth	-0.241	0.083	0.004
CWM mass	**- Decid + Brows - Earth**	**- Decid**	-0.113	0.142	0.01
		+ Brows	0.075		0.05
		- Earth	-0.122		0.05

Table S6. Comparison between significant predictors for observed and expected FD_{dev} values based on 1000 random permutations of the data trait table. The similar predictors in both models are indicated in bold.

References

Calba, S, Maris, V, Devictor, V. 2014 Measuring and explaining large-scale distribution of functional and phylogenetic diversity in birds: separating ecological drivers from methodological choices. Global Ecology and Biogeography, 23, 669–678.

Laliberté, E, Legendre P. 2010 A distance-based framework for measuring functional diversity from multiple traits. Ecology 91:299-305.

Pellissier, V, Barnagaud, JY, Kissling, WD, Şekercioglu, C, Svenning, JC. 2018 Niche packing and expansion account for species richness-productivity relationships in global bird assemblages. Global Ecology and Biogeography 27: 604–615.

Supplement S7. Sampling habitat and biotic predictors

(a) Vegetation sampling

Understorey vegetation was sampled between May and August 2012 in all forest plots. The percentage cover of all vascular plant species < 1.3 m in height was recorded in three 5×5 m subplots. The cover data for individual plant species were summed per subplot and averaged over the three subplots as a proxy for plot-level understorey abundance. The corresponding understorey species richness was used as a measure of plot-level understorey diversity. Forest overstorey composition was estimated as relative proportions of coniferous and deciduous trees, and we computed a Shannon index of vertical stratification based on averaged percentage cover of each stratum of vegetation, i.e., trees, shrubs, understorey and bare soil. We calculated an index of tree functional diversity for each plot, using a set of 9 tree functional traits: tree life span, tree height, leaf type (deciduous/evergreen) and specific leaf area (SLA), obtained from the LEDA trait base, and seed mass, root depth and foliar %N, %C and Ca contents measured from fresh leaves collected in the six regions during the study. For this, we calculated Rao's functional entropy as an abundance-weighted measure of tree functional diversity (total basal area per species was used as the measure of tree abundance) using the 'FD' R-package.

(b) Defoliating insect sampling

Defoliating insect activity was estimated by sampling leaf herbivory (leaf area loss or shoot mortality) on six individual trees per species in monocultures and three individual trees per species in mixed plots in spring and summer 2012 (Italy, Germany and Finland) and 2013 (Spain, Romania and Poland). Insect herbivory was estimated using the mean percentage crown damage over all trees for a given plot. To confirm that crown defoliation was owing to insect damage, herbivory was assessed on a leaf sample collected on each studied tree.

(c) Spider sampling

Spider abundance was sampled by foliage-beating method in spring and summer 2012 (Italy, Germany and Finland) and 2013 (Spain, Romania and Poland). In each forest plot, we selected four 'beating units' (i.e., a sapling or a low branch of adult tree) per target tree species in mixed plots and six units in monocultures. Each unit was beaten for spiders to fall on a 1×1 m screen located below the sampled foliage until no more new spiders were detected. All spider individuals collected were stored in 70% alcohol before being aged and identified. We used the total abundance of all adult and juvenile individuals per forest plot, since both life stages can be consumed by birds and bats.

(d) Earthworm sampling

Earthworms are both prey items for ground probing forest birds and contributing to overall biotic activity in forest soils by improving soil structure. Earthworm abundance was sampled in a central 10×10 m subplot in each forest plot in spring 2012 in Italy, Germany and Finland, and in autumn 2012 in Poland, Romania and Spain. We hand sorted litter over an area of 25×25 cm for epigeic earthworm species and removed litter over a larger area of 100×50 cm with mustard extraction of the soil for anecic species. We then hand sorted a soil sample of 25×25 cm and 20 cm depth from the middle of the 100×50 cm area for endogeic species. All earthworm individuals were summed per unit area and sampling method to determine total earthworm abundance at the plot level.

(e) Ungulate browsing

We measured browsing intensity by large mammal herbivores as a key non-trophic interaction affecting understorey structure and composition for forest birds and bats. Browsing intensity was estimated on understorey vegetation between 0.2 m and 3.0 m height, where ungulates

tend to browse predominantly and have the highest impact. It was assessed within four 5×5 m subplots established within each forest plot, where all woody species individuals were visually inspected for browsing damage. We estimated the percentage of biomass removed wherever evidence of browsing was found, and browsing intensity per plot was calculated as the mean biomass removed per plant individual, averaged over the four subplots.