

Supplementary materials

Vlaschenko et al. Bat assemblages are shaped by land cover types and forest age: a case study from Eastern Ukraine

Table S1 Classification of bats from *Vespertilionidae* family inhabiting Kharkiv region into different ecological groups, migratory status, and summer roost-sites selection (by Vlaschenko et al. 2021 Vlaschenko 2006; Strelkov and Il'in 1990 Russo et al. 2016; Dietz and Kiefer 2014; Boie and Dietz 2005).

Bat species	Migratory status	Roost-sites selection in breeding period	Ecological group
<i>M. daubentonii</i>	resident	tree cavities	water-associated
<i>M. dasycneme</i>	resident	roost in buildings	water-associated
<i>M. brandtii</i>	resident	tree cavities	forest-dwelling specialists
<i>M. nattereri</i>	resident	tree cavities	forest-dwelling specialists
<i>N. leisleri</i>	long-distance migrant	tree cavities	forest-dwelling specialists
<i>N. lasiopterus</i>	long-distance migrant	tree cavities	forest-dwelling specialists
<i>N. noctula</i>	partial migrant	tree cavities	forest-dwelling specialists
<i>E. serotinus</i>	resident	roost in buildings	urban- and rural-dwellers
<i>P. pygmaeus</i>	long-distance migrant	roosting both in trees and houses	generalists
<i>P. nathusii</i>	long-distance migrant	roosting both in trees and houses	generalists
<i>P. kuhlii</i>	resident	roost in buildings	urban- and rural-dwellers
<i>V. murinus</i>	long-distance migrant	roosting both in trees and houses	generalists
<i>Pl. austriacus</i>	resident	roost in buildings	urban- and rural-dwellers
<i>Pl. auritus</i>	resident	tree cavities	forest-dwelling specialists

Table S2. Results of the rarefaction analysis for all studied plots. s.e. - standard error, LCL - lower confidence limit, UCL - upper confidence limit.

Plot	Indices	Observed	Estimator	s.e.	LCL	UCL
Koziyivka	Species richness	3.000	3.000	0.479	3.000	4.488
	Shannon	2.139	2.200	0.201	2.139	2.593
	Simpson	1.968	2.019	0.185	1.968	2.382
Karavan	Species richness	8.000	8.000	0.251	8.000	8.560
	Shannon	2.919	2.963	0.232	2.919	3.417
	Simpson	1.906	1.914	0.133	1.906	2.174
Liptsy	Species richness	6.000	6.000	0.528	6.000	7.561
	Shannon	3.144	3.194	0.201	3.144	3.587
	Simpson	2.424	2.445	0.195	2.424	2.826
Neskuchne	Species richness	6.000	6.990	2.201	6.072	19.549
	Shannon	1.954	2.018	0.200	1.954	2.411
	Simpson	1.409	1.415	0.127	1.409	1.664
Starytsia	Species richness	6.000	6.991	1.856	6.089	16.981
	Shannon	1.717	1.772	0.208	1.717	2.181
	Simpson	1.302	1.306	0.086	1.302	1.474
Tetleha	Species richness	8.000	8.000	0.503	8.000	9.445
	Shannon	2.199	2.223	0.161	2.199	2.539
	Simpson	1.473	1.476	0.077	1.473	1.626
Pechenihy	Species richness	7.000	7.000	0.053	7.000	7.107

	Shannon	3.575	3.606	0.187	3.575	3.972
	Simpson	2.730	2.744	0.136	2.730	3.010
Pechenichy2	Species richness	9.000	9.499	1.321	9.030	17.428
	Shannon	4.991	5.035	0.195	4.991	5.418
	Simpson	3.832	3.853	0.201	3.832	4.247
Mokhnach	Species richness	8.000	8.000	0.544	8.000	9.589
	Shannon	4.932	5.029	0.279	4.932	5.577
	Simpson	4.004	4.070	0.306	4.004	4.670
Homilsha	Species richness	10.000	11.996	3.735	10.180	32.091
	Shannon	2.711	2.741	0.142	2.711	3.019
	Simpson	1.816	1.818	0.087	1.816	1.990
Yaremivka	Species richness	10.000	10.499	1.321	10.030	18.431
	Shannon	3.395	3.421	0.156	3.395	3.726
	Simpson	2.378	2.383	0.099	2.378	2.576

Table S3a. Effect of habitat variables on species richness. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
field	3.600	1	0.057
forest	3.159	1	0.075
lake	4.079	1	0.043
meadow	2.662	1	0.102
floodplain	1.668	1	0.196

Species richness Poisson vs habitats

formula: N_species ~ lake + meadow + field + forest + floodplain + (1 | Plot_Acr/Site)

Estimation of lambda by Laplace ML approximation (p_v).

Estimation of fixed effects by Laplace ML approximation (p_v).

family: poisson(link = log)

----- Fixed effects (beta) -----

	Estimate	Cond. SE	t-value
(Intercept)	-1.25032	1.19425	-1.047
lake	0.03433	0.01784	1.925
meadow	0.02960	0.01768	1.674
field	0.03397	0.01650	2.058
forest	0.02744	0.01548	1.773
floodplain	0.02852	0.02286	1.248

----- Random effects -----

Family: gaussian(link = identity)

--- Variance parameters ('lambda'):

lambda = var(u) for u ~ Gaussian;

Site:Plot. : 0.04785

Plot_Acr : 0.2165

--- Coefficients for log(lambda):

Group	Term	Estimate	Cond.SE
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Site:Plot.	(Intercept)	-3.04	0.4402
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Plot_Acr	(Intercept)	-1.53	0.473
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of obs: 101; # of groups: Site:Plot., 100; Plot_Acr, 11

----- Likelihood values -----
logLik
p_v(h) (marginal L): -202.5633
lambda leverages numerically 1 were replaced by 1- 1e-08 (as controlled by option
'regul_lev_lambda')

Table S3b. Effect of forest age variables on species richness. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
decid 11-40	2.227	1	0.135
decid 41-90	1.344	1	0.246
decid 91-150	0.122	1	0.726
decid >150	0.184	1	0.667
clearcut	0.095	1	0.757

Species richness Poisson vs forest age

formula: N_species ~ decid_11_40 + decid_41_90 + decid_91_150 + decid_more150 +
clearcut + (1 | Plot_Acr/Site)

Estimation of lambda by Laplace ML approximation (p_v).

Estimation of fixed effects by Laplace ML approximation (p_v).

family: poisson(link = log)

----- Fixed effects (beta) -----

	Estimate	Cond. SE	t-value
(Intercept)	0.8859226	0.233255	3.7981
decid_11_40	-0.0733676	0.031647	-2.3183
decid_41_90	0.0068897	0.006022	1.1442
decid_91_150	-0.0002255	0.004085	-0.0552
decid_more150	0.0066694	0.010257	0.6503
clearcut	-0.0110411	0.018483	-0.5974

----- Random effects -----

Family: gaussian(link = identity)

--- Variance parameters ('lambda'):

lambda = var(u) for u ~ Gaussian;

Site:Plot. : 0.06115

Plot_Acr : 0.08359

--- Coefficients for log(lambda):

Group	Term	Estimate	Cond.SE
Site:Plot.	(Intercept)	-2.794	0.392
Plot_Acr	(Intercept)	-2.482	0.5342

of obs: 101; # of groups: Site:Plot., 100; Plot_Acr, 11

----- Likelihood values -----

logLik

p_v(h) (marginal L): -200.6567

Table S4a. Effect of habitat variables on the number of individuals. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
field	4.044	1	0.044
forest	3.388	1	0.065
lake	4.728	1	0.029
meadow	2.895	1	0.088
floodplain	1.001	1	0.317

Number of individuals vs habitats, negative binomial
summary(fit_b_h_glm_nb)

formula: Number_of_individuals ~ lake + meadow + field + forest + floodplain +
(1 | Plot_Acr/Site)

Estimation of fixed effects by ML.

Estimation of NB_shape by 'outer' ML, maximizing p_v.

family: Neg.binomial(shape=0.4799)(link = log)

----- Fixed effects (beta) -----

	Estimate	Cond. SE	t-value
(Intercept)	0.80986	1.82329	0.4442
lake	0.05565	0.03254	1.7099
meadow	0.03539	0.02742	1.2905
field	0.02754	0.02474	1.1130
forest	0.02984	0.02381	1.2534
floodplain	-0.02064	0.03755	-0.5497

----- Likelihood values -----

logLik

p(h) (Likelihood): -400.2157

Table S4b. Effect of forest age variables on the number of individuals. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
decid 11-40	1.201	1	0.273
decid 41-90	0.127	1	0.721
decid 91-150	0.082	1	0.774
decid >150	0.377	1	0.538
clear-cut	1.403	1	0.997

```
#####Number of individuals vs forest age, negative binomial
summary(fit_b_h_glm_nb_forest_short)
formula: Number_of_individuals ~ decid_11_40 + decid_41_90 + decid_91_150 +
  decid_more150 + clearcut + (1 | Plot_Acr/Site)
Estimation of fixed effects by Laplace ML approximation (p_v).
Estimation of lambda and NB_shape by 'outer' ML, maximizing p_v.
family: Neg.binomial(shape=0.5225)( link = log )
----- Fixed effects (beta) -----
              Estimate      Cond. SE      t-value
(Intercept)    3.003998    0.448161    6.7029
decid_11_40   -0.102665    0.047807   -2.1475
decid_41_90    0.001619    0.011999    0.1349
decid_91_150   0.003598    0.008232    0.4371
decid_more150  0.013242    0.019117    0.6927
clearcut       -0.023975    0.033477   -0.7161
----- Random effects -----
Family: gaussian( link = identity )
--- Variance parameters ('lambda'):
lambda = var(u) for u ~ Gaussian;
Site:Plot. : 3.468e-05
Plot_Acr : 0.1297
# of obs: 101; # of groups: Site:Plot., 100; Plot_Acr, 11
----- Likelihood values -----
              logLik
p_v(h) (marginal L): -398.4236
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Table S5a Land cover types RDA ANOVA summary model table.

Permutation test for rda under reduced model

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ field + forest + floodplain + lake + meadow, data = data)

	Df	Variance	F	Pr(>F)
Model	5	0.04390	1.7722	0.015 *
Residual	96	0.47562		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova.cca(rda_hab_net, by = 'axis', step = 1000, model = 'reduced') ## nothing but first is marginal (p = 0.128, F = 2.72)

Permutation test for rda under reduced model

Forward tests for axes

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ field + forest + floodplain + lake + meadow, data = data)

	Df	Variance	F	Pr(>F)
RDA1	1	0.01693	3.4177	0.210
RDA2	1	0.01333	2.6907	0.272
RDA3	1	0.01001	2.0198	0.385
RDA4	1	0.00272	0.5487	0.958
RDA5	1	0.00091	0.1843	0.987
Residual	96	0.47562		

> anova.cca(rda_hab_net, by = 'terms', step = 1000, model = 'reduced') ## clearcut signif (0.026), lake signif (0.047) and meadow signif (0.04)

Permutation test for rda under reduced model

Terms added sequentially (first to last)

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ field + forest + floodplain + lake + meadow, data = data)

	Df	Variance	F	Pr(>F)
field	1	0.00568	1.1474	0.325
forest	1	0.01145	2.3101	0.048 *
floodplain	1	0.00700	1.4128	0.201
lake	1	0.01056	2.1306	0.049 *
meadow	1	0.00922	1.8602	0.106
Residual	96	0.47562		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>

Table S5b Forest age RDA ANOVA summary model table

Permutation test for rda under reduced model

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ decid_11_40 + decid_41_90 + decid_91_150 + decid_more150 + clearcut, data = data)

	Df	Variance	F	Pr(>F)
Model	5	0.05985	2.5001	0.001 ***
Residual	96	0.45966		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova.cca(rda_for_net, by = 'axis', step = 1000) ## first RDA is signif, p = 0.004, second RDA marginal (p = 0.08)

Permutation test for rda under reduced model

Forward tests for axes

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ decid_11_40 + decid_41_90 + decid_91_150 + decid_more150 + clearcut, data = data)

	Df	Variance	F	Pr(>F)
RDA1	1	0.03721	7.7718	0.001 ***
RDA2	1	0.01619	3.3809	0.109
RDA3	1	0.00334	0.6983	0.985
RDA4	1	0.00258	0.5397	0.968
RDA5	1	0.00053	0.1098	0.998
Residual	96	0.45966		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova.cca(rda_for_net, by = 'terms', step = 1000) ## decid_10 (p=0.002) and decid150 is signif. (p=0.004)

Permutation test for rda under reduced model

Terms added sequentially (first to last)

Permutation: free

Number of permutations: 999

Model: rda(formula = hel_com_net ~ decid_11_40 + decid_41_90 + decid_91_150 + decid_more150 + clearcut, data = data)

	Df	Variance	F	Pr(>F)
decid_11_40	1	0.03487	7.2820	0.001 ***
decid_41_90	1	0.00289	0.6032	0.720
decid_91_150	1	0.00218	0.4549	0.827
decid_more150	1	0.01549	3.2343	0.010 **

clearcut 1 0.00443 0.9260 0.472
 Residual 96 0.45966

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table S6 Breeding status for each bat species within the study plots (two species from urban- and rural-dwelling group are not included) B - breeding, NB - not breeding, mostly males

Plot	Bat species									
	MDA	MBR	MDS	NNO	NLE	NLA	PNA	PPY	VMU	PAU
KOZ	B				NB					B
KAR	B			B	B	B	B	B		B
LIP	B			B			B	B	B	
NES	B			B	B		B		B	NB
STR	B			B	B		NB	B		B
TET	B	NB		B	B		B	B		B
PEC	B		B	B	B		B	B		B
PEC2	B		B	B	B		B	B	B	B
MOK	B	B		B	B		B	B		B
HOM	B	B	B	B	B		B	B		B
YAR	B	B	NB	B	B		B	B	B	B

Table S7 The variability of b/h_s index by all studied plots.

Bat	Location (n - number of nights when each species was caught)										
	KOZ	TET	PEC	MOK	NES	HOM	YAR	LIP	PEC2	KAR	STR
MDA	n=4 median=0.36 mean=0.5 min=0.14 max=1.14	n=4 median=0.36 mean=0.42 min=0.13 max=0.83	n=6 median=0.32 mean=0.43 min=0.14 max=0.86	n=1 0.129	n=2 median=0.34 mean=0.34 min=0.14 max=0.55	n=9 median=0.27 mean=0.79 min=0.13 max=2.48	n=13 median=0.54 mean=1.24 min=0.14 max=7.56	n=2 median=0.21 mean=0.21 min=0.14 max=0.28	n=7 median=1.43 mean=1.51 min=0.14 max=3.14	n=3 median=0.14 mean=0.23 min=0.14 max=0.43	n=1 0.28
NNO	un	n=6 median=6.15 mean=6.88 min=0.8 max=14.4	n=7 median=4.29 mean=4.63 min=0.27 max=9.68	n=6 median=0.27 mean=0.63 min=0.13 0.2.14	n=4 median=2.84 mean=2.97 min=0.29 max=5.93	n=12 median=2.86 mean=4.13 min=0.14 max=16.71	n=12 median=3.43 mean=6.37 min=0.13 max=26.67	n=6 median=1.78 mean=2.36 min=1.0 max=5.43	n=8 median=3.71 mean=4.0 min=0.43 max=9.71	n=5 median=3.57 mean=4.8 min=2.57 max=11.57	n=7 median=0.71 mean=1.4 min=0.14 max=5.57
NLE	n=1 0.14	n=4 median=0.43 mean=0.53 min=0.27 max=1.0	n=3 median=0.21 mean=0.31 min=0.14 max=0.57	n=6 median=0.27 mean=0.53 min=0.13 max=1.71	n=3 median=0.14 mean=0.18 min=0.14 max=0.26	n=6 median=0.2 mean=0.25 min=0.14 max=0.53	n=3 median=0.18 mean=0.18 min=0.14 max=0.22	un	n=3 median=2.0 mean=2.24 min=0.86 max=3.85	n=6 median=0.57 mean=0.69 min=0.14 max=1.43	n=3 median=0.43 mean=0.38 min=0.14 max=0.57
PNA	un	n=4 median=0.28 mean=0.28 min=0.13 max=0.41	n=7 median=3.16 mean=3.26 min=0.53 max=6.0	n=5 median=0.13 mean=0.35 min=0.13 max=0.83	n=3 median=0.28 mean=0.27 min=0.13 max=0.41	n=11 median=0.28 mean=0.29 min=0.13 max=0.71	n=11 median=0.47 mean=1.19 min=0.14 max=3.17	n=6 median=0.64 mean=0.88 min=0.14 max=2.14	n=7 median=1.57 mean=1.92 min=0.14 max=6.14	n=2 median=0.28 mean=0.28 min=0.14 max=0.43	n=1 0.14
PPY	un	n=3 median=0.14 mean=0.18 min=0.13 max=0.29	n=6 median=0.34 mean=0.65 min=0.14 max=2.0	n=4 median=0.41 mean=1.55 min=0.13 max=5.24	un	n=7 median=0.40 mean=1.03 min=1.33 max=3.57	n=9 median=1.04 mean=1.50 min=0.14 max=4.66	n=4 median=0.43 mean=0.71 min=0.14 max=1.86	n=5 median=0.57 mean=0.83 min=0.14 max=2.14	n=3 median=0.14 mean=0.28 min=0.14 max=0.57	n=1 0.14
PAU	n=5 median=0.61 mean=0.72 min=0.29	n=5 median=0.28 mean=0.37 min=0.13	n=2 median=1.70 mean=1.70 min=0.14	n=4 median=0.14 mean=0.14 min=0.13	n=1 0.125	n=2 median=0.21 mean=0.21 min=0.14	n=3 median=0.15 mean=0.32 min=0.13	un	n=3 median=0.14 mean=0.28 min=0.14	n=3 median=0.14 mean=0.28 min=0.14	n=1 0.14

	max=1.44	max=1.0	max=3.25	max=0.17		max=0.28	max=0.69		max=0.57	max=0.57	
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Table S8a. Effect of habitat variables on breeding activity. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
Species	149.681	24	0.001
field	36.294	5	0.001
forest	31.653	5	0.001
lake	25.431	5	0.001
meadow	12.451	5	0.029
floodplain	11.733	5	0.038

Breeding activity vs habitats interaction with Species:

formula: SR ~ Species * (Field + forest + lake + meadow + floodplain) +

(1 | Location/Net_name)

Estimation of lambda by Laplace ML approximation (p_v).

Estimation of fixed effects by Laplace ML approximation (p_v).

family: binomial(link = logit)

----- Fixed effects (beta) -----

	Estimate	Cond. SE	t-value
(Intercept)	1.287e+00	0.339494	3.790895
SpeciesNLE	7.758e-02	1.398826	0.055461
SpeciesPNA	6.261e-01	0.571832	1.094902
SpeciesMDA	-2.570e+00	1.229186	-2.090616
SpeciesPAU	-1.175e+00	1.633014	-0.719560
Field	2.590e-03	0.001337	1.937039
forest	1.004e-03	0.000656	1.530234
lake	4.932e-03	0.002869	1.718915
meadow	5.123e-03	0.001833	2.795125
floodplain	1.769e-02	0.008175	2.164259
SpeciesNLE:Field	-1.351e-03	0.005215	-0.258979
SpeciesPNA:Field	-9.393e-03	0.002601	-3.611357
SpeciesMDA:Field	-4.845e-03	0.002981	-1.625228
SpeciesPAU:Field	-8.952e-03	0.003393	-2.638379
SpeciesNLE:forest	1.487e-03	0.002286	0.650364
SpeciesPNA:forest	-2.390e-03	0.001227	-1.947794
SpeciesMDA:forest	6.988e-03	0.002793	2.501909
SpeciesPAU:forest	2.597e-03	0.003063	0.847889
SpeciesNLE:lake	3.232e-02	0.047148	0.685430
SpeciesPNA:lake	7.780e-03	0.005250	1.481825
SpeciesMDA:lake	-1.807e-02	0.007204	-2.508924
SpeciesPAU:lake	-1.358e-03	0.010490	-0.129498
SpeciesNLE:meadow	-1.244e-02	0.006739	-1.846627
SpeciesPNA:meadow	3.551e-05	0.004057	0.008752
SpeciesMDA:meadow	-4.034e-03	0.003826	-1.054230
SpeciesPAU:meadow	-2.058e-04	0.006920	-0.029740
SpeciesNLE:floodplain	-2.476e-02	0.020556	-1.204759
SpeciesPNA:floodplain	-6.004e-02	0.034994	-1.715597
SpeciesMDA:floodplain	-2.858e-02	0.026668	-1.071717
SpeciesPAU:floodplain	-4.154e-02	0.023611	-1.759491

----- Random effects -----

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Family: gaussian( link = identity )
      --- Variance parameters ('lambda'):
lambda = var(u) for u ~ Gaussian;
Net_name:. : 0.1426
Location : 2.114e-09
      --- Coefficients for log(lambda):
      Group      Term Estimate Cond.SE
Net_name:. (Intercept) -1.948 0.3279
Location (Intercept) -19.97 1237
# of obs: 2836; # of groups: Net_name:., 76; Location, 11
----- Likelihood values -----
                        logLik
p_v(h) (marginal L): -858.7869

```

Table S8b. Effect of forest age variables on breeding activity. Significance of the fixed effects obtained by LRT.

Variable	chi2_LR	df	LTR p-value
Species	117.703	24	<0.001
decid_11-40	23.707	5	<0.001
decid_41-90	20.149	5	0.001
decid_91-150	21.625	5	<0.001
decid_>150	15.550	5	0.008
clearcut	15.930	5	0.007

#####Breeding activity vs forest age, binomial

formula: SR ~ Species * (decid_11.40 + decid_41.90 + decid_91_150 + decid_more150 + clearcut) + (1 | Location/Net_name)

Estimation of lambda by Laplace ML approximation (p_v).

Estimation of fixed effects by Laplace ML approximation (p_v).

family: binomial(link = logit)

----- Fixed effects (beta) -----

	Estimate	Cond. SE	t-value
(Intercept)	1.511e+00	0.4311978	3.50308
SpeciesNLE	-1.885e+00	1.9279032	-0.97752
SpeciesPNA	3.532e-01	0.6419112	0.55030
SpeciesMDA	-2.519e+00	1.4978143	-1.68207
SpeciesPAU	-1.192e+01	6.6026501	-1.80508
decid_11.40	1.444e-01	0.0559350	2.58094
decid_41.90	9.248e-03	0.0035210	2.62665
decid_91_150	-3.031e-04	0.0007713	-0.39292
decid_more150	-2.648e-02	0.0079057	-3.34994
clearcut	2.068e-02	0.0095306	2.17031
SpeciesNLE:decid_11.40	-2.092e-01	0.0768621	-2.72163
SpeciesPNA:decid_11.40	-2.747e-01	0.1554920	-1.76684
SpeciesMDA:decid_11.40	-1.787e-01	0.0714751	-2.49956
SpeciesPAU:decid_11.40	-1.947e-01	0.0739543	-2.63278
SpeciesNLE:decid_41.90	3.220e-03	0.0124879	0.25784
SpeciesPNA:decid_41.90	-1.604e-02	0.0060803	-2.63765
SpeciesMDA:decid_41.90	1.293e-03	0.0134806	0.09591
SpeciesPAU:decid_41.90	5.963e-02	0.0359083	1.66057
SpeciesNLE:decid_91_150	7.138e-03	0.0029758	2.39881
SpeciesPNA:decid_91_150	4.054e-03	0.0022377	1.81160
SpeciesMDA:decid_91_150	2.407e-03	0.0013275	1.81319
SpeciesPAU:decid_91_150	2.160e-02	0.0152397	1.41765
SpeciesNLE:decid_more150	1.790e-02	0.0156707	1.14252
SpeciesPNA:decid_more150	4.798e-02	0.0168684	2.84454
SpeciesMDA:decid_more150	4.538e-02	0.0335517	1.35244
SpeciesPAU:decid_more150	-3.801e-02	0.0386631	-0.98300
SpeciesNLE:clearcut	-2.332e-02	0.0327672	-0.71165
SpeciesPNA:clearcut	-4.684e-02	0.0182225	-2.57055
SpeciesMDA:clearcut	3.033e-03	0.0267464	0.11341
SpeciesPAU:clearcut	-3.292e-02	0.0425194	-0.77413


```

----- Random effects -----
Family: gaussian( link = identity )
    --- Variance parameters ('lambda'):
lambda = var(u) for u ~ Gaussian;
    Net_name:. : 0.2008
    Location : 1.745e-07
    --- Coefficients for log(lambda):
    Group      Term Estimate Cond.SE
Net_name:. (Intercept) -1.605 0.2989
    Location (Intercept) -15.56 225.5
# of obs: 2836; # of groups: Net_name:., 76; Location, 11
----- Likelihood values -----
                        logLik
p_v(h) (marginal L): -859.6061

```

Captions for Supplementary Figures

Figure S1. Detailed map of habitat composition of study plots.

Figure S2a. Habitat correlation before merging.

Figure S2b. Habitat correlation after merging several habitats.

Figure S3. Results of Redundancy Analysis revealing the relationship between the areas of different land cover types and assemblage structure at the plot level. **a)** Overlay of samples (at each mist-netting site) and species shown by grey arrows and orange 3-letter bat species abbreviations. **b)** Overlay of species shown with gray arrows and land cover types shown in green-blue: forest, lake, meadow, field and floodplain.

Figure S4a. Visualisation of GLMM results of revealing the relationship between the land cover types and number of individuals at the mist-netting site level.

Figure S4b. Visualisation of GLMM results of revealing the relationship between the forest age structure and number of individuals at the mist-netting site level.

Figure S5a. Sex ratio of *P. nathusii* (*PNA*) calculated using the total sample of all adult individuals and for each of 4 plots with more than 10 individuals.

Figure S5b. Sex ratio of *N. noctula* (*NNO*) calculated using the total sample of all adult individuals and for each of 9 plots with more than 10 individuals.

Figure S5c. Sex ratio of *M. daubentonii* (*MDA*) calculated using the total sample of all adult individuals and for each of 3 plots with more than 10 individuals.

Figure S6a-c Roosting tree of numerous colony of *P. pygmaeus* and *P. nathusii*.