Electronic supplement material: Appendix

My niche: within-species individual spatial niche specialisation affects within and between species interactions

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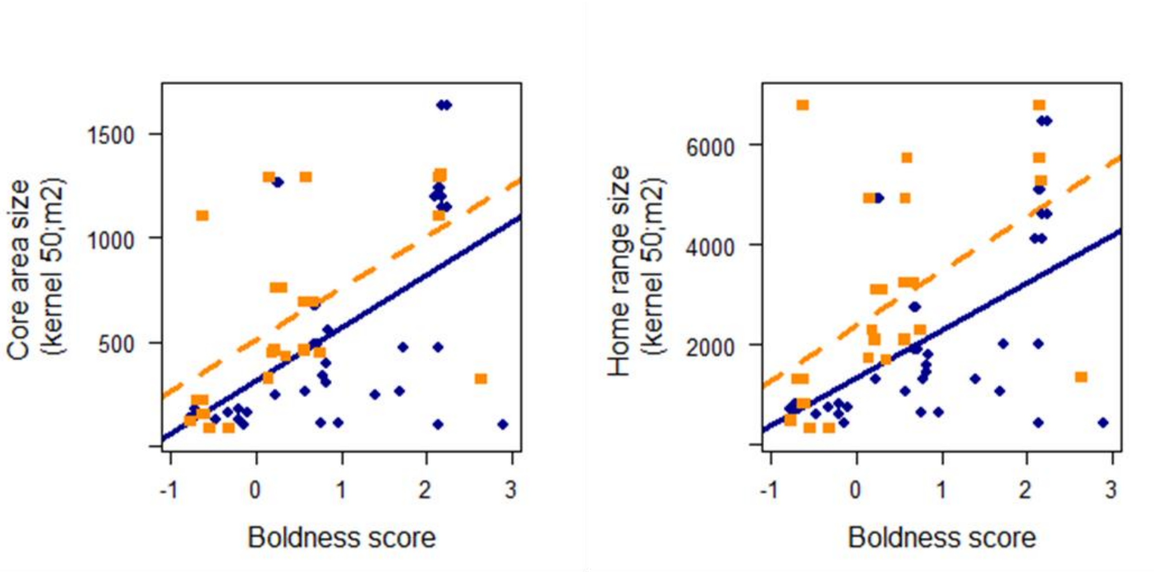
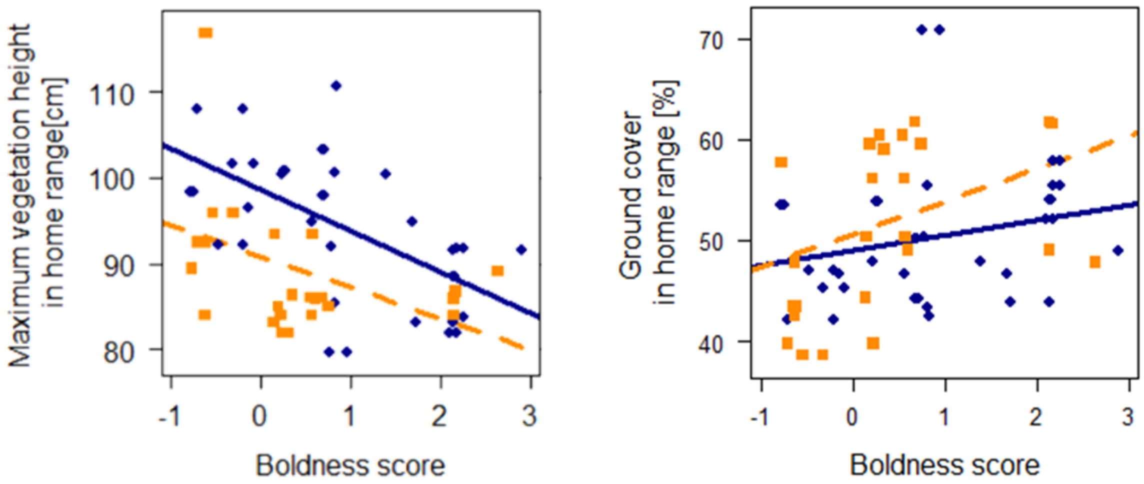
Table A1: Overview of the number of captured and recaptured individuals from the two study species (*M. glareolus*, *A. agrarius*) on each study site.

Grid	Captured individuals	Recaptured individuals
G2	54	48
G3	83	80
G4	44	29
G5	40	29
G6	49	41
Total	270	227



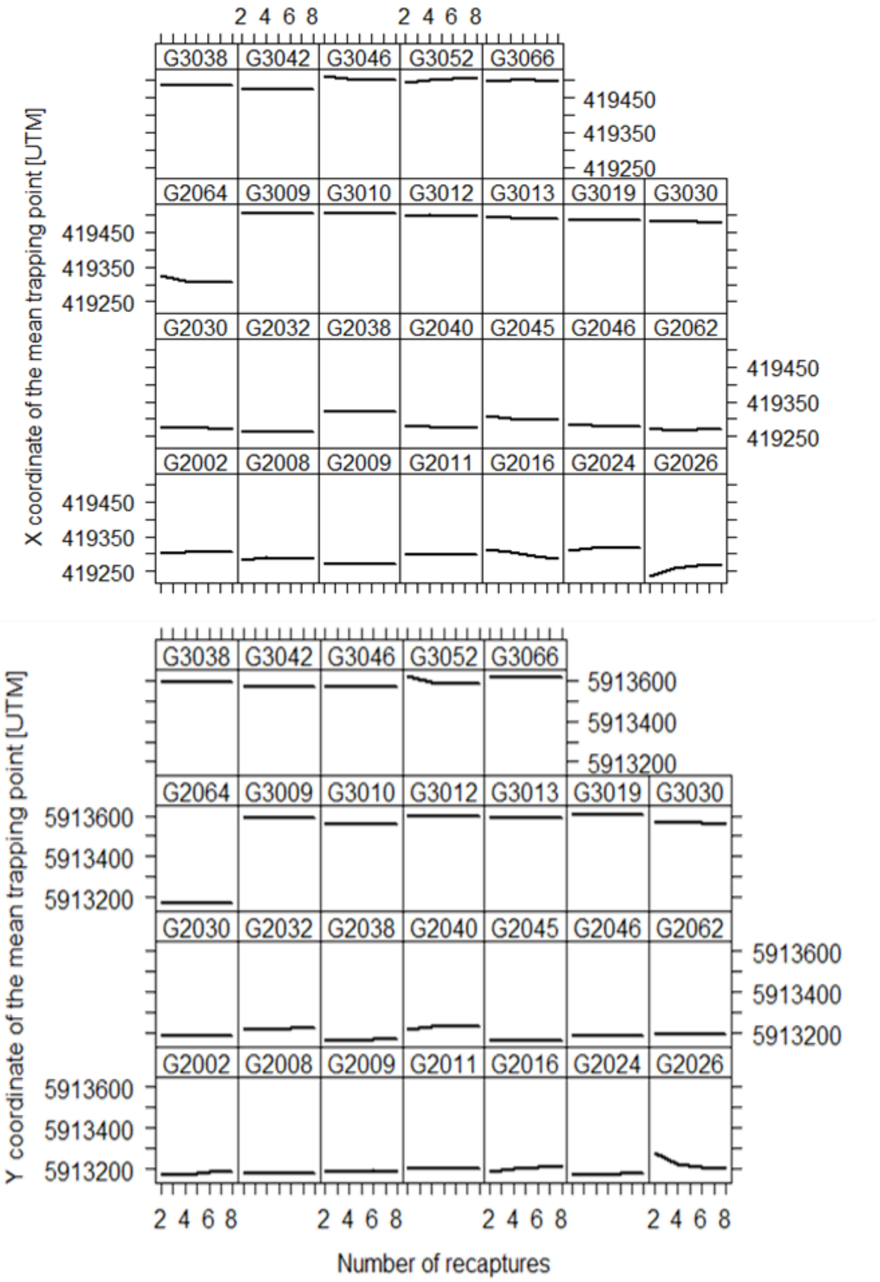
Variable	Correlation coefficient	Co-variance	CI low	CI high
Core area size (kernel 50)	**0. 49**	**0.58**	**0.299**	**0.801**
Home range size (kernel 95)	**0. 47**	**0.60**	**0.278**	**0.816**

Figure A1 Covariance of boldness and home range and core area size respectively for *M. glareolus* (n = 21, blue solid line and dots) and *A. agrarius* (n = 15, orange dashed line and squares) tracked via automated VHF telemetry. Home ranges are based on 95 % of location points, core areas on 50 % of location points. Represented are covariance values and credibility intervals, as well as correlation coefficients to represent the strength of association between variables. Intervals different from zero represent significant covariances and are marked in bold.



Variable	Correlation coefficient	Co-variance	CI low	CI high
Maximum vegetation height in home range	**-0.40**	**-0.57**	**-0.787**	**-0.211**
Ground cover in home range	**0.32**	**0.18**	**0.025**	**0.751**

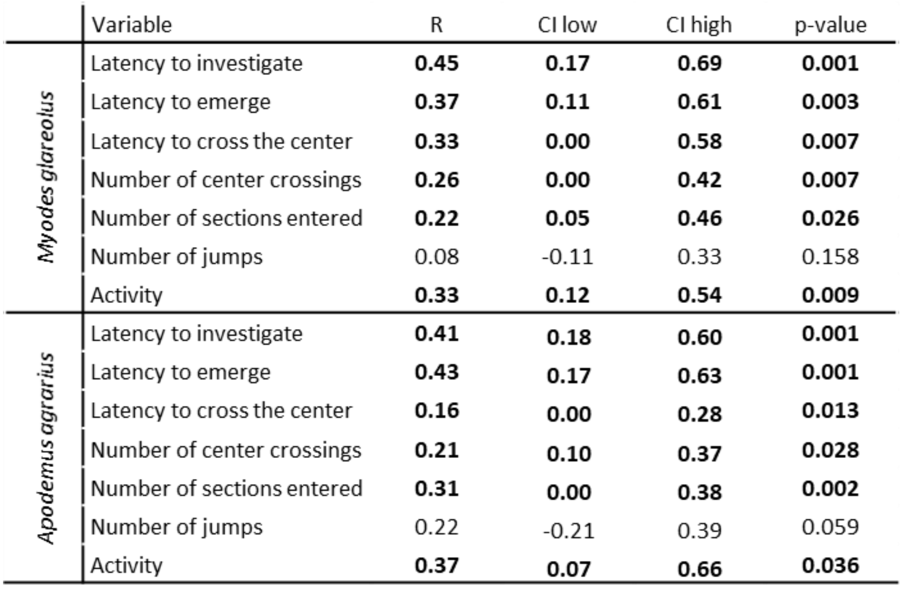
Figure A2 Covariance between boldness and microhabitat structure in home ranges of bank voles (*M. glareolus,* solid line and circles) and striped field mice (*A. agrarius,* dashed line and squares). We measured the maximum vegetation height (in cm) and estimated the percentage of ground cover (10 cm above ground) based on photographs in one square meter surrounding each trap location. Using QGIS we interpolated maximum vegetation height and percentage of ground cover on the basis of an inverse weighing of the distance between points to assess habitat characteristics for the whole area of the trapping grid. Subsequently, we extracted maximum vegetation height and vegetation cover from these GIS models for each simulated location point within individual home ranges and core areas (for more details see Schirmer et al. 2019). Represented are covariance values and credibility intervals, as well as correlation coefficients to represent the strength of association between variables. Intervals different from zero represent significant covariances and are marked in bold.



Variable	Factor	χ^2	Df	p-value
X coordinate of mean trapping point	No.Recaptures	1.50	1	0.220
Y coordinate of mean trapping point	No.Recaptures	0.52	1	0.473

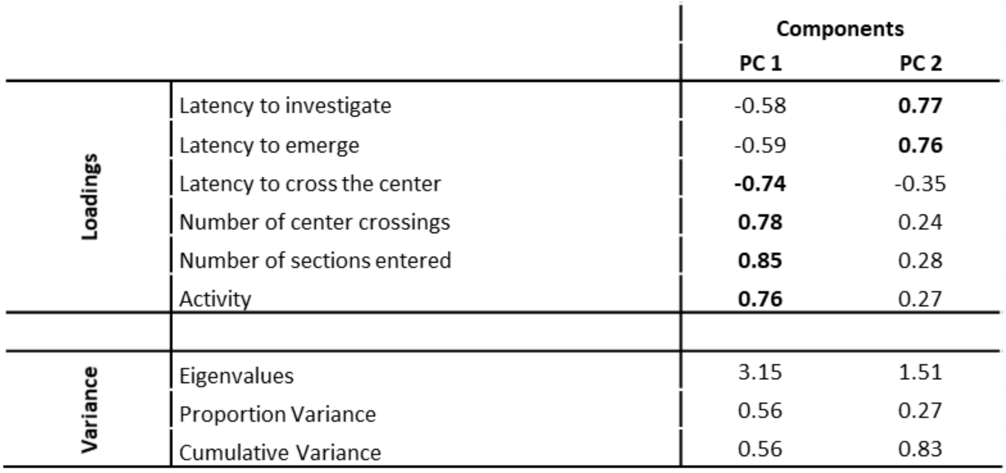
Figure A3 | X and Y coordinates of mean trapping points in dependence of the number of recaptures for a subset of individuals (n = 26) which were trapped 8 times. Neither coordinate was significantly dependent on the number of recaptures of individuals based on calculated generalised linear mixed-effects models.

Table A2 Repeatability of behavioural variables quantified in a combined open-field and dark-light test for *M. glareolus* (n = 62) and *A. agrarius* (n = 44). R stands for the repeatability coefficient, CI_low represents the lower 95% confidence interval, CI_high the upper 95% confidence interval and SE the standard error. Repeatabilities different from zero are indicated in bold.



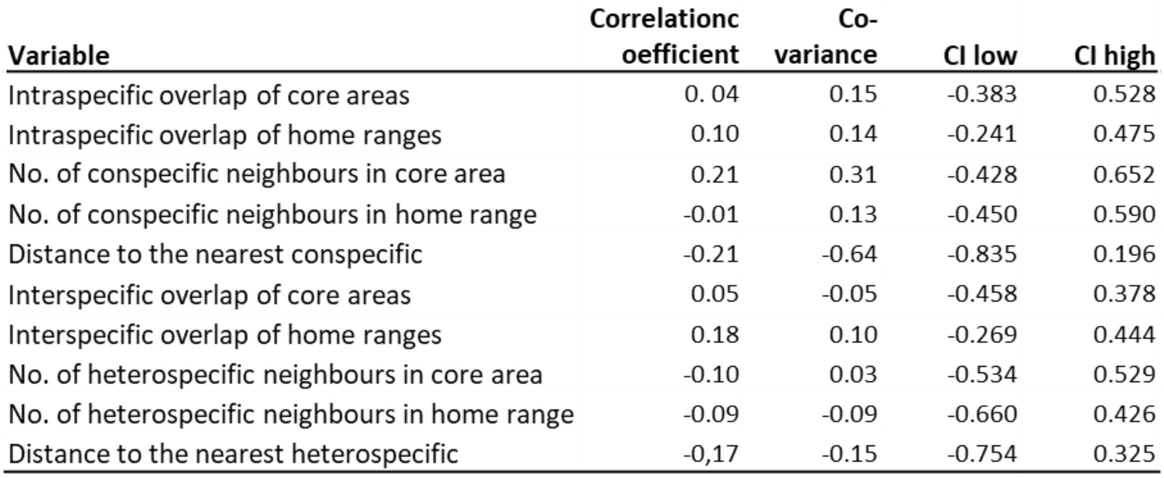
	Variable	R	CI low	CI high	p-value
Myodes glareolus	Latency to investigate	**0.45**	**0.17**	**0.69**	**0.001**
	Latency to emerge	**0.37**	**0.11**	**0.61**	**0.003**
	Latency to cross the center	**0.33**	**0.00**	**0.58**	**0.007**
	Number of center crossings	**0.26**	**0.00**	**0.42**	**0.007**
	Number of sections entered	**0.22**	**0.05**	**0.46**	**0.026**
	Number of jumps	0.08	-0.11	0.33	0.158
	Activity	**0.33**	**0.12**	**0.54**	**0.009**
Apodemus agrarius	Latency to investigate	**0.41**	**0.18**	**0.60**	**0.001**
	Latency to emerge	**0.43**	**0.17**	**0.63**	**0.001**
	Latency to cross the center	**0.16**	**0.00**	**0.28**	**0.013**
	Number of center crossings	**0.21**	**0.10**	**0.37**	**0.028**
	Number of sections entered	**0.31**	**0.00**	**0.38**	**0.002**
	Number of jumps	0.22	-0.21	0.39	0.059
	Activity	**0.37**	**0.07**	**0.66**	**0.036**

Table A3 Results of the principle component analysis, corrected for species, for *M. glareolus* and *A. agrarius* (n = 126). PC 1 represents the principle component interpreted as exploration, PC 2 represents the component interpreted as boldness. The highest loading of each variable, signifying which component represents the variable best, is marked in bold.



		Components	
		PC 1	**PC 2**
Loadings	Latency to investigate	-0.58	**0.77**
	Latency to emerge	-0.59	**0.76**
	Latency to cross the center	**-0.74**	-0.35
	Number of center crossings	**0.78**	0.24
	Number of sections entered	**0.85**	0.28
	Activity	**0.76**	0.27
Variance	Eigenvalues	3.15	1.51
	Proportion Variance	0.56	0.27
	Cumulative Variance	0.56	0.83

Table A4 Covariances between exploration and the respective spatial interaction variables. Represented are the covariance values, their credibility intervals and the correlation coefficients to represent the strength of association between variables.



Variable	Correlationc oefficient	Co-variance	CI low	CI high
Intraspecific overlap of core areas	0. 04	0.15	-0.383	0.528
Intraspecific overlap of home ranges	0.10	0.14	-0.241	0.475
No. of conspecific neighbours in core area	0.21	0.31	-0.428	0.652
No. of conspecific neighbours in home range	-0.01	0.13	-0.450	0.590
Distance to the nearest conspecific	-0.21	-0.64	-0.835	0.196
Interspecific overlap of core areas	0.05	-0.05	-0.458	0.378
Interspecific overlap of home ranges	0.18	0.10	-0.269	0.444
No. of heterospecific neighbours in core area	-0.10	0.03	-0.534	0.529
No. of heterospecific neighbours in home range	-0.09	-0.09	-0.660	0.426
Distance to the nearest heterospecific	-0,17	-0.15	-0.754	0.325

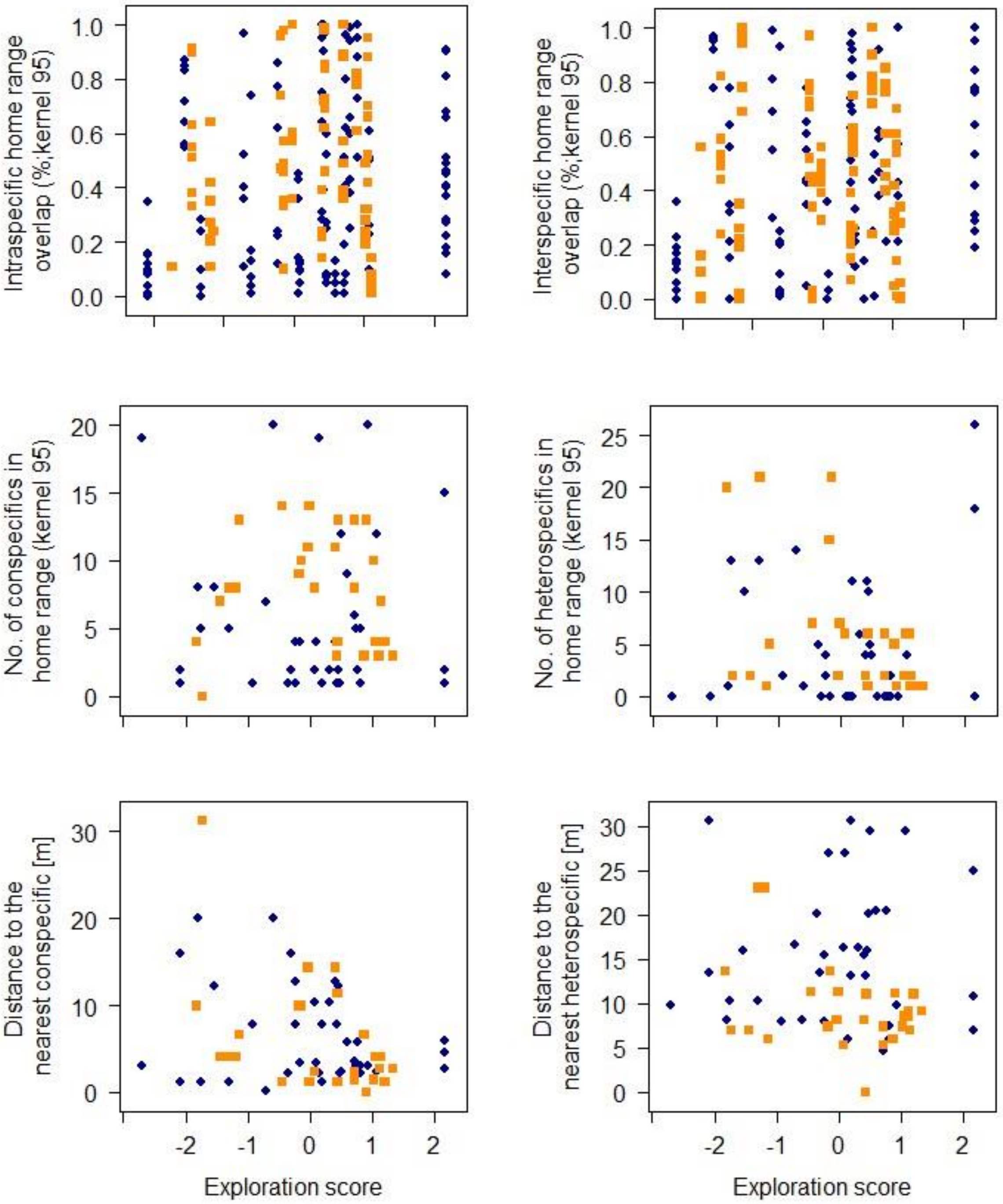


Figure A4 Covariance between exploration and spatial patterns at the home range scale. Presented are intra- and interspecific overlap, number of con- and heterospecific neighbours and the distance to the nearest con- or heterospecific of bank voles (*M. glareolus*, n = 21, dots) and striped field mice (*A. agrarius*, n = 15, squares). Results on the core area scale are similar, we therefore refrain from presenting them.

Table A5 Results for the fixed effects of Bayesian mixed-effects models on spatial patterns in home ranges (kernel 95) and core areas (kernel 50) of bank voles and striped field mice. Represented are the mean values for the variables based on the posterior distribution of the data, the lower and upper level of the 95 % credibility interval (CI) the effective sample size based on permutations and the adjusted p values based on Bayesian statistics.

Variable	**Fixed factor**	**Post.mean**	**Lower CI 95%**	**Upper CI 95%**	**Eff.samp**	**pMCMC**
Intraspecific overlap of core areas	Sex	0.136	-0.051	0.300	1000	0.112
	Species	-0.007	-0.205	0.186	1214	0.950
	Dif_Bold	0.000	-0.001	0.001	1000	0.956
	DyadSex	0.000	-0.005	0.007	698	0.912
Intraspecific overlap of home range	Sex	0.103	-0.113	0.309	1000	0.344
	Species	0.072	-0.152	0.306	1000	0.516
	Dif_Bold	0.000	-0.001	0.001	1000	0.872
	DyadSex	0.001	-0.006	0.007	1000	0.836
Interspecific overlap of core areas	Sex	-0.001	-0.169	0.171	1000	0.992
	Species	0.045	-0.109	0.232	1000	0.604
	Dif_Bold	0.000	-0.001	0.001	1000	0.960
	DyadSex	0.000	-0.006	0.006	1000	0.990
Interspecific overlap of home range	Sex	-0.036	-0.265	0.199	1000	0.750
	Species	0.026	-0.204	0.241	1000	0.822
	Dif_Bold	0.000	-0.001	0.001	1000	0.824
	DyadSex	0.001	-0.006	0.007	1000	0.790
No of conspecific neighbours in core area	Sex	-0.294	-0.794	0.252	1000	0.292
	Species	-0.161	-0.675	0.401	1000	0.538
No of conspecific neighbours in home range	Sex	0.119	-0.516	0.710	1000	0.682
	Species	0.456	-0.190	1.063	1000	0.132
No of heterospecific neighbours in core area	Sex	-0.009	-0.754	0.707	1000	0.980
	Species	-0.077	-0.879	0.701	1000	0.852
No of heterospecific neighbours in home range	Sex	0.335	-0.798	1.390	1000	0.528
	Species	0.424	-0.527	1.390	1000	0.434
Distance to the nearest conspecific	Sex	-0.930	-3.138	1.689	1000	0.424
	Species	-0.104	-2.280	2.194	1000	0.920
	DyadSex	-0.056	-0.345	0.223	1000	0.738
Distance to the nearest heterospecific	Sex	0.608	-2.006	3.399	1000	0.630
	Species	-2.395	-4.933	0.207	1000	0.076
	DyadSex	-0.012	-0.296	0.307	1000	0.896

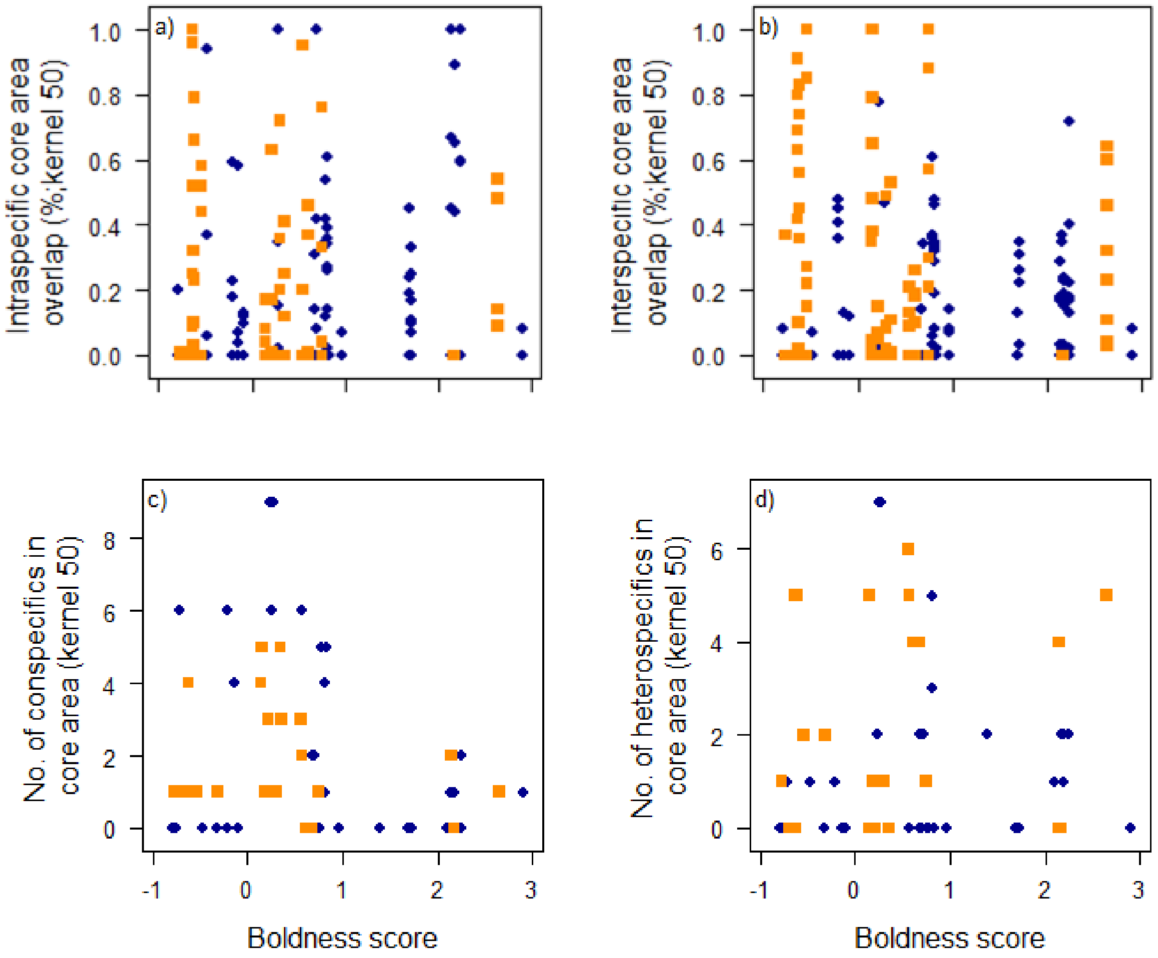
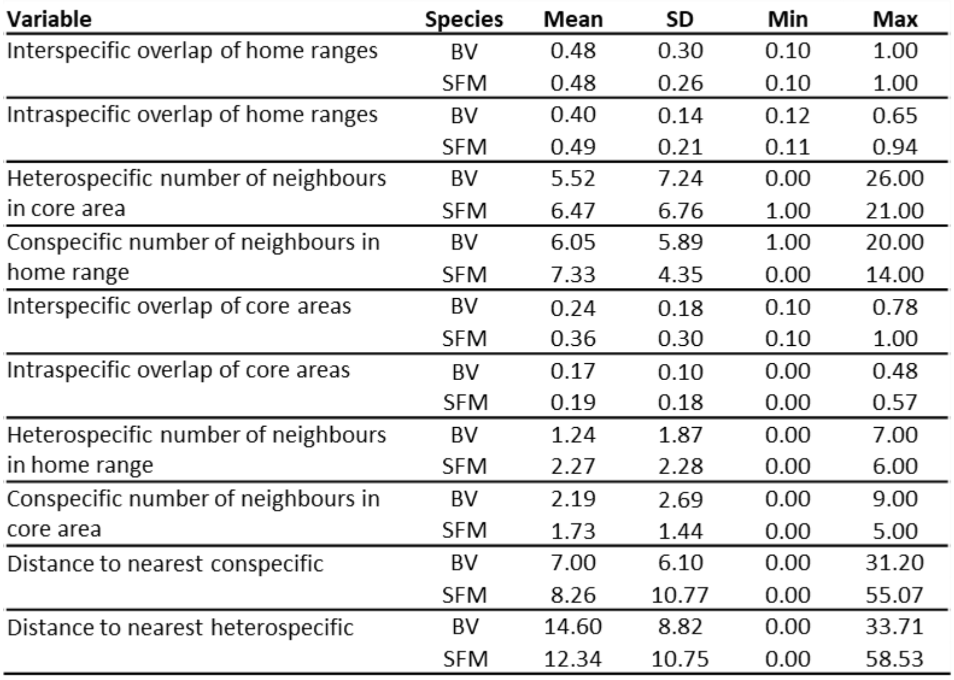


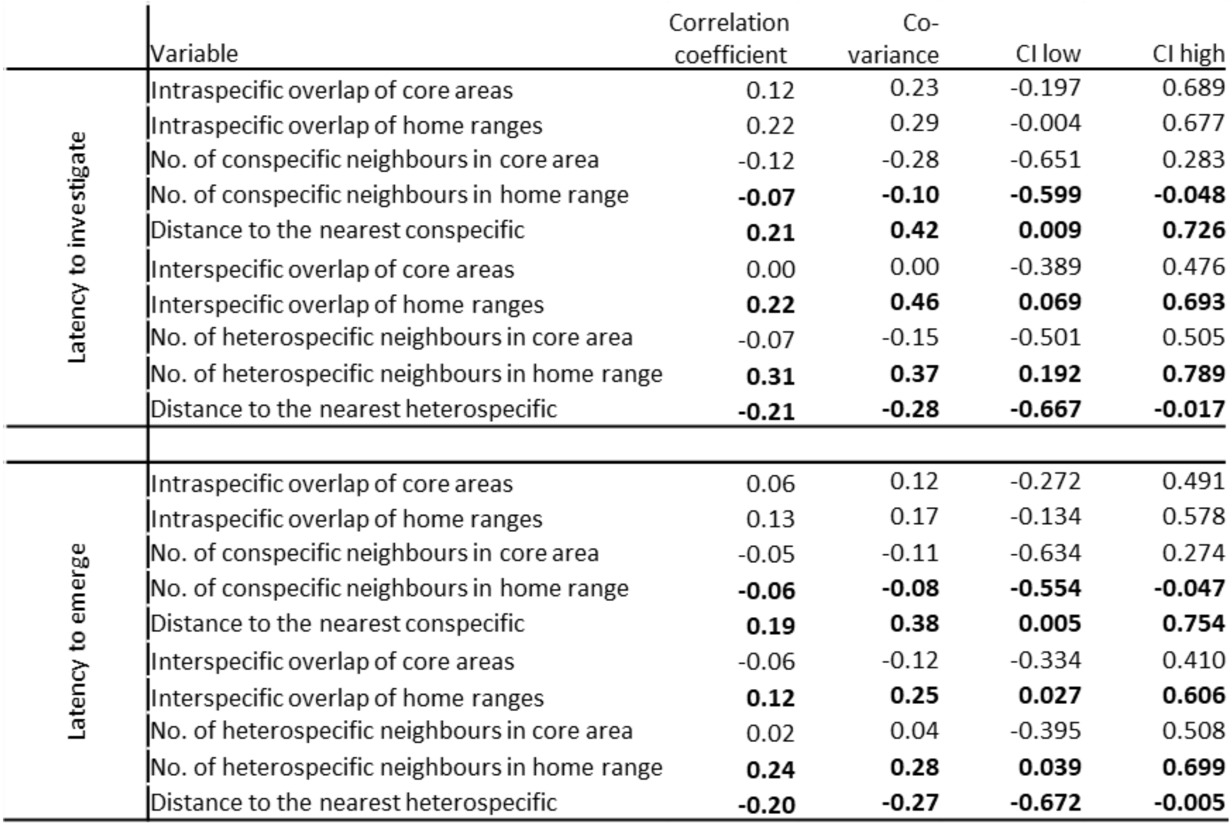
Figure A5 Covariance between boldness and spatial patterns at the core area scale. Presented are intra- and interspecific overlap (a, b) and number of con- and heterospecific neighbours (c, d) of bank voles (*M. glareolus*, n = 21, dots) and striped field mice (*A. agrarius*, n = 15, squares).

Table A6 Descriptive statistic of spatial variables for bank voles (BV) and striped field mice (SFM). Given are mean, SD as the standard deviation, Min the minimum and Max the maximum value.



Variable	Species	Mean	SD	Min	Max
Interspecific overlap of home ranges	BV	0.48	0.30	0.10	1.00
	SFM	0.48	0.26	0.10	1.00
Intraspecific overlap of home ranges	BV	0.40	0.14	0.12	0.65
	SFM	0.49	0.21	0.11	0.94
Heterospecific number of neighbours in core area	BV	5.52	7.24	0.00	26.00
	SFM	6.47	6.76	1.00	21.00
Conspecific number of neighbours in home range	BV	6.05	5.89	1.00	20.00
	SFM	7.33	4.35	0.00	14.00
Interspecific overlap of core areas	BV	0.24	0.18	0.10	0.78
	SFM	0.36	0.30	0.10	1.00
Intraspecific overlap of core areas	BV	0.17	0.10	0.00	0.48
	SFM	0.19	0.18	0.00	0.57
Heterospecific number of neighbours in home range	BV	1.24	1.87	0.00	7.00
	SFM	2.27	2.28	0.00	6.00
Conspecific number of neighbours in core area	BV	2.19	2.69	0.00	9.00
	SFM	1.73	1.44	0.00	5.00
Distance to nearest conspecific	BV	7.00	6.10	0.00	31.20
	SFM	8.26	10.77	0.00	55.07
Distance to nearest heterospecific	BV	14.60	8.82	0.00	33.71
	SFM	12.34	10.75	0.00	58.53

Table A7 Covariances of single variables comprising the boldness score in the manuscript and spatial interaction variables. We decided to use the PCA scores of the second component as a quantitative measure of boldness in the Bayesian mixed-effects models presented in the manuscript, rather than the single measured variables from the individual difference test, since the test itself measures six variables and picking one of them as a measure of boldness would neglect the underlying grouping structure of the data. Therefore, we present the covariances between the single variables and the spatial variables only here. Latency to investigate represents the latency until an individual stuck its head out of the pipe from the test set up, while the latency to emerge represents the latency until an individual left the pipe with its whole body. Represented are the covariance values their credibility intervals and the correlation coefficients to represent the strength of association between variables. Intervals different from zero represent significant covariances and are marked in bold.



	Variable	Correlation coefficient	Co-variance	CI low	CI high
Latency to investigate	Intraspecific overlap of core areas	0.12	0.23	-0.197	0.689
	Intraspecific overlap of home ranges	0.22	0.29	-0.004	0.677
	No. of conspecific neighbours in core area	-0.12	-0.28	-0.651	0.283
	No. of conspecific neighbours in home range	**-0.07**	**-0.10**	**-0.599**	**-0.048**
	Distance to the nearest conspecific	**0.21**	**0.42**	**0.009**	**0.726**
	Interspecific overlap of core areas	0.00	0.00	-0.389	0.476
	Interspecific overlap of home ranges	**0.22**	**0.46**	**0.069**	**0.693**
	No. of heterospecific neighbours in core area	-0.07	-0.15	-0.501	0.505
	No. of heterospecific neighbours in home range	**0.31**	**0.37**	**0.192**	**0.789**
	Distance to the nearest heterospecific	**-0.21**	**-0.28**	**-0.667**	**-0.017**
Latency to emerge	Intraspecific overlap of core areas	0.06	0.12	-0.272	0.491
	Intraspecific overlap of home ranges	0.13	0.17	-0.134	0.578
	No. of conspecific neighbours in core area	-0.05	-0.11	-0.634	0.274
	No. of conspecific neighbours in home range	**-0.06**	**-0.08**	**-0.554**	**-0.047**
	Distance to the nearest conspecific	**0.19**	**0.38**	**0.005**	**0.754**
	Interspecific overlap of core areas	-0.06	-0.12	-0.334	0.410
	Interspecific overlap of home ranges	**0.12**	**0.25**	**0.027**	**0.606**
	No. of heterospecific neighbours in core area	0.02	0.04	-0.395	0.508
	No. of heterospecific neighbours in home range	**0.24**	**0.28**	**0.039**	**0.699**
	Distance to the nearest heterospecific	**-0.20**	**-0.27**	**-0.672**	**-0.005**

A13 Exemplary R code of a calculated Bayesian mixed model investigating the covariance between boldness and spatial parameters

```
##MCMC model: Covariance between boldness and distance to the nearest conspecific
library(MCMCglmm)

##Load data
DataDis <- read.delim2("C:/.../DataDistance.txt")

#set priors
##create matrix variances of both covariates
pvar1<-matrix(c(var(DataDis$Boldness,na.rm=TRUE),0,0, var(DataDis$DistanceConspecific, na.rm=TRUE)), 2,2)
```

```
##the distance to the nearest conspecific has only been measured once, therefore the within-individual
correlation is fixed to nearly 0
prior1<-list(G=list(G1=list(V=diag(2)*pvar1/2,n=2),G2=list(V=diag(2)*pvar1/2,n=2)),
R=list(V=diag(c(1,0.0001),2,2),nu=1,fix=2))


#Run MCMC model
##Boldness and the distance to the nearest conspecific have not been measured at the same time, therefore the
within-individual covariance was fixed to 0
mod.Dis<-MCMCglmm(cbind(Boldness,DistanceConspecific)~ trait-
1+Sex+Species,random=~us(trait):PIT+us(trait):Grid, rcov=~idh(trait):units,
family=c("gaussian","gaussian"),data=DataDis, nitt=101000, thin=100, burnin=1000, prior=prior1, verbose=FALSE)

summary(mod.Dis)
autocorr(mod.Dis$VCV)
plot(mod.Dis$VCV)
plot(mod.Dis$Sol)
posterior.mode(mod.Dis$VCV)
mod.Dis$DIC
head(mod.Dis$Sol)

#calculation of among-individual correlations
CorDis<-
mod.Dis$VCV[,"traitDistanceConspecific:traitBoldness.PIT"]/sqrt(mod.Dis$VCV[,"traitBoldness:traitBoldness.PIT"]
*mod.Dis$VCV[,"traitDistanceConspecific:traitDistanceConspecific.PIT"])

#extract covariance and credibility interval
posterior.mode(CorDis)
HPDinterval(CorDis, 0.95)
```