

Supplementary Material

Appendix 1 - Details on the hair identification protocol.

A total of 83 dormouse wooden nest-boxes (210×120×160) mm with an entrance hole of 30 mm) were installed in August 2013. Nest boxes were constructed using pressure-treated plywood; these were mounted at 1,5 meters, facing the tree trunks, trying to prevent the occupation by bird species from occupying them (Morris et al. 1990, Sarà et al. 2005).

Hair-tubes made from PVC flexible tubes (250-300 mm length; 75 mm diameter) were installed and attached to horizontal tree branches with metal wire and baited following the sampling protocol described in Mortelliti & Boitani (2007) and Amori et al. (2011).

Hazelnuts (*Corylus avellana*, L.) were glued into the inner part of the tube. Hairs were identified to species using reference collection and atlas (Teerink 1991, De Marinis & Agnelli 1993, Lombardi & Ragni 2012). As a preliminary step, guard hairs were first cleaned with 70% alcohol and then were dry on paper towels. The configuration of medulla was investigated through a microscope (10x), then hair was pressed in celluloid sheet (thickness 1 mm) to get imprints of cuticle pattern by applying acetone. Imprints were analysed through a binocular microscope (40x) and further examined based on cuticle and scale patterns using identification keys. Nest types, pellets and gnawed hazelnuts were identified with the aid of field guides (Olsen 2013).

Different types of nests of the two rodents are showed in the image below:

(a-b) *Glis glis*;

(c-d) *Muscardinus avellanarius*.



Appendix 2 - Description of the 12 explanatory variables measured and estimated at each sampling plot.

Forest category (F_cat): The forest category is a combination of the geographical/ecological distribution of the type, tree species composition. Its name usually reflects the most abundant tree species of the stand. In our study, this information was provided by the forest types map of the Molise region (Vizzarri et al. 2015) and then verified *in situ* during the field surveys.

Forest management (F_man): the silvicultural system adopted to achieve specific stand structural and management objectives, based on the biological requirements of the trees. The silvicultural treatments integrates specific harvesting, regeneration, and stand tending methods to maintain forests healthy and vigorous, and to achieve a predictable yield from the stand over time. In our study, this information was provided by the forest types map of the Molise region (Vizzarri et al. 2015) and then verified *in situ* during the field surveys. The main forest management systems in the study area are: coppice (usually with standards), coppice in conversion to high forests, and high forest.

Age: the age of trees within the forest stands. It is determined by counting the tree's rings of the trees belonging to the most frequent class of diameter at the breast height (DBH). The increment borer was used to collect tree's cores during the field survey and then analysed in laboratory using dendrochronological techniques.

Tree density (T_density): mean number of trees per hectare ($\text{pt} \cdot \text{ha}^{-1}$). A quantitative measure of tree stocking expressed in terms of number of trees per unit area. Human interventions affect the tree density of both living trees and stand dead trees. T_density was estimated using the data collected per each sampling plot during the field surveys.

Mean of the heights (Mean_height): the arithmetic mean of the heights of all the living trees (in m) with DBH higher than 7.5 cm within the sampling plots.

σ^2 Height (Stdev_height): the standard deviation of the heights of all the living trees (in m) with DBH higher than 7.5 cm within the sampling plots.

Stand basal area (Basal_area): Basal area of a forest stand is the sum of the basal areas of all the living trees (in $\text{m}^2 \cdot \text{ha}^{-1}$). The basal area (g) is the cross-sectional area of a tree trunk at breast height, then calculated as follows:

$$g = \frac{\pi}{4} \cdot d^2$$

where d is the DBH.

Mean DBH: the DBH of the tree with the mean basal area within the sampling plot (cm). At first we calculated the mean basal area (\bar{g}) of the stand trees as follows:

$$\bar{g} = \frac{G}{n}$$

where G is the basal area of the stand ($\text{m}^2 \text{ha}^{-1}$) and n is the number of the stand trees ($\text{pt} \cdot \text{ha}^{-1}$). Then the mean DBH is calculated using the equation:

$$\text{mean DBH} = \sqrt{\bar{g} \cdot \frac{4}{\pi}}$$

$\sigma^2\text{DBH}$: the standard deviation of the DBH of all the living trees measured within the sampling plot (cm).

CWD : the volume of coarse woody debris measured within the sampling plot (dead trees, snag, and stumps), including lying deadwood (downed trees and logs) ($\text{m}^3 \cdot \text{ha}^{-1}$). For standing dead trees the DBH threshold value was 10 cm, while for the lying deadwood only the lying longer than 1 m and ≥ 10 cm in diameter at cutting point were measured. Volume ($V\ CWD$) was then calculated as follows:

$$V\ CWD = \frac{\pi}{4} \cdot d^2 \cdot l$$

where d is the diameter of the CWD while l is the length. The volume of each CWD were then summed up within the sampling plot and reported to the ha.

Volume (V): the volume of all the living trees within each sampling plot having a DBH greater than 7.5 cm as estimated by using the equations proposed by the Italian National Forest Inventory and referred to a 1 ha area (Gasparini & Tabacchi 2011).

Tree species richness (SR): the number of tree species occurring within each sampling plot. The value is based on the ground observations.

Appendix 3 - Details on the spatialization procedure.

Numerical predictors selected in the top-ranked models, *i.e.*, SR, T_density, Basal_area, Mean_height and Stdev_height, were spatialized over the study area by applying a regression kriging technique. Kriging is a method to interpolate the values of a dependent variable at points between field observations. Unlike classical statistics, which relies on the independence of data points, kriging assumes that observations are not independent (Hudak et al. 2002). Regression kriging represents a modification of ordinary kriging and relies on interpolating a poorly sampled variable (the primary variable) with the help of a well-sampled variable (the secondary variable; Papritz & Stein, 1999). It prescribes to use multiple regression to describe the relationship between the primary variable the secondary predictors, then applying kriging on the regression residuals (Hudak et al. 2002). In our study, each numerical predictors that was selected in the top-ranked models was interpolated over the study area including Forest category and Forest management as secondary variables in the regression kriging procedure. These secondary variables were derived from the forest types map (Vizzarri et al. 2015). We assessed the predictive accuracy of the interpolation phase by applying a 10-fold cross validation procedure and calculating the mean absolute percentage error (MAPE). MAPE values follow:

Variable	MAPE (mean + sd)
SR	5.12 ± 10.1
T_density	3.11 ± 2.91
Basal_area	5.70 ± 16.46
Mean_height	18.35 ± 10.75
Stdev_height	5.63 ± 5.63

Tab. S1 - Summary of presence (1) and absence (0) of two arboreal rodent species (*G. glis* and *M. avellanarius*) in the 83 sampling sites; “-” indicate no data; I-II-III-IV represent the number of replicate.

Sampling plot	<i>Glis glis</i>				<i>Muscardinus avellanarius</i>			
	I	II	III	IV	I	II	III	IV
1	0	-	-	-	-	-	-	-
2	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0
5	0	0	0	1	0	0	0	0
6	0	0	0	0	0	1	1	1
7	0	0	0	0	0	1	0	0
8	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0
10	0	0	0	0	1	1	1	1
11	0	0	0	0	0	0	0	1
12	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0
14	0	0	0	1	0	0	0	0
15	0	0	0	0	0	0	0	0
16	0	0	0	0	0	-	0	0
17	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0
21	0	0	0	1	0	1	1	1
22	1	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0
24	0	0	0	1	0	0	0	0
25	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	1
27	1	0	0	0	0	0	0	0
28	0	0	0	0	-	0	1	1
29	-	-	-	0	-	-	-	0
30	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0
32	0	0	-	1	0	0	-	0
33	0	-	-	-	1	1	1	1
34	-	0	0	0	-	0	0	0
35	0	0	0	0	0	0	0	0
36	0	0	0	1	0	0	0	1
37	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	1	1
40	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0
42	0	1	0	0	0	0	0	1
43	0	0	0	1	0	0	0	0
44	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0

Sampling plot	<i>Glis glis</i>				<i>Muscardinus avellanarius</i>			
	I	II	III	IV	I	II	III	IV
46	0	0	0	0	0	0	0	0
47	0	0	1	1	1	0	0	0
48	0	0	0	0	0	0	0	0
49	0	0	0	0	1	1	1	1
50	0	1	0	1	0	0	0	0
51	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0
53	0	0	0	1	0	0	0	0
54	0	0	0	1	0	0	0	0
55	0	0	0	1	0	0	0	0
56	0	0	0	1	0	0	0	0
57	0	0	0	1	0	0	0	0
58	0	0	1	0	0	0	0	0
59	0	0	0	0	0	0	0	0
60	0	0	0	0	0	0	0	0
61	0	0	0	0	0	0	0	0
62	0	0	0	1	0	0	0	0
63	0	0	0	0	0	0	0	0
64	0	0	0	1	0	0	0	0
65	0	0	0	1	0	0	0	0
66	0	0	0	0	0	0	0	0
67	0	0	0	0	0	0	0	0
68	0	0	0	-	0	0	0	0
69	0	0	1	0	0	0	0	0
70	0	0	0	0	0	0	0	0
71	0	0	0	1	0	0	0	0
72	0	0	1	0	0	0	0	0
73	0	0	0	1	0	0	0	0
74	0	0	0	1	0	0	0	0
75	0	0	0	0	0	0	0	0
76	0	0	1	1	0	0	0	0
77	0	0	0	1	0	0	0	1
78	0	0	0	0	0	0	0	0
79	0	0	0	0	0	0	0	0
80	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	0	0
82	0	0	0	0	0	1	0	0
83	1	1	0	0	0	1	0	0

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Tab. S2 - Top-ranked GLMMs derived from the model selection procedure. W indicates the Akaike weight of each model. The goodness-of-fit of the models was assessed by calculating the conditional (in parentheses) and marginal coefficients of determination for GLMM. Continuous variables in fixed effect part enter as linear and quadratic terms and “:” indicate interaction between predictors.

Species	Models (fixed effect terms)	Models (random effect terms)	AICc	ΔAICc	W	R ² c (R ² m)
<i>G. glis</i>	Pocc~Basal_area+F_cat+F_man:Mean_height	1 replicate	182.2	0	0.111	0.560 (0.439)
	Pocc~Basal_area+T_density+F_man:Basal_area	1 replicate	182.7	0.41	0.090	0.497 (0.363)
	Pocc~Basal_area+ F_man:Mean_height	1 replicate	182.7	0.46	0.088	0.555 (0.439)
	Pocc~Basal_area+F_cat+ T_density+F_man:SR+F_man:F_cat	1 replicate	182.9	0.68	0.079	0.555 (0.422)
	Pocc~Basal_area+F_cat+ T_density+F_man:Mean_height	1 replicate	182.9	0.68	0.079	0.556 (0.431)
	Pocc~Basal_area+T_density	1 replicate	183.2	0.91	0.071	0.406 (0.254)
	Pocc~Basal_area+F_cat+ T_density	1 replicate	183.2	0.95	0.069	0.409 (0.251)
	Pocc~Basal_area+F_cat+F_man:F_cat	1 replicate	183.4	1.14	0.063	0.605 (0.496)
	Pocc~Basal_area+F_cat+T_density+F_man:Basal_area	1 replicate	183.5	1.26	0.059	0.506 (0.362)
	Pocc~Basal_area+F_cat+F_man:Mean_height+F_man:T_density+F_man:Stdev_height	1 replicate	183.6	1.39	0.055	0.637 (0.527)
	Pocc~Basal_area+T_density+F_man:Mean_height	1 replicate	183.7	1.44	0.054	0.544 (0.422)
	Pocc~Basal_area+F_man:T_density	1 replicate	183.9	1.69	0.048	0.504 (0.369)
	Pocc~Basal_area+T_density+F_man:Stdev_height	1 replicate	184.0	1.76	0.046	0.475 (0.335)
	Pocc~Basal_area+ F_man:Stdev_height	1 replicate	184.0	1.78	0.046	0.471 (0.335)
Pocc~Basal_area+F_man:Mean_height+F_man:Stdev_height	1 replicate	184.2	1.93	0.042	0.564 (0.443)	
<i>M. avellanarius</i>	Pocc~Mean_height+Stdev_height+F_man:T_density	1 replicate	151.3	0	0.472	0.648 (0.632)
	Pocc~Mean_height+F_cat+Stdev_height+F_man:T_density	1 replicate	151.9	0.58	0.353	0.638 (0.622)
	Pocc~Mean_height+F_cat+F_man:T_density	1 replicate	153.3	1.99	0.175	0.634 (0.620)

Tab. S3 - Top-ranked OMs derived from the model selection procedure. ψ = probability of occupancy, p = detection probability, W = Akaike weight of each model, pseudo- R^2 = Nagelkerke's coefficient of determination. Continuous variables enter as linear and quadratic terms, with “:” indicating interaction between predictors.

Species	Models	AICc	Δ AICc	W	pseudo- R^2
<i>C. glis</i>	$\psi \sim$ Basal_area + T_density + F_cat + F_man + Mean_height:F_man $p \sim$ Basal_area	192.0	0.00	0.192	0.424
	$\psi \sim$ Basal_area + T_density + F_man + Mean_height:F_man $p \sim$ Basal_area	192.1	0.07	0.185	0.403
	$\psi \sim$ Basal_area + F_man + A.S.Rich:F_man $p \sim$ Basal_area + T_density	192.6	0.54	0.146	0.340
	$\psi \sim$ Basal_area + Mean_height $p \sim$ T_density + Basal_area	192.9	0.91	0.121	0.334
	$\psi \sim$ Basal_area + Mean_height + F_man + T_density:F_man $p \sim$ Basal_area	193.3	1.24	0.103	0.394
	$\psi \sim$ Basal_area + F_man + A.S.Rich:F_man $p \sim$ Basal_area	193.4	1.42	0.094	0.351
	$\psi \sim$ Basal_area + F_man + A.S.Rich + Mean_height $p \sim$ Basal_area	193.6	1.61	0.086	0.371
	$\psi \sim$ Basal_area + F_cat + Mean_height + Stdev_height $p \sim$ Basal_area	194.0	1.94	0.072	0.347
<i>M. avellanarius</i>	$\psi \sim$ Stdev_height + F_cat + T_density $p \sim$ Mean_height + Stdev_height + F_cat + T_density	130.3	0.00	0.726	0.570
	$\psi \sim$ Mean_height + Stdev_height $p \sim$ Mean_height + T_density + Stdev_height	132.2	1.95	0.274	0.528

Fig. S1 - First (second) row depicts maps of predicted occurrence probabilities for *G. glis* (left) and *M. avellanarius* (right) by GLMM (OM). Occurrence probability values, which range from 0 (blue) to 1 (red), were projected over the study area by spatializing the predictors selected in the top-ranked models (see also Appendix 3).

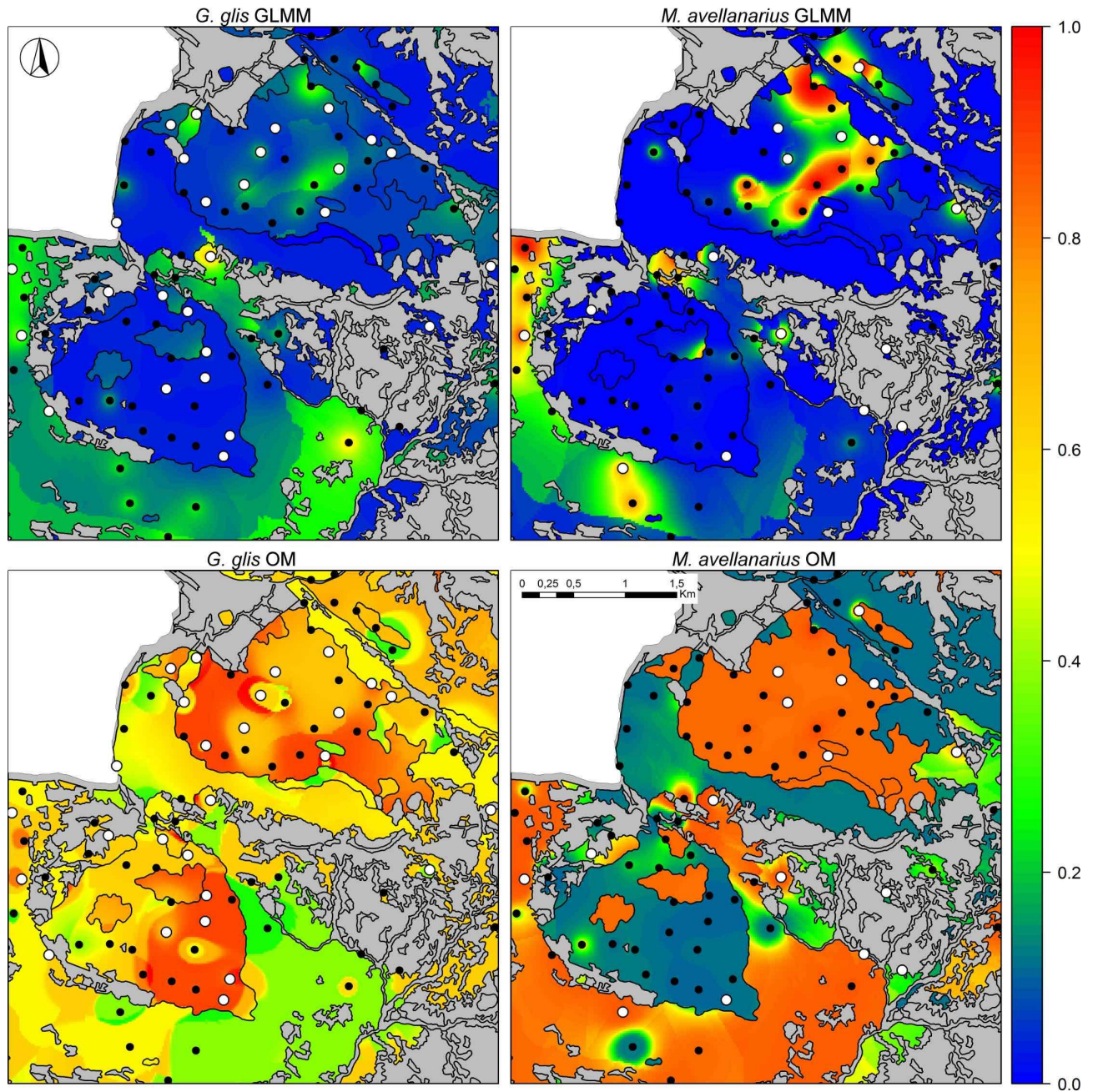
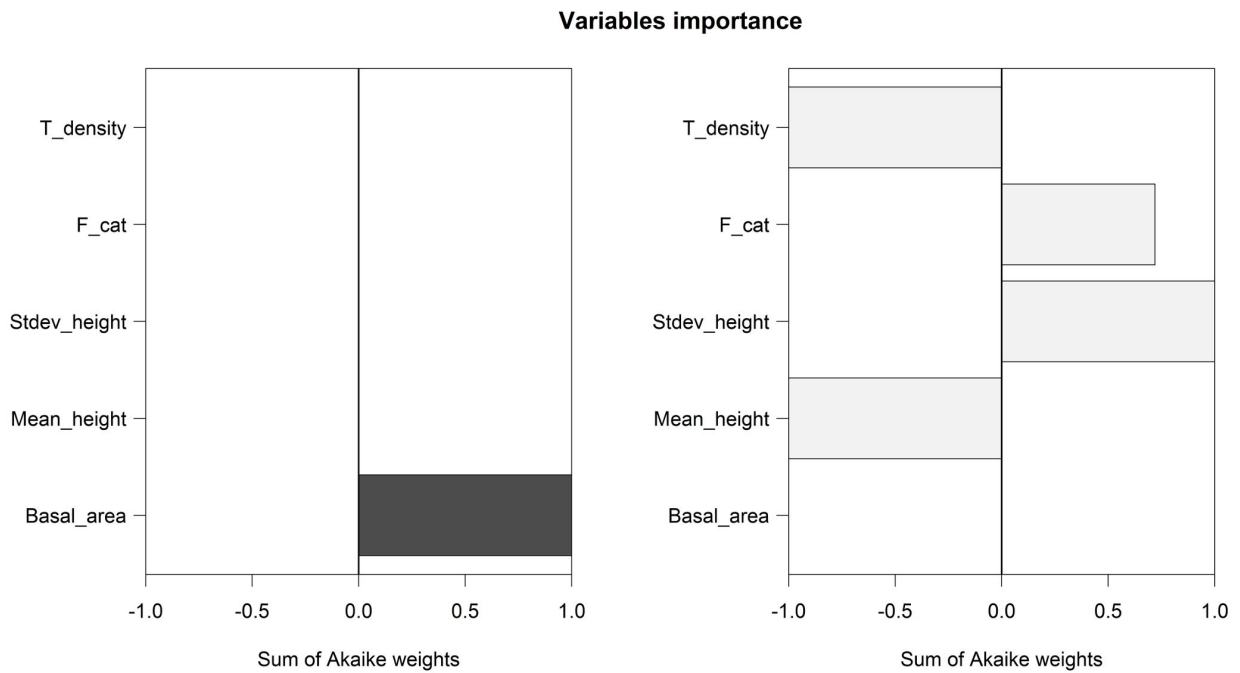


Fig. S2 - Detectability variables importance for edible (dark grey) and hazel (light grey) dormice, as the cumulative sum of Akaike weights over the top-ranked models.



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