Frugivore species maintain their structural role in the trophic and spatial networks of seed dispersal interactions

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Electronic Supplementary Material

Appendix S1. Study system and sampling methodologies

Figure S1. Representation of the study system and sampling design. A) A landscape view of the Bandujo-Puertos de Marabio site, showing habitat heterogeneity with forest patches, remnant trees, pastures, heathland and rocky outcrops. B) View of study plot indicating vantage points for monitoring fruit consumption by birds (yellow stars), point-counts for monitoring bird abundance and perching behavior (red dots), and seed deposition sampling stations with different types of seed traps (blue and purple squares, yellow dots). C) Transects for mammal scat sampling related to one study plot (main and additional transect represented by the white and yellow lines, respectively) and detail of a mammal scat on a rocky habitat.

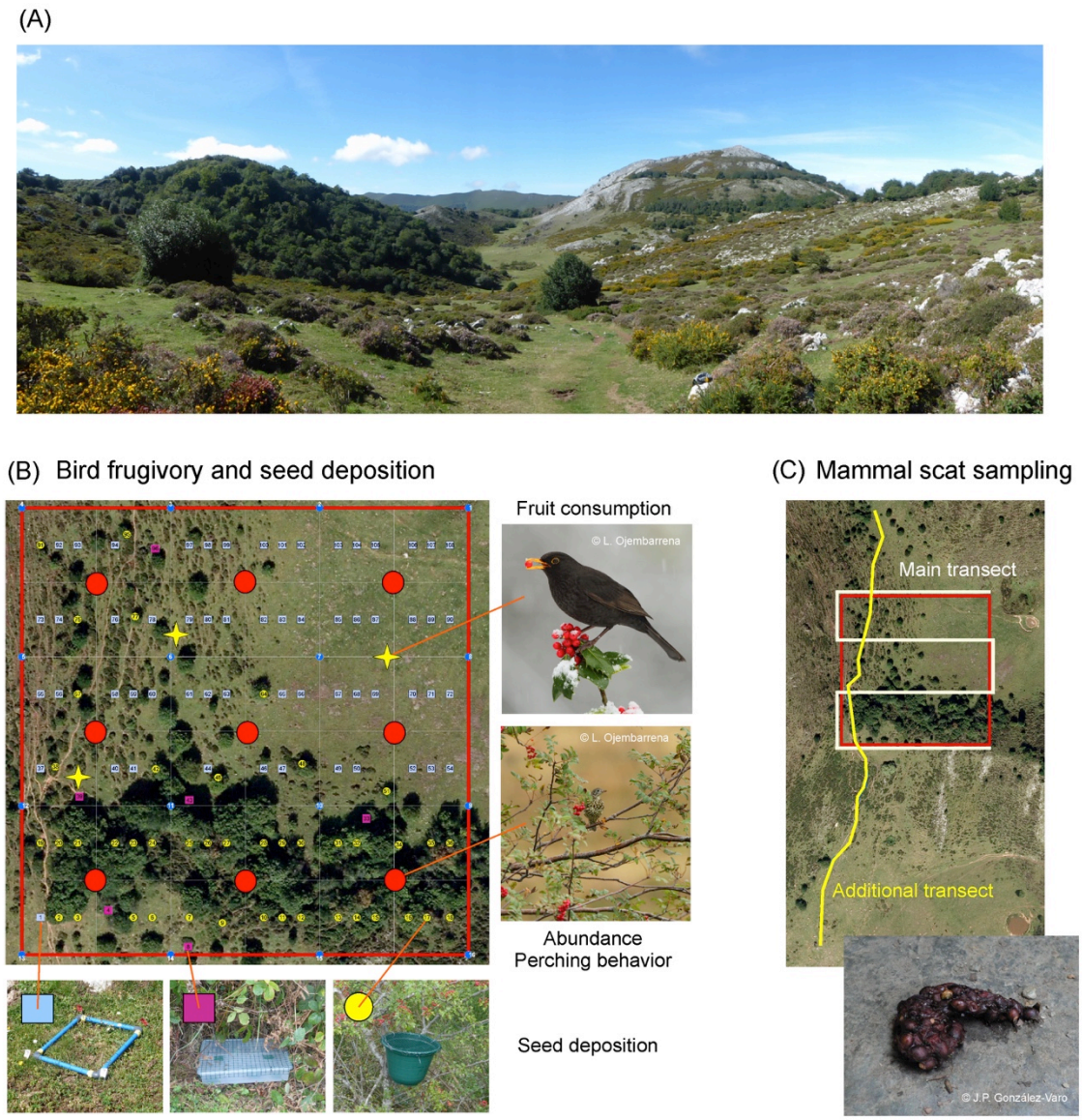


Table S1: Geographical description of the fourteen 2.25-ha study plots in the Cantabrian Range (Asturias, Spain).

Plot code	Site	Elevation (m) asl	Geographic coordinates (N-W)		Forest cover (%)
P1	Sierra de Peña Mayor	1034	43° 17' 18.1"	05° 29' 56.0"	19.98
P2	Sierra de Peña Mayor	1001	43° 17' 50.4"	05° 30' 12.2"	31.31
P3	Sierra de Peña Mayor	1067	43° 18' 09.5"	05° 30' 32.6"	8.87
P4	Sierra de Peña Mayor	1092	43° 18' 38.7"	05° 30' 44.7"	68.74
G1	Sierra de Peña Mayor	993	43° 17' 15.3"	05° 30' 28.0"	11.12
G2	Sierra de Peña Mayor	1078	43° 17' 29.8"	05° 30' 32.8"	18.88
G3	Sierra de Peña Mayor	1093	43° 17' 47.4"	05° 30' 46.4"	39.28
B1	Bandujo-Puertos de Marabio	1124	43° 14' 37.2"	06° 05' 03.7"	3.11
B2	Bandujo-Puertos de Marabio	1145	43° 14' 35.2"	06° 05' 41.4"	26.66
B3	Bandujo-Puertos de Marabio	1183	43° 14' 18.6"	06° 05' 38.9"	47.32
B4	Bandujo-Puertos de Marabio	1253	43° 14' 09.7"	06° 06' 21.3"	20.88
M1	Bandujo-Puertos de Marabio	1020	43° 13' 09.5"	06° 07' 19.0"	33.54
M2	Bandujo-Puertos de Marabio	1020	43° 13' 01.1"	06° 07' 37.1"	11.36
M3	Bandujo-Puertos de Marabio	1012	43° 12' 20.2"	06° 07' 25.7"	54.93

Table S2 Frugivore species sorted by functional type (thrushes, other birds and mammals), family, abbreviation codes and traits included in the piecewise SEMs (relative abundance and body mass; see Table S6 in Appendix S4). Abundance of frugivores was estimated as the proportion of occurrences of each species relative to the total number of plot-based observation events (N = 238; 17 rounds x 14 plots). Body mass data were obtained from Elton Traits (Wilman et al., 2014).

Frugivore species	Family	Code	Abundance	Body mass (g)
Thrushes				
Turdus iliacus	Turdidae	*Tur ili*	0.36	61.2
Turdus merula	Turdidae	*Tur mer*	0.90	102.7
Turdus philomelos	Turdidae	*Tur phi*	0.32	67.7
Turdus pilaris	Turdidae	*Tur pil*	0.02	106
Turdus torquatus	Turdidae	*Tur tor*	0.08	109
Turdus viscivorus	Turdidae	*Tur vis*	0.02	117.4
Other birds				
Erithacus rubecula	Muscicapidae	*Eri rub*	0.79	17.7
Garrulus glandarius	Corvidae	*Gar gla*	0.08	159.5
Phylloscopus collybita/ibericus	Phylloscopidae	*Phy* spp	0.07	8.3
Sylvia atricapilla	Sylviidae	*Syl atr*	0.21	16.7
Mammals				
Canis lupus/familiaris	Canidae	*Can* spp	0.01	32183.3
Capreolus capreolus	Cervidae	*Cap cap*	0.33	22500
Cervus elaphus	Cervidae	*Cer ela*	0.32	165015.9
Martes martes/foina	Mustelidae	*Mar* spp	0.18	1420.4
Meles meles	Mustelidae	*Mel mel*	0.15	13000
Mustela nivalis/erminea	Mustelidae	*Mus* spp	0.01	111.6
Sus scrofa	Suidae	*Sus scr*	0.13	96118.1
Vulpes vulpes	Canidae	*Vul vul*	0.36	5476.2

Reference

Wilman, H., Belmaker, J., Simpson, J., de la Rosa, C., Rivadeneira, M.M., & Jetz, W. (2014) EltonTraits 1.0: Species‐level foraging attributes of the world's birds and mammals. *Ecology, 95***,** 2027-2027

Table S3 Fleshy-fruited species included in the study, family and abbreviation codes.

Feshy-fruited species	Family	Code
Crataegus monogyna	Rosaceae	*Cra mon*
Ilex aquifolium	Aquifoliaceae	*Ile aqu*
Malus sp.	Rosaceae	*Mal* sp.
Prunus avium	Rosaceae	*Pru avi*
Rosa sp.	Rosaceae	*Ros* sp.
Rubus fruticosus	Rosaceae	*Rub fru*
Sambucus nigra	Adoxaceae	*Sam nig*
Smilax aspera	Smilacaceae	*Smi asp*
Sorbus aria	Rosaceae	*Sor ari*
Sorbus aucuparia	Rosaceae	*Sor* auc
Taxus baccata	Taxaceae	*Tax bac*

Appendix S2. Seed dispersal matrices

In order to obtain the trophic and spatial networks we built trophic and spatial matrices following a three-step approach (Fig. S2). First, we estimated *raw matrices* for birds and mammals separately, based on field data obtained from different methodologies, and representing the number of dispersed seeds by different frugivore species (trophic network; Fig. S2A) and in different fine-scale habitats (spatial network; Fig. S2B). In the case of the raw spatial matrix of birds, cell values represented observations of different birds perching on different fine-scale habitats. Second, we transformed raw matrices into *proportional matrices*, in which each cell represented the proportion of seeds relative to the total number of seeds of the raw matrix. In the case of the proportional spatial matrix of birds, we corrected it by a seed dispersal rate, by multiplying the values of each bird species by the proportion of seeds dispersed by the bird species in the trophic interaction matrix. This product matrix was transformed again into proportional, by dividing the value of each cell by the total sum of cell values in the product matrix (for simplicity, this step was omitted from Fig. S2). Third, for both the trophic and the spatial case, we merged bird and mammal proportional matrices in a single *final matrix*, after multiplying the proportional matrices by a total number of seeds according to a ratio 70.9:1 for, respectively, birds and mammals (and with a 10^N coefficient enabling the transformation of any proportional value into an integer value).

Figure S2 Procedure followed to construct our seed dispersal matrices: (A) trophic interaction matrix, and (B) spatial matrix of seed deposition fine-scale habitats (H). Interactions were weighted by using a bird:mammal ratio based on the seed rain (seeds/m^2) generated by both birds and mammals (see green box).

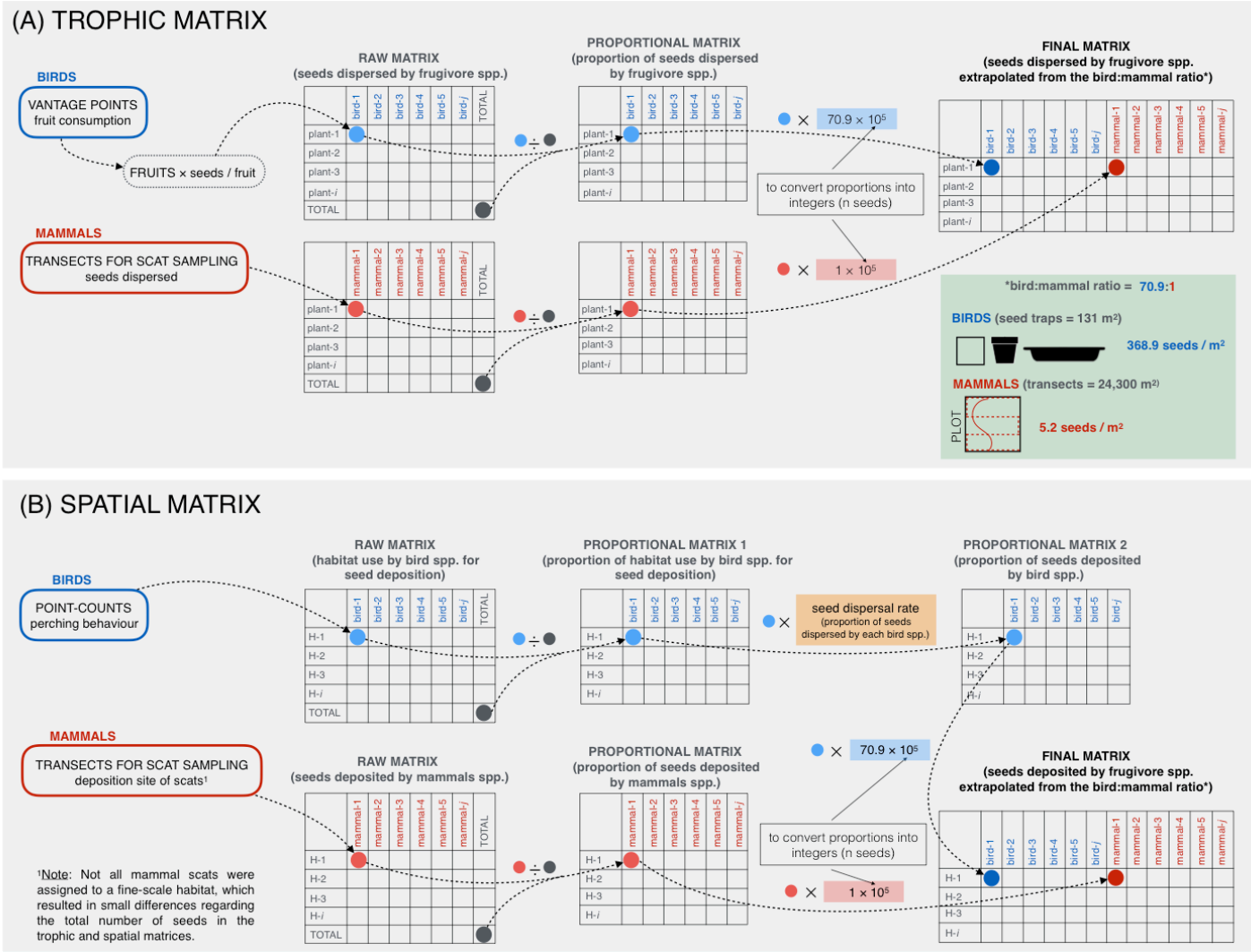


Table S4 Trophic interaction matrix, with plant species as rows and frugivores as columns. Matrix cells show the estimated number of seeds dispersed as a result of each interaction.

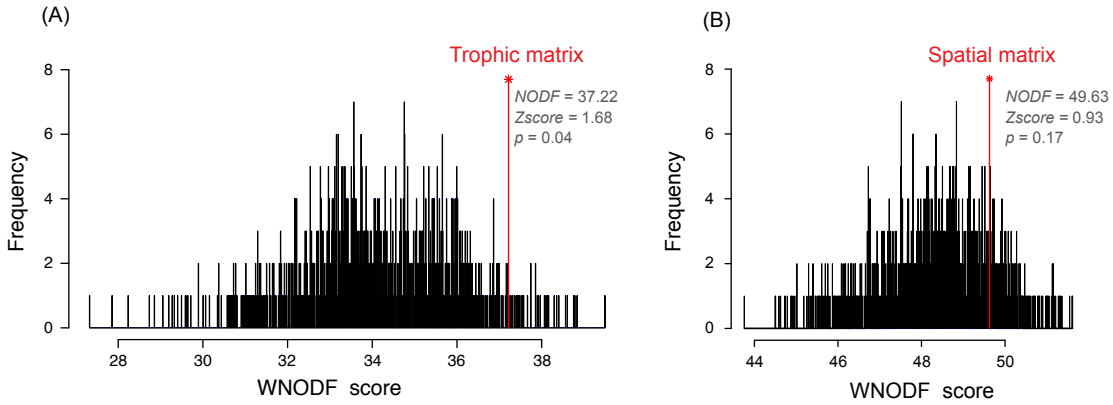
	Erithacus rubecula	*Garrulus glandarius*	*Phylloscopus* spp	*Sylvia atricapilla*	*Turdus iliacus*	*Turdus merula*	*Turdus philomelos*	*Turdus pilaris*	*Turdus torquatus*	*Turdus viscivorus*	*Canis* spp	*Capreolus capreolus*	*Cervus elaphus*	*Martes* spp	*Meles meles*	*Mustela* spp	*Sus scrofa*	*Vulpes vulpes*	TOTAL
Crataegus monogyna	39994	0	0	5516	332365	1441169	184801	81367	0	20687	0	2	136	23	116	0	14	319	2106509
Ilex aquifolium	4137	0	0	28961	1050881	1932132	165493	0	0	24824	0	6	6	12	2	0	2	2	3206458
Rubus fruticosus	20687	9654	0	103433	0	38615	16549	0	0	0	1066	101	444	8713	35029	0	13154	32108	279553
Sambucus nigra	12412	0	8275	318574	0	28961	0	0	0	0	0	0	1	0	2	0	0	0	368225
Sorbus aria	0	0	0	5516	0	71714	44131	0	44131	430282	0	0	2	34	7	0	0	98	595915
Sorbus aucuparia	4137	0	0	17928	0	358568	17928	0	0	4137	0	11	2	118	122	0	0	361	403312
Taxus baccata	2758	1379	0	9654	6896	64818	95159	6896	0	34478	0	0	0	148	660	0	0	32	222878
Malus sp.	0	0	0	0	0	0	0	0	0	0	11	0	1	2	7	0	0	24	45
Rosa sp.	0	0	0	0	0	0	0	0	0	0	0	0	4	2579	2415	12	0	1635	6645
Smilax aspera	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	3
Prunus avium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	458	0	0	1	459
TOTAL	84125	11033	8275	489582	1390142	3935977	524061	88263	44131	514408	1077	120	596	11630	38820	12	13170	34580	7190002

Table S5 Spatial matrix of seed deposition, with habitats as rows and frugivores as columns. Matrix cells show the estimated number of seeds dispersed per frugivore species in each fine-scale habitat.

	Erithacus rubecula	*Garrulus glandarius*	*Phylloscopus* spp	*Sylvia atricapilla*	*Turdus iliacus*	*Turdus merula*	*Turdus philomelos*	*Turdus pilaris*	*Turdus torquatus*	*Turdus viscivorus*	*Canis* spp	*Capreolus capreolus*	*Cervus elaphus*	*Martes* spp	*Meles meles*	*Mustela* spp	*Sus scrofa*	*Vulpes vulpes*	TOTAL
Fleshy – fruited shrub	922	0	0	4175	0	76716	0	0	0	0	0	13	0	0	178	0	0	78	82082
Fleshy – fruited tree	39148	121	202	44134	1122755	5202291	132788	1075	269	31332	0	23	128	1074	2346	0	12	2061	6579759
Non-fleshy-fruited tree	5739	134	60	5368	49110	167816	13406	0	0	25692	0	57	20	1841	3868	0	0	1830	274941
Heather	102	0	10	0	0	9589	1277	0	0	0	0	12	163	2249	5750	0	4073	6987	30212
Pasture	410	0	0	0	11854	134253	3830	0	0	627	1128	24	281	5970	25993	13	9715	21569	215667
Rock	0	0	0	0	0	4795	0	0	0	0	0	0	32	123	0	0	0	2388	7338
TOTAL	46321	255	272	53677	1183719	5595460	151301	1075	269	57651	1128	129	624	11257	38135	13	13800	34913	7189999

Appendix S3. Nestedness significance

Figure S3 Significance test for Nestedness under the CRT (Conserve Row Totals) null model implemented in *FALCON* (Beckett, Boulton, & Williams, 2014). (A) Trophic network; (B) Spatial network. Only the trophic network was significantly nested under this null model.



Reference

Beckett, S.J., Boulton, C.A., & Williams, H.T.P. (2014) FALCON: a software package for analysis of nestedness in bipartite networks. *F1000Research, 3*, 185. doi: 10.12688/f1000research.4831.1

Appendix S4. Piecewise structural equation modeling

Table S6 Piecewise SEM model specifications including distributions for response variables and R-squared values. Model types include generalized linear models (GLM) and linear models (LM). In the four piecewise SEMs (Fig. 4), we specified correlated error structures between the topological metrics (*z*, *c*, *ND* and *d'*) of both the trophic and the spatial network.

Response variable	Model	Distribution	Predictors	R^2
z – trophic	GLM	Gamma (link = log)	Abundance + Log(body mass)	0.02
z – spatial	GLM	Gamma (link = log)	Abundance + Log(body mass)	0.21
c – trophic	GLM	Gamma (link = log)	Abundance + Log(body mass)	0.54
c – spatial	GLM	Gamma (link = log)	Abundance + Log(body mass)	0.51
ND – trophic	LM	Gaussian	Abundance + Log(body mass)	0.30
ND – spatial	LM	Gaussian	Abundance + Log(body mass)	0.61
d' – trophic	LM	Gaussian	Abundance + Log(body mass)	0.33
d' – spatial	GLM	Gamma (link = log)	Abundance + Log(body mass)	0.78

Table S7 Piecewise SEM coefficients from each pathway (arrows) and correlated error structures (~~) associated to the four models shown in Fig. 4. Values in bold-italics are statistically significant ($p < 0.05$).

Piecewise SEM model	Path	Estimate	SE	*df*	*p* value
within-module degree (*z*)	*Abundance* → $z_{trophic}$	0.256	0.456	14	0.607
	Abundance → $z_{spatial}$	0.722	0.451	14	0.132
	Body mass → $z_{trophic}$	0.014	0.090	14	0.876
	Body mass → $z_{spatial}$	-0.029	0.084	14	0.734
	$z_{trophic}$ ~~ $z_{spatial}$	0.781	NA	17	***<0.001***
among-module connectivity (*c*)	*Abundance* → $c_{trophic}$	0.373	0.134	15	***0.014***
	Abundance → $c_{spatial}$	0.439	0.149	15	***0.010***
	Body mass → $c_{trophic}$	-0.059	0.025	15	***0.031***
	Body mass → $c_{spatial}$	-0.054	0.027	15	0.068
	$c_{trophic}$ ~~ $c_{spatial}$	0.023	NA	18	0.190
normalised degree (*ND*)	*Abundance* → $ND_{trophic}$	0.529	0.25	15	***0.050***
	Abundance → $ND_{spatial}$	0.869	0.187	15	***<0.001***
	Body mass → $ND_{trophic}$	0.074	0.046	15	0.125
	Body mass → $ND_{spatial}$	0.073	0.034	15	0.052
	$ND_{trophic}$ ~~ $ND_{spatial}$	0.776	NA	18	***<0.001***
Specialization (*d'*)	*Abundance* → $d'_{trophic}$	-0.425	0.157	15	***0.016***
	Abundance → $d'_{spatial}$	-2.623	0.826	15	***0.021***
	Body mass → $d'_{trophic}$	-0.004	0.029	15	0.894
	Body mass → $d'_{spatial}$	0.777	0.152	15	***<0.001***
	$d'_{trophic}$ ~~ $d'_{spatial}$	0.690	NA	18	***0.001***