Text S1. Detailed description of the methodology for the estimation of the abundance and the richness of thrushes

The estimation of the abundance of different species of thrushes was based on direct observations of thrushes entering different sampling cells. Observations were made from five stations in different vantage positions in elevated outcrops (hill tops), located along the central axis of the plot (Fig. S1). Sampling season extended from October 2009 to February 2010, and accounted for a cumulative observation time of 105 h. This observation time was allocated between stations across the sampling season in a balanced number of 1-h observation periods (i.e. 1-h periods were assigned to the different stations in order to achieve similar times of cumulative observation between stations).

In each observation period, one well-trained observer counted and identified, at the species level, all thrushes seen (or heard) in different sectors of the surveyed area. The six species of thrushes under study are distinguishable from each other by their different plumage (figure S1) and/or song patterns. Due to the elevated location of vantage positions (ca. 70 m difference in elevation from the lowest point of the plot) and the open structure of forest cover in almost all the plot (most forest patches are small, with low canopy density, and very scattered; figure S1), the observer achieved high visual detectability of birds (with the help of high-quality 8x30 binoculars) in almost all plot cells, even those furthest away (ca. 200 m) from vantage positions. High acoustic detectability was also achieved, as the alarm or flocking songs of thrushes are loud and easily distinguishable, both between species and from background noise. Moreover, during the sampling season (fall-winter), thrushes do not show territorial behaviors, and all species show similar foraging behavior patterns: they move frequently from one perch to another, searching for food. Territorial calls

are, thus, mostly absent, and songs are associated with alarm or flocking behaviors and are evident for all species. Therefore, differences between species in terms of visual or acoustic detectability are considered negligible.

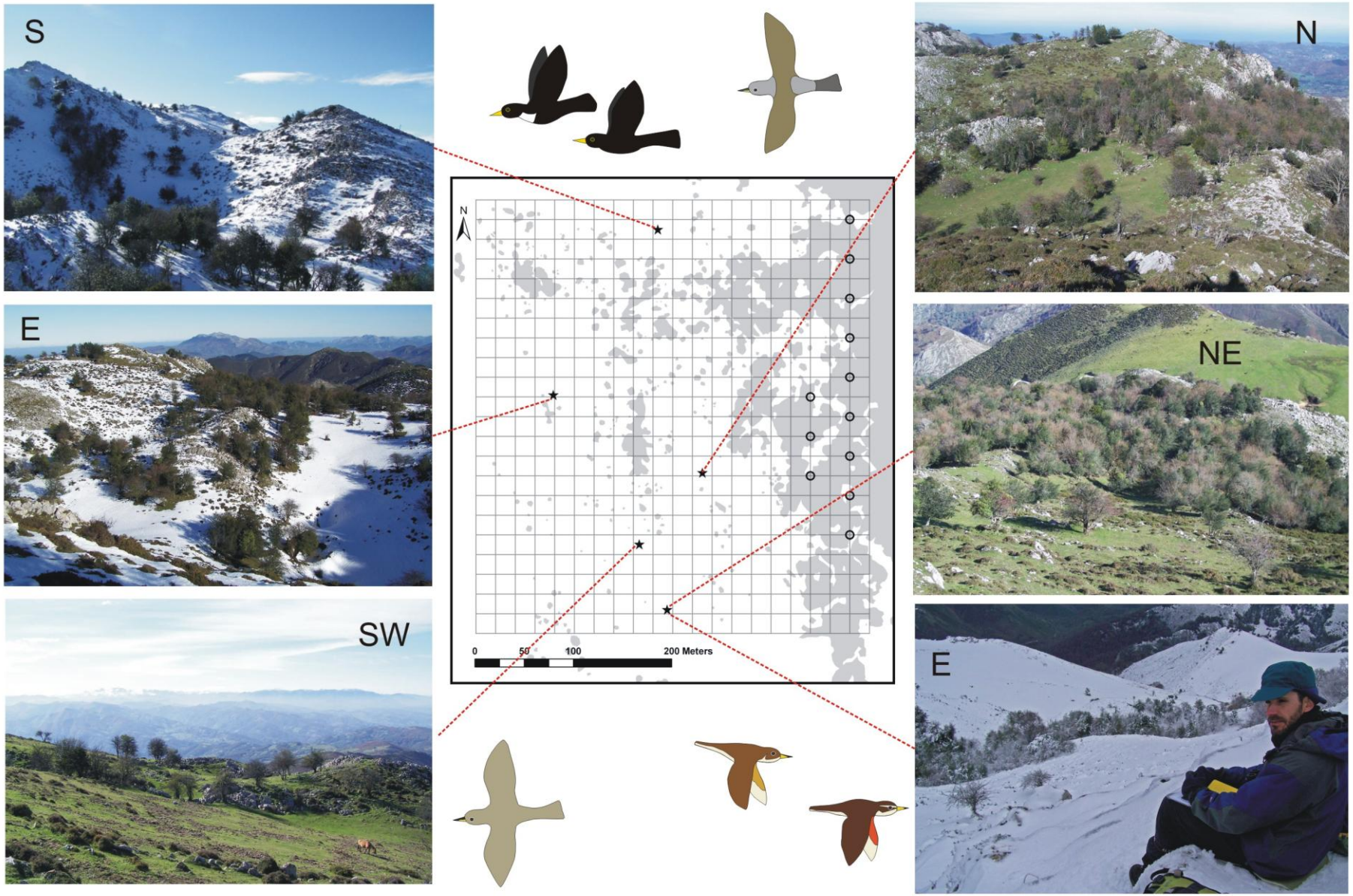
Although the detectability of birds from vantage positions was high across almost the entire plot, it decreased sharply in the easternmost sector of the plot, due to the larger size of forest patches, the denser forest canopy and a small-scale topographical effect (abrupt slope) in the area (figure S1). Therefore, complementary bird observation was accomplished in this sector from positions within the forest. Twelve forest point-count positions were established, each one corresponding to the center of a group of four cells (figure S1). Observations were made based on 10 min periods, recording any thrush heard or seen within the four surrounding cells. The total observation time from each point count was 110 minutes. No differences in bird detectability between vantage positions and point-count positions were evidenced.

Bird sightings were assigned to the different geo-referenced sampling cells covered from each vantage or point-count position, with the help of printed maps. In some cases, the consecutive sightings of a given species could have corresponded to the same individuals remaining within, or repeatedly entering a given cell. In these doubtful cases, we considered as independent those sightings separated by at least five minutes. Also, those sightings potentially corresponding to a given individual bird in different cells -or in the same cell on different days- were considered to be as valid as those from different individuals.

Rather than assessing the actual size of bird populations, our goal was to provide a measure of bird abundance in functional terms, i.e. an estimation of the total activity of frugivorous thrushes across the season in the study plot. For this, we calculated the abundance of birds per cell as the cumulative number of birds heard or

seen in each cell through the season, for both each bird species and all species together. We divided the cumulative number of birds by the total observation time for each cell, calculating the number of birds per 10-h of observation. Weighting by total observation time per cell enabled the comparison of abundance between cells, correcting for overestimation in those cells observed from different positions and thus accounting for longer observation times.

Figure S1. Scheme of the study plot (central panel) representing the configuration of the forest cover (gray area), the plot subdivision into 20x20 m sampling cells, and the vantage (black stars) and point-count (circles) positions for bird observation. Pictures represent detailed views of different sectors of the study plot captured from different vantage positions (each view is linked to the corresponding vantage position by a dotted red line, letters inside pictures indicate the orientation of the view, e.g. S = southwards; photo credits by Daniel Martínez). The different species of thrushes are also illustrated (upper row: *Turdus torquatus*, *T. merula*, *T. pilaris*; lower row: *T. viscivorus*, *T. philomelos*, *T. iliacus*; artwork by Daniel Martínez).


S
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200 Meters

Text S2: Frugivore assemblage composition analyses

To search for major trends of variability in the composition of the assemblage of frugivorous thrushes across the studied landscape, we used a non-metric multidimensional scaling analysis (NMDS [1]). NMDS is an iterative search for the ranking and placement of n entities (samples) in k dimensions (ordination axes) that minimizes the stress of the k-dimensional configuration. The ‘‘stress’’ value is a measure of departure from monotonicity in the relationship between the dissimilarity (distance) in the original p-dimensional space and in the reduced k-dimensional ordination space. NMDS is therefore used to find the configuration in a given number of dimensions which preserves rank-order dissimilarities in species composition as closely as possible, such that distance along an NMDS axis corresponds to relative difference in community composition. In our case, the original sample was composed of the log-transformed average abundances of the six different thrush species in each of the 110 sampled blocks. NMDS analysis was performed with the Ginkgo software ([2,3]; available at http://biodiver.bio.ub.es/ginkgo/).

A matrix of Bray-Curtis dissimilarities between all 110 blocks was calculated and subjected to NMDS. A minimum stress value of 0.059 was achieved from 44 random starts in two dimensions. NMDS also calculated PCA rotated axes (NMDS1 and NMDS2) that provided scores for each sampled block. Despite the low stress value (probably derived from the small number of species), these NMDS score vectors were considered to represent gradients in the composition of the frugivore guild across the whole studied landscape, with similar score values representing similar composition in frugivore assemblage (figure S2).

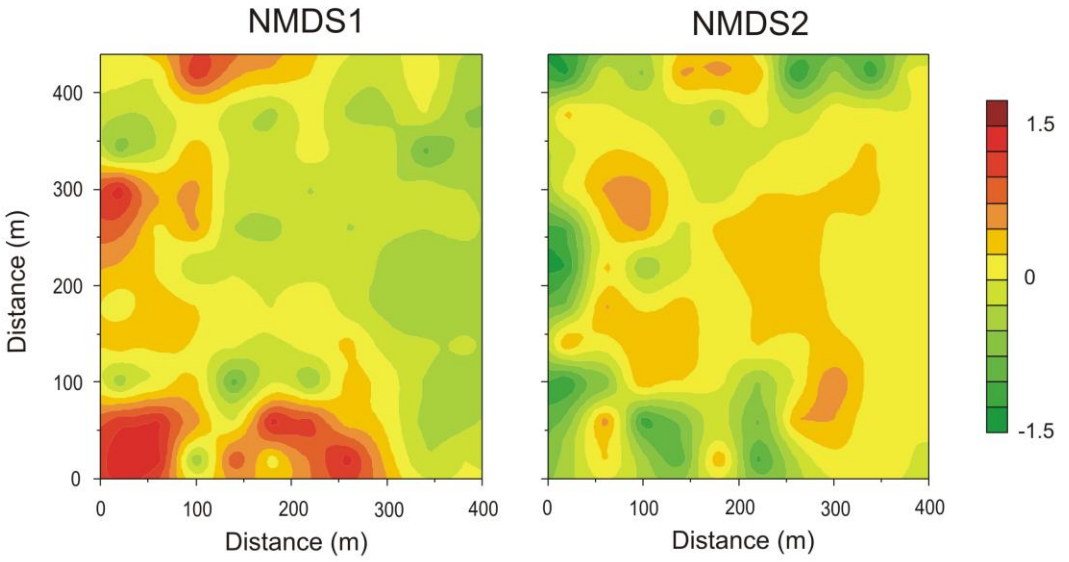
References:

1. Quinn, G. P. & Keough, M. J. 2002 *Experimental design and data analysis for biologist*. Cambridge University Press, Cambridge.

2. Bouxin, G. 2005 Ginkgo, a multivariate analysis package. *J. Veg. Sci.* **16**, 353-359

3. De Cáceres, M., Oliva, F., Font, X. & Vives, S. 2007 Ginkgo, a program for non-standard multivariate fuzzy analysis. *Adv. Fuzzy Sets Syst.* **2**, 41-56.

Figure S2. Distribution of the scores of PCA-rotated axes (NMDS1 and NMDS2) of the non-metric multidimensional scale analysis on the log-abundances of the six different species of frugivorous thrushes (*Turdus* spp.) across the study plot. Colored contours are interpolated from the values of the corresponding variable in the centroid of each 40x40 m block of the plot. The color scales are shown.



Text S3. Dutilleul's method for correction of spatial autocorrelation constraints

The Dutilleul's method [1,2] is a procedure to correct the degree of significance of the coefficients of correlation between spatially autocorrelated variables. Spatial autocorrelation in ecological data constrains statistical inference by causing pseudo-replication among samples and hence increasing the probability of Type-I error [2]. The effects of autocorrelation are equivalent to a reduction of the effective sample size from an original pool of observations involved in a given statistical test. Therefore, the estimated degree of spatial autocorrelation can be used to determine how much smaller the effective sample size is than the number of original observations. By taking into account spatial autocorrelation, the Dutilleul's method provides a modified t-test for assessing the degree of correlation between two spatially explicit variables, and it estimates a corrected number of degrees of freedom from which to re-calculate the degree of significance of original correlation coefficients between the two variables.

References

1. Dutilleul, P. 1993 Modifying the t test for assessing the correlation between two spatial processes. *Biometrics* **49**, 305-314.

2. Legendre, P., Dale, M., Fortin, M.-J., Gurevitch, J., Hohn, M. & Myers, D. 2002 The consequences of spatial structure for the design and analysis of ecological field surveys. *Ecography* **25**, 601-515.

Table S3. Correlations among the different attributes of the assemblage of frugivorous thrushes, between assemblage attributes and the different components of seed dispersal, and between assemblage attributes or seed dispersal components and the proportion of forest cover. Pearson correlation coefficients and their significance degree, corrected by Dutilleul's method, are shown (n. s. = $p > 0.05$, * = $p < 0.05$, ** = = $p < 0.01$, *** = $p < 0.001$).

	Abundance of thrushes (log)	NMDS1	NMDS2	Richness of thrushes	Forest cover (arcsin sqrt)	n
Abundance of thrushes (log)	-	-0.58 ***	0.24 n. s.	0.76 ***	0.79 ***	110
NMDS1	-	-	-0.13 n. s.	-0.62 ***	-0.55 **	110
NMDS2	-	-	-	0.33 *	0.16 n. s.	110
Richness of thrushes	-	-	-	-	0.74 ***	
Abundance of seeds (log)	0.76 ***	-0.51 *	0.16 n. s.	0.74 ***	0.82 ***	110
Richness of seeds (log)	0.75 ***	-0.55 **	0.15 n. s.	0.74 ***	0.84 ***	110
Seed arrival rate (arcsin sqrt)	0.72 ***	-0.54 **	0.21 n. s.	0.74 ***	0.83 **	110
Seed colonization rate (arcsin sqrt)	0.54 **	-0.37 *	0.20 n. s.	0.58 **	0.48 *	86

Table S4. Summary of the spatial simultaneous autoregressive models (SAR) considering, as predictor variables, the components of the frugivore assemblage, and, as response variables, quantitative and qualitative components of seed dispersal. These models have been run with a sample size (n = 86 blocks) equivalent to that of the model corresponding to seed colonization rate in the main text. The total variance explained by the predictors (r^2), the degree of significance of the whole model (*F*-value based), the value of the un-standardized (±SE) and standardized regression coefficient of each predictor, and their degree of significance (*t*-value based), are also shown.

Abundance of seeds (log)				
Model	$r^2 = 0.60$		$F = 30.27$	$p < 0.001$
Predictor	SAR Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Bird abundance (log)	0.90±0.18	0.54	4.90	< 0.001
NMDS 1	0.23±0.19	0.10	1.19	0.23
NMDS 2	-0.21±0.16	-0.10	-1.33	0.18
Bird richness	0.25±0.09	0.32	2.69	0.009
Richness of seeds (log)				
Model	$r^2 = 0.56$		$F = 25.30$	$p < 0.001$
Predictor	SAR Coeff (±SE)	Stand. Coeff.	*t*	*p*
Bird abundance (log)	0.11±0.04	0.34	3.07	0.003
NMDS 1	0.01±0.04	0.01	0.15	0.88
NMDS 2	-0.04±0.03	-0.09	-1.27	0.21
Bird richness	0.06±0.01	0.34	3.48	< 0.001
Seed arrival rate (arcsin sqrt)				
Model	$r^2 = 0.55$		$F = 25.06$	$p < 0.001$
Predictor	SAR Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Bird abundance (log)	0.13±0.05	0.28	2.56	0.012
NMDS 1	0.02±0.05	0.03	0.37	0.708
NMDS 2	-0.02±0.04	-0.04	-0.52	0.607
Bird richness	0.10±0.03	0.48	3.91	< 0.001

Table S5. Summary of the spatial simultaneous autoregressive models (SAR) considering, as predictor variables, forest cover and the components of the frugivore assemblage and, as response variables, quantitative and qualitative components of seed dispersal. The total variance explained by the predictors (r^2), the degree of significance of the whole model (*F*-value based), the value of the un-standardized (±SE) and standardized regression coefficient of each predictor, and their degree of significance (*t*-value based), are also shown.

Abundance of seeds (log)				
Model	$r^2 = 0.73$	n = 110	$F = 56.38$	$p < 0.001$
Predictor	Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Forest cover (arcsin sqrt)	1.83±0.35	0.49	5.19	< 0.001
Abundance of thrushes (log)	0.34±0.15	0.21	2.25	0.03
NMDS 1	0.18±0.20	0.06	0.88	0.38
NMDS 2	-0.24±0.17	-0.07	-1.36	0.18
Richness of thrushes	0.20±0.09	0.22	2.26	0.03

Richness of seeds (log)				
Model	$r^2 = 0.77$	n = 110	$F = 69.18$	$p < 0.001$
Predictor	Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Forest cover (arcsin sqrt)	0.45±0.07	0.60	6.89	< 0.001
Abundance of thrushes (log)	0.04±0.03	0.12	1.42	0.16
NMDS 1	-0.02±0.04	-0.04	-0.61	0.54
NMDS 2	-0.02±0.03	-0.04	-0.76	0.45
Richness of thrushes	0.03±0.01	0.14	1.99	0.05

Seed arrival rate (arcsin sqrt)				
Model	$r^2 = 0.71$	n = 110	$F = 51.31$	$p < 0.001$
Predictor	Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Forest cover (arcsin sqrt)	0.54±0.09	0.56	5.91	< 0.001
Abundance of thrushes (log)	0.03±0.04	0.06	0.66	0.51
NMDS 1	-0.02±0.05	-0.02	-0.30	0.76
NMDS 2	-0.00±0.05	-0.00	-0.03	0.97
Richness of thrushes	0.04±0.01	0.18	2.12	0.02

Seed colonization rate (arcsin sqrt)				
Model	$r^2 = 0.36$	n = 86	$F = 9.86$	$p < 0.001$
Predictor	Coeff. (±SE)	Stand. Coeff.	*t*	*p*
Forest cover (arcsin sqrt)	0.05±0.18	0.03	0.25	0.80
Abundance of thrushes (log)	0.06±0.06	0.15	1.05	0.29
NMDS 1	-0.00±0.06	-0.00	-0.07	0.95
NMDS 2	0.02±0.05	0.03	0.38	0.71
Richness of thrushes	0.08±0.03	0.40	2.62	0.01

Table S6. Correlations between the abundance (log-transformed) of different species of frugivorous thrushes and the different variables representing the quantitative and qualitative components of seed dispersal. Pearson correlation coefficients and their degree of significance, corrected by Dutilleul's method, are shown (n = 110; n. s. = $p > 0.05$, * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$).

	Abundance of seeds (log)	Richness of seeds (log)	Seed arrival rate (arcsin sqrt)	Seed colonization rate (arcsin sqrt)
T. iliacus	0.69 **	0.69 **	0.66 **	0.44 *
T. merula	0.59 ***	0.57 ***	0.55 ***	0.42 **
T. philomelos	0.46 *	0.51 **	0.42 *	0.28 *
T. pilaris	0.18 n. s.	0.23 n. s.	0.21 n. s.	0.15 n. s.
T. torquatus	0.37 **	0.36 *	0.28 *	0.17 n. s.
T. viscivorus	0.48 **	0.47 *	0.43 *	0.27 *