Supporting Information

Appendix 1 – *Details of field data collection*

The environmental variables were sampled in a grid of 440, 20 x 20 m cells (Fig. S1), which is an appropriate combination of grain and extent sizes to represent the spatial scale at which frugivory and seed dispersal by thrushes operate (García and Chacoff 2007; García et al. 2011). In fact, the scale of our grid was used to parameterize the activity of each bird species (see Appendix 2 and Morales et al. 2013).

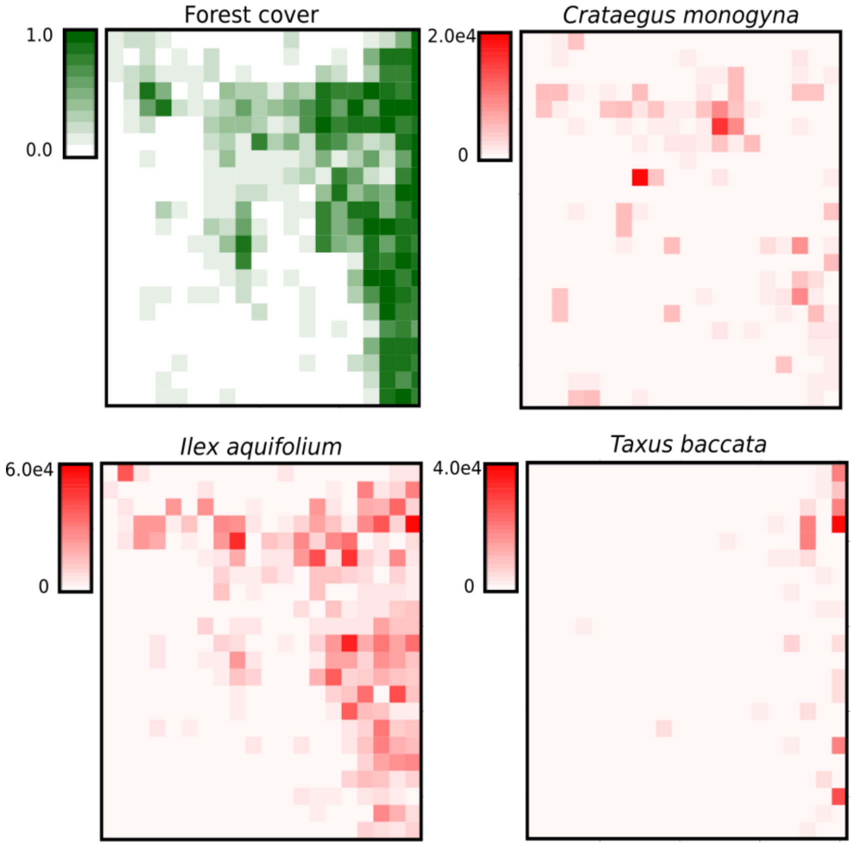

Fig. S1 – Location of the study site with its associated forest cover, and fruit production of *C. monogyna*, *I. aquifolium* and *T. baccata*. The proportion forest cover per cell was based on a 1:5000-scale ortophoto image whereas fruit abundance was sampled during the 2009 fruiting season. Green and red hues represent the proportion of forest cover and total number of fruits, respectively. Note the scale differences between species.

Forest cover and fruit abundance. We developed a Geographical Information System (GIS, ArcGIS 9.3) based on a recent (2011) 1:5000-scale ortophotomap image of the study plot. The GIS platform incorporated a grid of 440 20 x 20 m cells as well as a layer of digitized forest cover. In each cell we estimated from GIS the amount of forest cover (in m^2, and irrespective of tree species identity). At the beginning of the 2009 fruiting season (September) we also sampled visually the standing crop of each tree of any fleshy-fruited species by means of a semi-quantitative Fruiting Abundance Index (FAI; considering six intervals: 0 = without fruits; 1 = 1-10 fruits; 2 = 11-100; 3 = 101-1,000; 4 = 1,001-10,000; 5 $\geq$ 10,001; Saracco et al. 2004). We incorporated into the GIS platform position, species and FAI of each individual tree. We calculated the abundance of fruits of different tree species as the sum of the crops of all fruiting trees. Crops were extrapolated from FAI ranks, taking into account the fit between the crop size of a sub-sample of trees and the assigned FAI index, by following an allometric equation ($\textit{crop size} = 1.77 \times e^{1.92 FAI}$; $R^2 = 0.80$; n = 136 trees, Herrera et al. 2011).

Density and richness of birds. From October to February of 2009 we performed direct observations of thrushes in our study plot from five vantage positions in elevated outcrops, and 12 point-count positions within forest patches (Fig. S2). For each individual bird we recorded the species and sampling cell in which it was observed. Due to avoid species-area constraints measuring richness indexes, we combined the data corresponding to each four adjacent cells, and that resulted into 110 40 x 40 blocks (Fig. S2). Total observation time was 270 hours. For further information about this methodology, see García et al. (2013), García and Martínez (2012) and Morales et al. (2013).

Seed rain. In 2009 we monitored the occurrence of seeds dispersed by thrushes in sampling stations across the whole plot. We placed ten sampling stations (separated from each other by 2 m) along the central longitudinal axis of 220 sampling cells (20 x 20 m), and following a checkerboard design (see García and Martínez, 2012). In each station we set up a permanently labeled, open-ground 50 x 50 cm quadrat where all seeds dispersed by birds were collected and counted. Each sampling station was assigned to covered (tree canopy) or open (pasture, rock) microhabitats, corresponding to the structural features of the area covered by (or above) the quadrat. In each sampling station we estimated the number of dispersed seeds per tree species as the sum of seeds found in two consecutive surveys (late November 2009 and early January 2010). For each sampling cell we calculated (a) the seed density and (b) the seed richness as the average number of seeds and plant species, respectively. Furthermore, we also calculated (c) the seed density in open habitat, defined as the seed density of sampling stations in open divided by the per-block percentage of open habitat (see Fig S2).

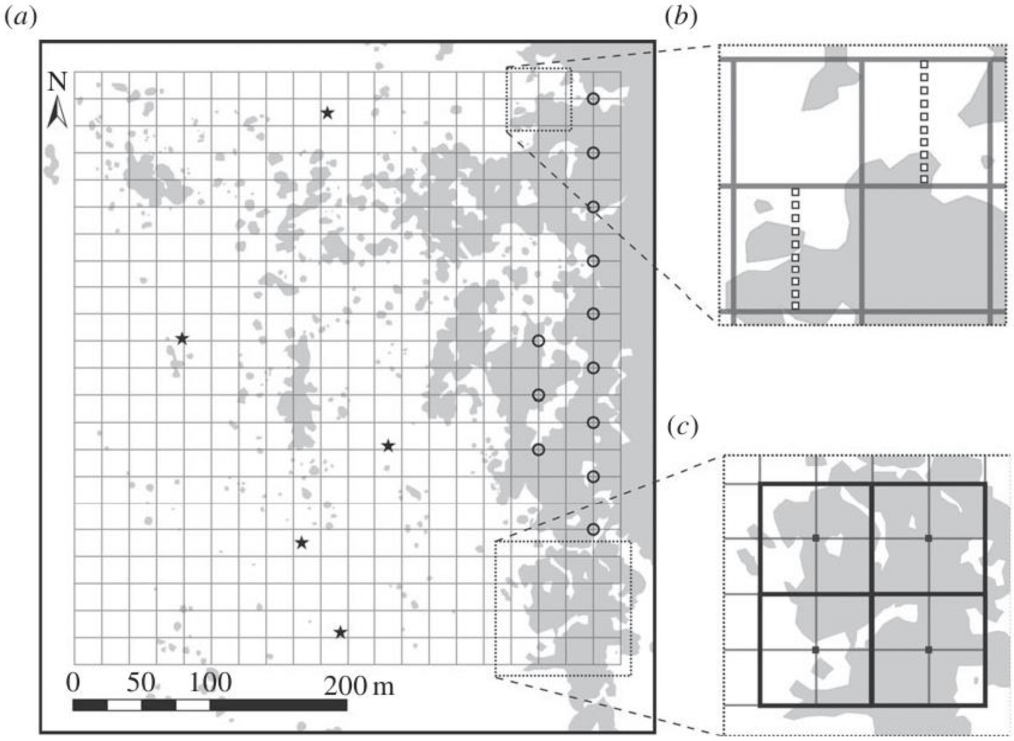

Fig. S2 – Scheme of the study plot representing: (a) the configuration of the forest cover (grey area), the plot subdivision into 20 x 20m sampling cells, and the vantage (black stars) and point-count (circles) positions for bird observation; (b) a detail of the position of the sampling stations (white quadrats) along the central longitudinal axis of cells, following a chess-board design; and (c) a detail of four of the 40 x 40 m blocks (squares outlined in black and showing a black- dotted centroid) used to combine the data corresponding to each group of four adjacent sampling cells.

Movement patterns of birds. We recorded the activity of thrushes over observation sequences from the above-defined vantage positions during October to February of 2007 – 9 (see Fig. S2). For each bird movement we visually tracked its bouts with binoculars and printed maps of plot cells. During bird activity we calculated (a) the flight distance of each movement bout (i.e. euclidean distance between the centroids of the starting and the ending cells; see Fig. 1), (b) the perching/landing habitat [i.e. tree canopy (forest) vs. tree uncovered pasture or rock (open)], and (c) the number and species of fruits consumed. Birds were followed until lost, that is when the individual bird left the plot or disappeared into the canopy.

REFERENCES

García, D. and Chacoff, N.P. 2007. Scale-dependent effects of habitat fragmentation on hawthorn pollination, frugivory, and seed predation. -Conservation Biology. 21: 400–411.

García, D. and Martínez, D. 2012. Species richness matters for the quality of ecosystem services: a test using seed dispersal by frugivorous birds. -Proceedings of the Royal Society of London B. 279: 3106-3013.

García, D. et al. 2013. Functional heterogeneity in a plant-frugivore assemblage enhances seed dispersal resilience to habitat loss. -Ecography. 36: 197-208.

García, D. et al. 2011. The spatial scale of plant–animal interactions: effects of resource availability and habitat structure. -Ecological Monographs. 81: 103–121.

Herrera, J.M. et al. 2011. Regional vs local effects of habitat loss and fragmentation on two plant-animal interactions. -Ecography. 34. 606–615.

Morales, J.M. et al. 2013. Frugivore behavioural details matter for seed dispersal: a multi-species model for Cantabrian thrushes and trees. -Plos ONE. 6:e65216.

Saracco, J.F. et al. 2004. How do frugivores track resources? Insights from spatial analyses of bird foraging in a tropical forest. -Oecologia. 139: 235–245.

Supporting Information

Appendix 2 – *Model details and parameterizations*

In order to assess the relative contribution of each bird species to the total seed rain, Morales et al. (2013) fitted bird trajectories using decision-based probabilities fitted to observational data in a grid-based landscape (see *Study site* and Fig. 1). Model included various mechanistic rules which simulate (a) Residence time, fruit consumption and gut passage time, (b) Bird movement and (c) Habitat deposition of seeds, with the aim to simulate the spatial-explicit seed deposition as the interplay between bird activity and habitat structure. Rules were parameterized for each one of the six species of thrushes. Thus simulations generate values of spatially-explicit seed rain (belonging to different dispersed fleshy-fruited tree and bird disperser species), and seed dispersal distance (distance between source and deposition cells).

The calculations described below (i.e. eq. 1, 2 and 3) are used first to estimate parameters from observed data (computing likelihood functions), and later-on to compute probability density distributions with the aim to generate mechanistic rules of bird activity with the previously fitted parameter values (see Fig. S3). To obtain maximum-likelihood estimates of each parameter, we minimized the negative log-likelihood using the Nelder-Mead algorithm (Nelder & Mead 1965) with several overdispersed starting points with the *bbmle* library (Bolker & R Development Core Team 2014). The model was implemented in R statistical language (R Development Core Team 2014). Below we describe the general simulation procedure and how we parameterize mechanistic rules.

a) Residence time, fruit consumption and gut passage time

Every time a simulated bird arrives to a landscape cell, it spends there an amount of time drawn from a Gamma distribution fitted to the observed perching time for each species (i.e. shape parameter: 0.569 to 1.472; scale parameter: 0.269 to 1.114; range of species-based estimates based on observed data). Bird resident time in a given cell (perching time) is independent of fruit consumption (there is no previous evidence about this; Morales et al. 2013) and the decisions by the simulated birds (i.e. stay or leave to a new landscape cell) are made once perching time expired.

Frugivory events depend on both fruit availability at the cell and observed fruit consumption rates (García et al. 2013). To model fruit consumptions we consider both observed consumption rates and fruit availability at the landscape cell. Simulated birds potentially consumed fruits drawn from a zero-inflated Poisson distribution fitted to the observed number of fruits consumed by each bird species (i.e. Probability of fruit consumption: 0.335 to 0.531; Average number of fruits per feeding bout: 5.145 to 6.560; range of species-based estimates based on observed data). Simulated birds do not have built-in preferences for fruit species, and so plant species identity depends on fruit species abundance at the landscape cell (Morales et al 2013). If the potentially consumed fruits are higher than the number available in the landscape cell, simulated birds consume the minimum between above-mentioned values.

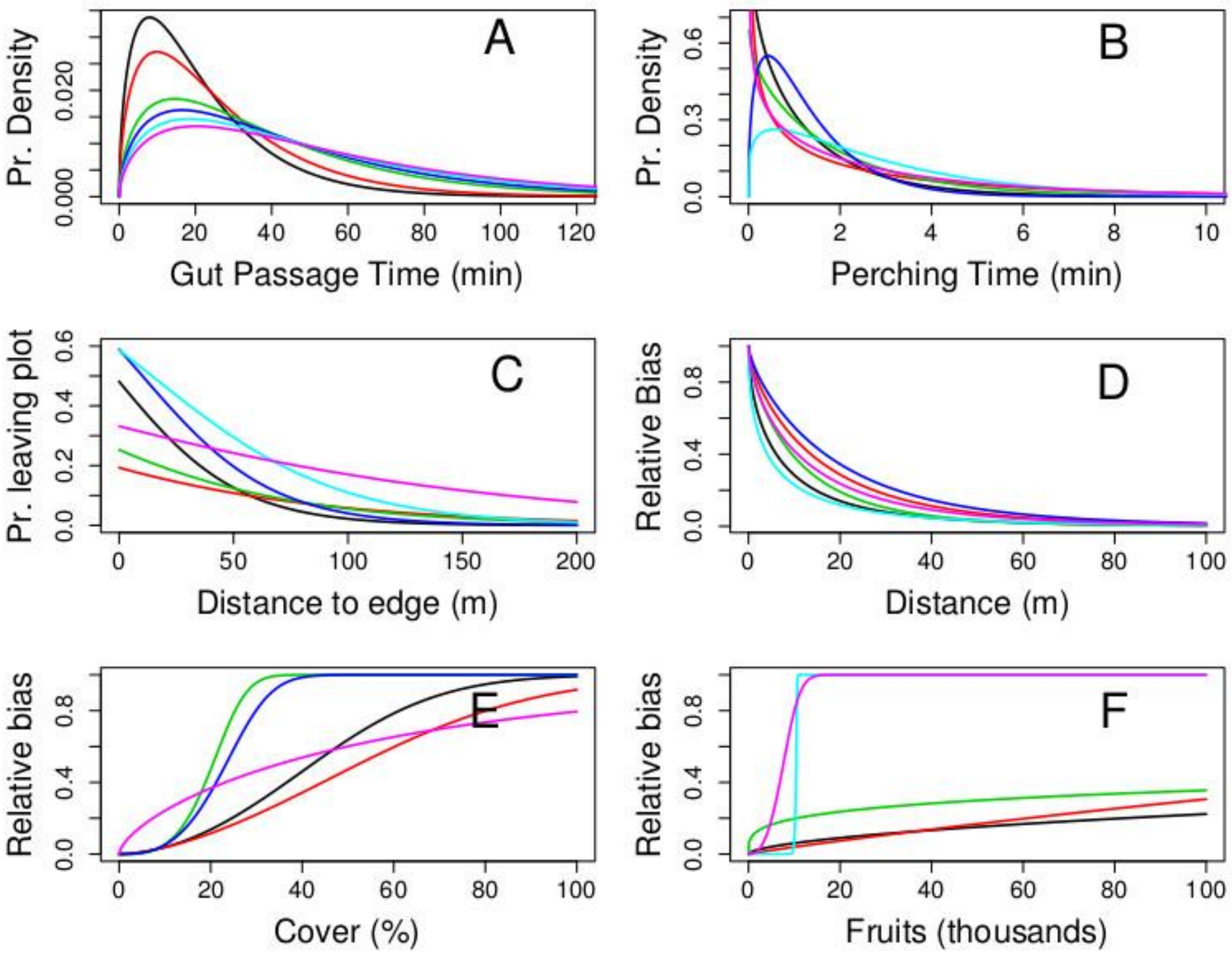

Fig. S3 – Mechanistic functions fitted describing the residence time, gut passage time and bird movement for each *Turdus* species. (A) Gut passage time follows a Gamma distribution with scale parameter related to bird size. (B) Perching time is Gamma distributed and fitted to data from direct observations. (C) The probability of leaving the study plot decreased with distance to the plot edge. (D) Movement to a landscape cell decreased with distance from source cell. (E, F) Movement bias increased with forest cover and with fruit abundance. The *Turdus* species are: *T. iliacus* (black), *T. philomelos* (red), *T. merula* (green), *T. pilaris* (blue), *T. torquatus* (cyan) and *T. viscivorus* (magenta). No effect of fruit abundance was found for *T. pilaris* and no effect of cover for *T. torquatus*.

Once a frugivore event occurs, ingested seeds spend a gut-passage time (GPT) inside simulated birds. GPTs distributions were fitted to empirical data based on experimental retention times of 18 hand-raised and wild captive birds of *Turdus merula* (M. Sobral, A.R. Larrinaga & L. Santamaría unpublished data). GPTs were drawn from a Gamma distribution with a common shape parameter (i.e. 1.59), but with a bird species-specific scale parameter (i.e. 0.029 to 0.074) based on the relationship between the *Turdus* body size and GPT using 8 species from Turdidae and Silvidae (Herrera 1984; see Morales et al. 2013).

b) Bird movement

When the perching time expires, the movements of simulated birds depend on three main factors, namely (i) stay in the same landscape cell, (ii) move to a new cell, or (iii) leave the study plot. First, model computes the probability to leave the study plot (v) based on the distance to the nearest plot border (B):

$$logit\ (v) = a_0 + b_0 B \quad (1)$$

where a_0 and b_0 are parameters fitted to each bird species based on observed data. Second, if simulated birds decide to stay in the plot, three factors affect its decision, namely (i) distance from the current to the destination cell, (ii) proportion of forest cover, and (iii) the number of fruits at the destination cell. With all these factors, model computed a discrete probability distribution based on hyperbolic tangent functions [tanh (x)] as follows:

$$\begin{aligned} d_i &= 1 - \tanh\left(\left(\delta_{ij}/a_d\right)^{b_d}\right) \\ c_i &= \tanh\left(\left(\mathrm{cover}_i/a_c\right)^{b_c}\right) \\ f_i &= \tanh\left(\left(\mathrm{fruit}/a_f\right)^{b_f}\right) \qquad (2) \\ \mathbf{k} &= \frac{[\mathbf{d} \otimes \mathbf{c} \otimes \mathbf{f}]}{\sum [\mathbf{d} \otimes \mathbf{c} \otimes \mathbf{f}]} \end{aligned}$$

where the scale (i.e. a_d, a_c and a_f) and shape parameters (i.e. b_d, b_c and b_f) control the shape of the probability along factors; above-mentioned scale and shape parameters were estimated for each bird species based on observed bird trajectories, forest cover and fruit abundances (Morales et al. 2013). The vectors **d**, **c** and **f** hold the probability of choosing the *i*-th landscape cell given the distance to current location (*d*), forest cover (*c*) and fruit abundance (*f*), and they are multiplied to get a discrete probability vector **k** to choose landscape cells. Once a simulated bird decided where to go, it flew at a speed of 6 m per second following a straight line to and from perches.

c) Microhabitat deposition of seeds

Apart from the above-described procedures, we implement here two mechanistic processes in the current version. First, we include the number of seeds per dropping and fleshy-fruited species based on counts of seeds in bird droppings in our study site (Martínez et al. 2008). For each simulated track birds defecate monospecific droppings (87.6% droppings had one species; Martínez et al. 2008), with a number of seeds drawn from a random Poisson distribution, and a mean value depending on each fleshy-fruited species (namely, *C. monogyna*: 2.1 ± 1.1, *I. aquifolium* 3.4 ± 1.8, and *T. baccata*: 2.1 ± 1.8; mean ± SD; Martínez et al. 2008). Second, we assume within-cell habitat seed deposition depended on the proportion of bird observations perching in forest cover and open habitats. For each simulated track, birds defecate in each habitat (i.e. forest vs. open habitats) depending on (1) the foraging activity (based on fruit consumption and movement in the landscape) and (2) the proportion of forest cover per cell (Fig. 1). The probability of seed defecation (*k*) along the proportion of forest cover (*C*) follows:

$$logit\,(k) = a_0 + b_0C \quad (3)$$

where a_0 and b_0 are parameters fitted to each bird species based on observed data. Both the probability distributions related to bird movement decisions (see Fig. 1) and to the within-cell habitat of defecation (eq. 3) are simulated to generate the seed rain with the fitted parameter values.

Here we show the results of the species parameterization at habitat perching, which describes the probability of perching based on the proportion of forest cover per cell (Table S1). Bird species reacted differently to the proportion of forest cover (Fig. S3). For the most abundant *T. iliacus* and *T. merula*, they preferentially perch in forest even with high low proportions of forest cover. For *T. viscivorus*, *T. pilaris* and *T. torquatus*, by contrast, they have high probability to perch in open when the forest proportion is low. *T. philomelos* preferentially perch in forest but it had low probabilities in open when the proportion of forest cover was < 0.2 (Fig. S4).

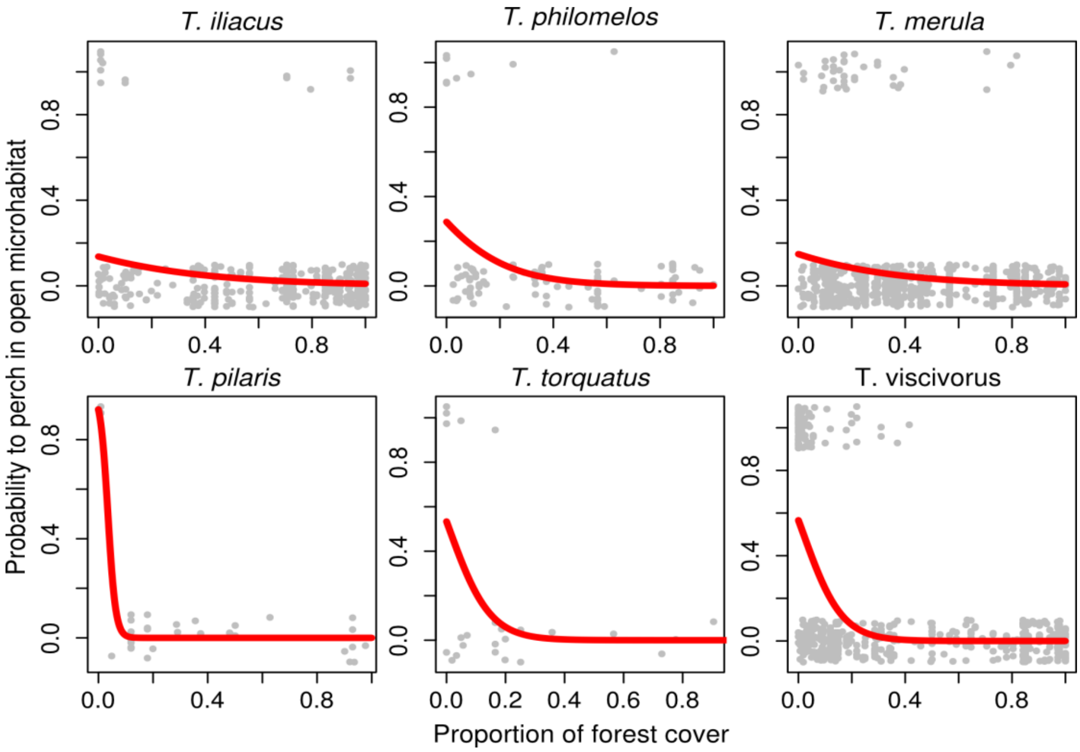

Fig. S4 – Functions fitting the probability of perching in open habitat based on the proportion of forest cover per cell. For each species model functions were logit distributed and fitted to field data. Observed values are in grey dots, whereas fitted functions are plotted in red lines. During simulations, fitted functions were sampled in order to simulate bird perching in each microhabitat with the fitted parameter values (Table S1).

Table S1. Parameters with ± SE (in parenthesis) for logit distributions of the probability of perch in open habitat depending on the proportion of forest cover per cell. The calculations described in eq. (3) were used to compute likelihood functions to estimate parameters from observed within-cell perching habitats.

	Intercept (a0)	**Scale (b0)**	**Expected (median)**	**N**
T. iliacus	-1.843(0.424)	-2.810(0.888)	0.0200	343
T. philomelos	-0.911(0.496)	-6.281(2.689)	0.0408	101
T. merula	-1.748(0.284)	-3.216(0.898)	0.0526	635
T. pilaris	2.472(1.943)	-70.93(51.77)	4.250e-06	32
T. torquatus	0.1360(0.758)	-14.49(8.450)	0.0947	24
T. viscivorus	0.267(0.196)	-13.83(2.210)	0.0614	478

REFERENCES

Bolker B. and R Development Core Team 2014. bbmle: Tools for general maximum likelihood estimation. -R package version 1.0.17. http://CRAN.R-project.org/package=bbmle

García, D. et al. 2013. Functional heterogeneity in a plant-frugivore assemblage enhances seed dispersal resilience to habitat loss. -Ecography. 36: 197–208.

Herrera, C.M.1984. Adaptation to frugivory of Mediterranean avian seed dispersers. -Ecology 65: 609-617.

Martínez, I. et al. 2008. Differential seed dispersal patterns generated by a common assemblage of vertebrate frugivores in three fleshy-fruited trees. -Ecoscience. 15: 189–199.

Morales, J.M. et al. 2013. Frugivore behavioural details matter for seed dispersal: a multi-species model for Cantabrian thrushes and trees. -Plos ONE. 6: e65216.

Nelder, J.A. and Mead R. 1965 A simplex method for function minimization -Computer Journal. 7: 303-313.

Supporting Information

Appendix 3 – *Validation of modeled seed dispersal components*

In order to test the validity of model predictions, we simulated bird tracks within our grid-based landscape (Fig. 1 in main text). We wanted to mimic a realistic frugivore assemblage, and we thus used the abundance of species of thrushes observed during 2009 fruiting season; namely, 49.1% of *Turdus iliacus*, 20.7% *T. merula*, 17.2% *T. viscivorus*, 10.5% *T. philomelos*, 1.6% *T. pilaris*, and 1.0% *T. torquatus*. For each simulation run we calculated six seed dispersal components related to the seed density and richness and seed density in open (see main text). Apart from these measures we also calculated and validated with observational data the density and richness of thrushes (for a similar approach with observational data, see García and Martínez 2012). The grain of the seed dispersal components agreed with the field sampling design (i.e. 110 40 x 40 m blocks; see Appendix 1). We simulated 500 bird tracks, and ran 30 times, with the aim to fit the magnitude of simulated seeds with that samped under field conditions (see Fig. S5).

The amount of variation in the observed data explained by simulations was calculated as the generalized coefficient of determination (adjusted R^2) assuming Gaussian errors, whereas the spatial concordance in the distribution of observed and simulated seed and bird values were calculated by means of a partial Mantel-r test between observed and simulated values using the ***vegan*** library (Oksanen et al. 2007). All analyses were performed within the R environment (R development core team 2013).

Simulated seed rain was able to explain an important fraction of the variability of the observed data. For bird density and richness, there existed spatial concordance in the distribution of both field and simulated values (bird density: $R^2 = 0.616$; bird richness: $R^2 = 0.568$). We also observed an agreement in the distribution of seed rain (Seed density: $R^2 = 0.543$ and seed richness: $R^2 = 0.538$; Fig. S5), except for the seed density in open with lower capacity of prediction of observed patterns ($R^2 = 0.166$).

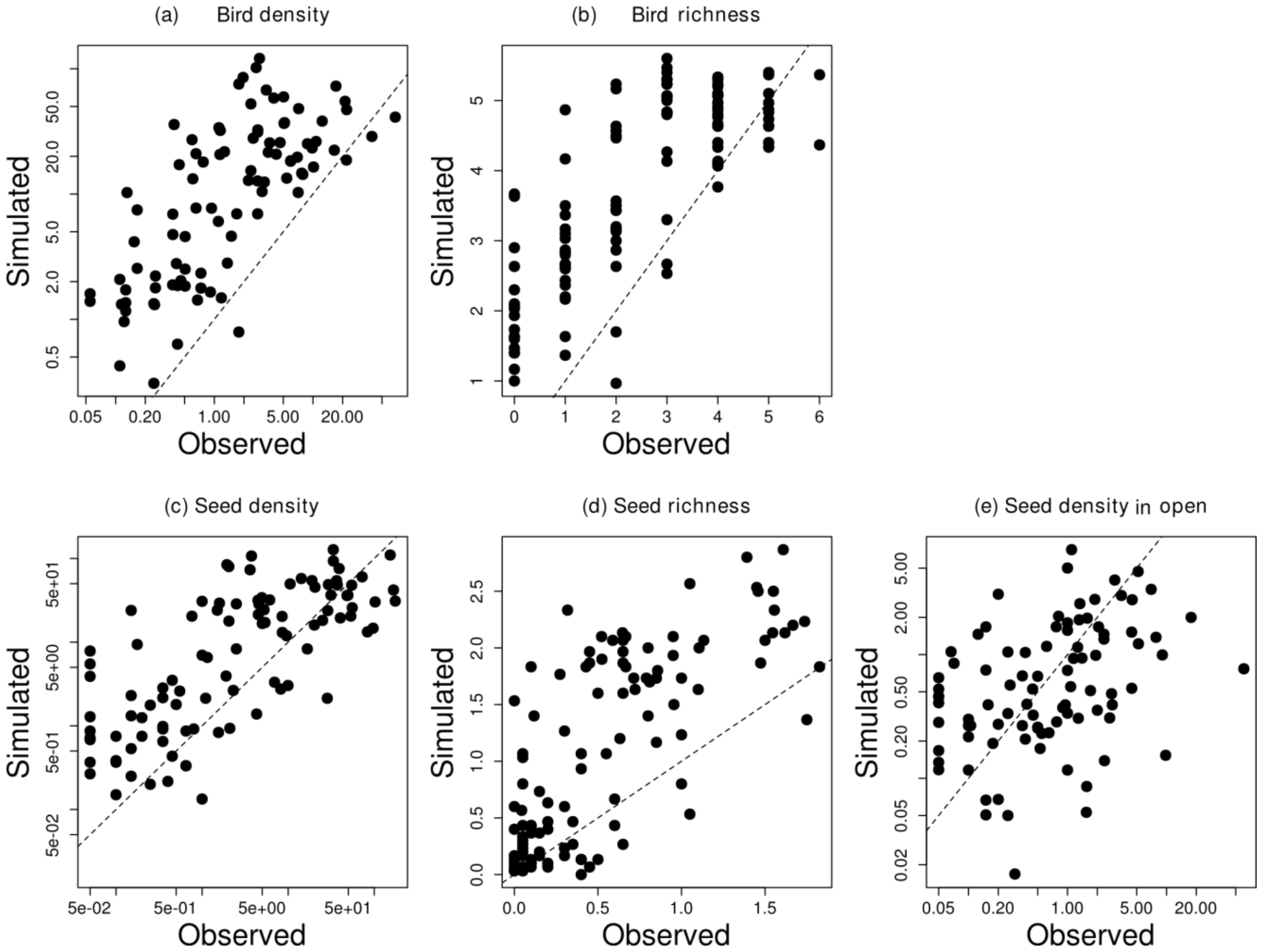

Fig. S5 - Observed vs. simulated values of the seed dispersal components. Figures compared cell-based values of (a) bird density and (b) richness, (c) seed density and (d) richness and (e) seed density in open. Simulations and observational data were compared at the same spatial grain (see Appendix 1). Dashed lines (representing the 1:1 values) showed the agreement between simulations and observations (i.e. dots along the 1:1 line highly matched between simulations and observations).

The model bias, measured as the proportion of the net difference between model simulations and observations, tended to be larger and positive for simulated values of the density and richness of birds (129.2 and 20.8%, respectively), and seed diversity (51.1%), whereas it was negative for simulated values (i.e. was larger for observed than simulated values) for seed density (39.0%) and seed density in open (74.9%). In general, there was a high spatial concordance of observed and simulated values, tending to be higher for seed rain (i.e. Mantel-r = 0.450 for seed density, 0.490 for seed richness and 0.429 for seed density in open) than for bird density and richness (Mantel-r = 0.389 and 0.374, respectively).

REFERENCES

García, D. and Martínez, D. 2012. Species richness matters for the quality of ecosystem services: a test using seed dispersal by frugivorous birds. -Proceedings of the Royal Society of London Series B-Biological Sciences. 279: 3106-13.

Oksanen, J. et al. 2013. Vegan: Community Ecology Package. R package version 2.0-7. http://CRAN.R-project.org/package=vegan

R Development Core Team. 2013. R: A language and environment for statistical computing. (ed) R Foundation for Statistical Computing, Vienna, Austria.

Supporting Information

Appendix 4 – *Detailed description of simulated scenarios of bird loss*

We performed simulation experiments to examine how gradients of bird loss affect to seed dispersal components. In our study system field data suggest that changes in the abundance and richness of birds could cascade into key components of the seed dispersal functionality (García et al. 2013; García and Martínez, 2012). We thus developed scenarios which entail the loss of the current species composition of the frugivore guild, and depended on the species sensitivities to likely drivers of global change.

We started from the current abundance and richness of the six species of thrushes. We based the initial bird composition on the abundances observed in 2009 fruiting season (i.e. 49.1% relative abundance of *Turdus iliacus*, 20.7% *T. merula*, 17.2% *T. viscivorus*, 10.5% *T. philomelos*, 1.6% *T. pilaris*, and 1.0% *T. torquatus*). We developed three scenarios (one random and two non-random), which modified linearly both the abundance and richness of birds. Given birds have different sensitivity to disturbances and they did not completely extinct in non-random scenarios (see below), we thus decided to generate sequences of 20 loss-spans ranging from 1 to 75% reduction of bird abundance (Fig. S6). In essence the main objective of having three scenarios was to create a baseline (random scenario) to compare likely functional changes derived from anthropogenic drivers (non-random scenarios). Below we describe each simulated scenario.

Random loss. This scenario assumes that forces provoking alterations were equally acting over all birds. With that scenario we wanted to construct a gradient *sensu stricto* of alteration of species composition, independent on the functional diversity (Lavorel and Garnier, 2002; Naeem and Wright, 2003; Solan et al. 2004; Larsen et al. 2005; Duffy, 2009). Translated to our study system, the most abundant bird species would be more resilient to loss due to their higher relative abundance. For instance, *T. iliacus* is the most abundant bird, and thus its function is likely to be the most reluctant to be loss under such scenario; in other words, increasing losses of our frugivore guild would cascade into seed dispersal patterns derived from a frugivore guild dominated by *T. iliacus*. On the other way round, rare species (such as *T. torquatus* and *T. pilaris*) have higher chances to be loss, and that reduce their imprint on the seed dispersal processes.

We therefore generated a gradient of bird loss based on its observed abundances (Fig. S6a). Latter gradient reduced the abundance of individual birds with the condition that all species have equal chances to be loss, and that resulted into a seed dispersal output with increasing role by fewer but commoner species (i.e. sampling effect; Hooper and Vitousek, 1998; Fargione and Tilman, 2005).

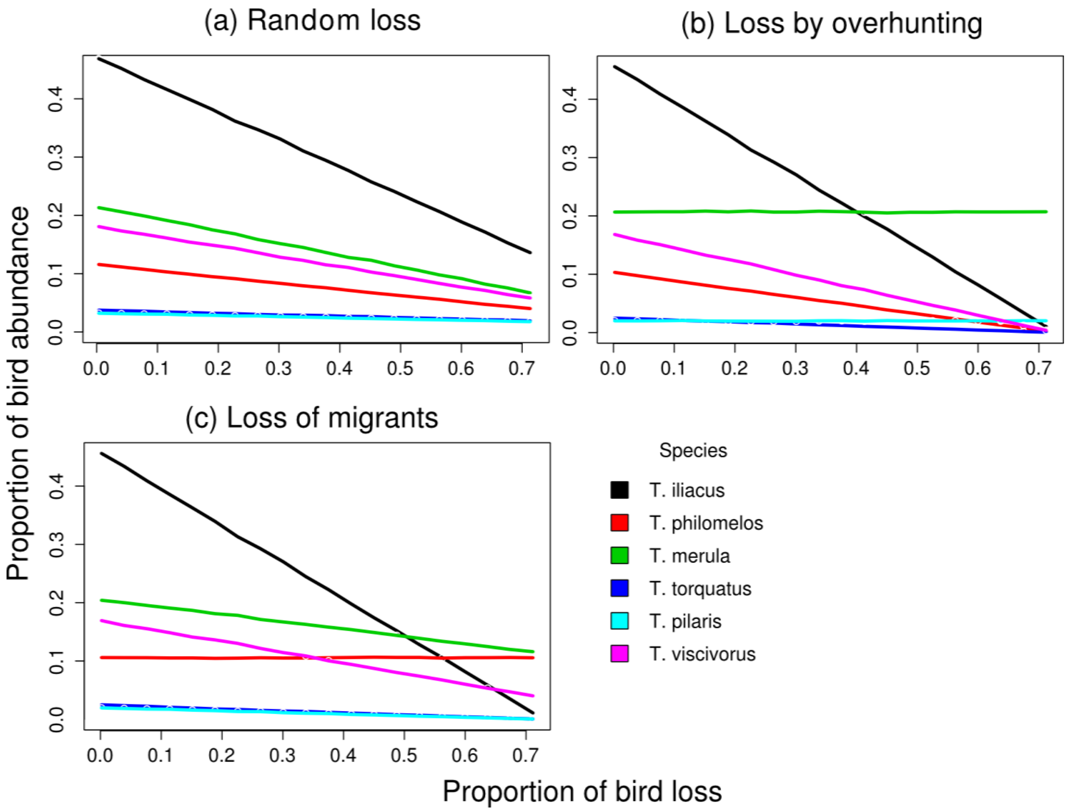

Fig. S6 – Bird abundance over three gradients of (a) random loss, (b) loss by overhunting and (c) loss of migrant birds. We represent the abundance of bird averaged after 50 realisations. Colour lines represent the relative abundance of the six bird species. Starting from the initial relative bird composition observed in 2009, we modified species abundances based on the species sentivities to each x driver. Pay attention that the proportion of bird loss ranges from 1 to 75%, due to birds species have different sensitivity to each disturbance and they did not completely extinct in non-random scenarios (see details for each scenario)

Loss by overhunting. European songbirds have declined during the past century due to hunting, due to biocides and habitat destruction (Berthold et al. 1998). In Europe thrushes are small-game passerines hunted when they migrate from summer (North Europe) to winter quarters (Mediterranean basin; McCulloch et al. 1992). Some of them (e.g. *T. viscivorus, T. iliacus, T. philomelos*) suffer increasing hunting pressures in Southern Europe (Payevsky and Vysotsky, 2003), and changes in hunting regimes may lead to population loss by over-exploitation.

Since wildlife conservation depends on regional agreements, a given species may be protected or not depending on each region or country. For instance, *T. merula* may be hunted in some regions of France and Italy, but not in Spain (EU parliament and council 2009), due its recent reduction in population sizes (SEO/Birdlife 2012). In Spain, there is even discrepancies between regions in the conservation policy of game birds, only protected in those regions where these species breeds. For instance, *T. viscivorus* and *T. philomelos* are non-game species in Asturias (North Spain), but they are in other regions (e.g. Andalucía, Cataluña, Valencia). In our case we modified the abundance of four species of thrushes (namely, *T. iliacus, T. viscivorus, T. philomelos* and *T. pilaris*) over a gradient of bird loss (Fig. S6b). Despite all these four species are non-game species in our study region (Asturias), we assumed this scenario as a *proxy* of alteration of thrush populations within a broader context of bird hunting.

Loss of migrant species. Migratory passerines are very sensitive to changes in climatic factors, and such changes may affect their distribution, population-based processes and phenology (Leech and Crick, 2007). Recent studies predict lower arrival rates of wintering thrushes into Southern Europe, which may be attributed to multiple causes. For instance, thrushes could arrive in low numbers due to global warming, and the concomitant amelioration of environmental conditions in breeding areas (Rivalan et al. 2007). Another possible cause could be habitat degradation and breeding collapse in Northern Europe, which may reduce thrush populations (Newton, 2004; Robinson and Green, 2004; Beale et al. 2006).

In the Cantabrian range (North Iberian Peninsula), *T. iliacus* and *T. pilaris* were regular non-breeder overwintering species, and their arrival time usually depends on environmental conditions in North Europe (Herrera, 1998; Telleria, et al. 2005). When they arrive to the Cantabrian range (November), they feed on *C. monogyna* and *I. aquifolum* fruits, and they continue southwards when fruits are completely depleted (January). *T. torquatus* breeds in scarce numbers in the Cantabrian range (but not in our study site), and it is a regular migrant species (September and October) from

North Europe. This species uses the Cantabrian range mostly as a stopover along its traveling to winter quarters (Mountains of South Iberian Peninsula and Atlas Mountains). Apart from the latter species, our study site host resident (presumably breeding) species, namely *T. merula*, *T. viscivorus* and *T. philomelos,* whose numbers increase with the arrival of overwintering individuals.

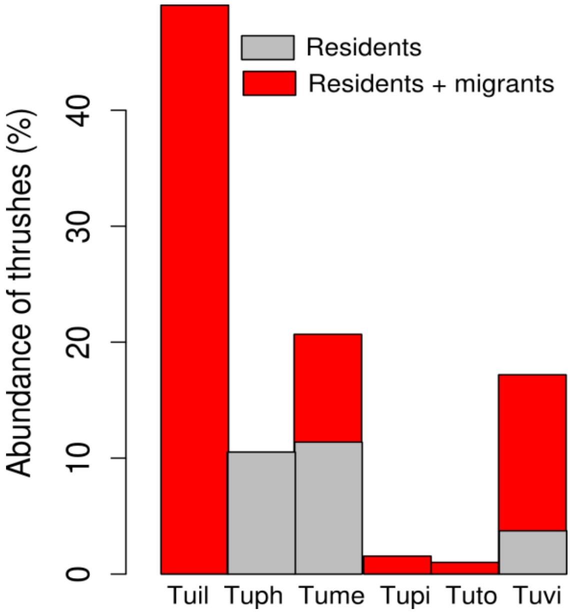

Fig. S7 – Relative abundance of “residents” and “residents and migrant” per bird species. Data were calculated from censuses performed in our study site. For details about data collection, see Appendix 1. Bird species are *T. iliacus* (Tuil), *T. philomelos* (Tuph), *T. merula* (Tume), *T. pilaris* (Tupi), *T. torquatus* (Tuto) and *T. viscivorus* (Tuvi).

We therefore constructed scenarios which reduce the abundance of migrant birds, in order to mimic an amelioration of wintering conditions in North Europe or a reduction of their breeding populations (Fig. S6c). We calculated the abundance and richness of the “resident” thrushes based on the censuses performed in early October: the abundance and richness during that period are reasonable to calculate the guild of resident thrushes in our study site. In that period *T. philomelos* was the most abundant species (44.9% of relative observations), followed by *T. merula* (41.5%) and *T. viscivorus* (13.6%); neither *T. illacus*, *T. pilaris* and *T. torquatus* were observed in early October (Fig. S7). Overall, we detected 45.7 birds/10h in early October which represented a 25.6% reduction relative to that calculated for the whole sampling period (i.e. from October to February, representing both migrants and residents). There existed thus species-based differences in the abundance of “residents” (Fig. S7): the observed “residents” of *T. philomelos* were equivalent (100% relative abundance) to that of the whole period, followed by *T. merula* (55.0% of relative abundance) and *T. visvivorus* (21.7%). Results thus suggest that the observed population of *T. philomelos* in our study site would not receive much overwinter individuals or, alternatively, that "residents" would be replaced by "migrants" when they disperse to southern localities. By contrast, the abundance of *T. viscivorus* increased four times in our locality probably as a result of overwinters. For simulations, we thus reduced the relative abundance of each thrush species (representing both breeders and migrants) up to values representing the abundance and composition of "residents" (Fig. S7).

REFERENCES

Beale, C.M. 2006. Climate change may account for the decline in British ring ouzels Turdus torquatus. -Journal of animal ecology. 75: 826–35.

Berthold, P. et al. 1998. 25-year study of the population development of Central European songbirds: a general decline, most evident in long-distance migrants. -Naturwissenschaften. 353: 350–353.

Duffy, J.E. 2009. Why biodiversity is important to the functioning of real-world ecosystems. -Frontiers in Ecology and the Environment. 7: 437–444.

EU parliament and council 2009. Directive 2009/147/EC of the European parliament and of the council of 30 November 2009 on the conservation of wild birds. http://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX:32009L0147

Fargione, J.E. and Tilman, D. 2005. Diversity decreases invasion via both sampling and complementarity effects. -Ecology Letters. 8: 604–611.

García, D. and Martínez, D. 2012. Species richness matters for the quality of ecosystem services: a test using seed dispersal by frugivorous birds. -Proceedings of the Royal Society of London Series B-Biological Sciences. 279: 3106–13.

García, D. et al. 2013. Functional heterogeneity in a plant-frugivore assemblage enhances seed dispersal resilience to habitat loss. -Ecography. 36: 197–208.

Herrera, C.M. 1998. Long-term dynamis of Mediterranean frugivorous birds and fleshy fruits: a 12-year study. -Ecological monographs. 68: 511–538.

Hooper, D. and Vitousek, P. 1998. Effects of plant composition and diversity on nutrient cycling. -Ecological Monographs. 68: 121–149.

Larsen, T.H. et al. 2005. Extinction order and altered community structure rapidly disrupt ecosystem functioning. -Ecology letters. 8: 538–47.

Lavorel, S. and Garnier, E. 2002. Predicting changes in community composition and ecosystem functioning from plant traits: revisiting the Holy Grail. -Functional Ecology. 16: 545–556.

Leech, D.I. and Crick, H.Q.P. 2007. Influence of climate change on the abundance, distribution and phenology of woodland bird species in temperate regions. -Ibis. 149: 128–145.

McCulloch, M. et al. 1992. The hunting of migratory birds in Europe: a ringing recovery analysis. -Ibis. 134: 55–65

Morales, J.M. et al. 2013. Frugivore Behavioural Details Matter for Seed Dispersal: A Multi-Species Model for Cantabrian Thrushes and Trees. -PLoS ONE. 8: e65216.

Naeem, S. and Wright, J.P. 2003. Disentangling biodiversity effects on ecosystem functioning: deriving solutions to a seemingly insurmountable problem. -Ecology Letters. 6: 567–579.

Newton, I. 2004. The recent declines of farmland bird populations in Britain: an appraisal of causal factors and conservation actions. -Ibis. 146: 579–600.

Payevsky, V.A. and Vysotsky, V.G. 2003. Migratory Song Thrushes Turdus philomelos hunted in Europe: survival rates and other demographic parameters. -Avian Science. 3. 13-20.

Rivalan, P. et al. 2007. Contrasting responses of migration strategies in two European thrushes to climate change. -Global Change Biology. 13: 275–287.

Robinson, R. and Green, R. 2004. Demographic mechanisms of the population decline of the song thrush Turdus philomelos in Britain. -Journal of Animal Ecology. 73*: 670-682*

SEO/BirdLife 2012. Programas de seguimiento de SEO/BirdLife en 2011. SEO/BirdLife. Madrid

Solan, M.et al. 2004. Extinction and ecosystem function in the marine benthos. -Science, 306: 1177–80.

Telleria, J. et al. 2005. Conservation of seed-dispersing migrant birds in Mediterranean habitats: Shedding light on patterns to preserve processes. -Biological Conservation. 124: 493–502.