



## What is long-distance dispersal? And a taxonomy of dispersal events

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# What is long-distance dispersal? And a taxonomy of dispersal events

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## Abstract

1 Dispersal is a key individual-based process influencing many life-history attributes,  
2 scaling up to population-level properties (e.g., metapopulation connectivity). A  
3 persistent challenge in dispersal ecology has been the robust characterization of  
4 dispersal functions (kernels), a fundamental tool to predict how dispersal processes  
5 respond under global change scenarios. Especially the rightmost tail of these func-  
6 tions, i.e. the long-distance dispersal (LDD) events, are difficult to characterize  
7 empirically and to model in realistic ways. But, when is it a LDD event? In the  
8 specific case of plants, dispersal has three basic components: 1) a distinct (sessile)  
9 source, the maternal plant producing the fruits or the paternal tree acting as a  
10 source of pollen; 2) a distance component between source and target locations;  
11 and 3) a vector actually performing the movement entailing the dispersal event.  
12 Here we discuss operative definitions of LDD based on their intrinsic properties: 1)  
13 events crossing geographic boundaries among stands; and 2) events contributing  
14 to effective gene flow and propagule migration. Strict-sense long distance disper-  
15 sal involves movement both outside the stand geographic limits and outside the  
16 genetic neighborhood area of individuals. Combinations of propagule movements  
17 within/outside these two spatial reference frames results in four distinct modes  
18 of LDD. Beyond traditional statistical approaches to characterize distributions,  
19 Extreme Value Analysis (EVA) can be used to properly and explicitly evaluate  
20 the properties of frequency and extent of LDD events. We discuss conditions  
21 where global change scenarios truncate dispersal processes, leading to the loss of  
22 key dispersal services in natural populations. Proper characterization of the LDD

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- 23 events helps to assess, for example, how the ongoing defaunation of large-bodied  
24 frugivores pervasively entails the loss of crucial LDD functions.

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## 25 Introduction

26 Dispersal is a key individual-based process influencing many life-history attributes  
27 and scaling up to population-level properties (e.g., metapopulation connectivity,  
28 Cousens *et al.* 2008). In the specific case of plants, largely sessile organisms,  
29 dispersal has three basic components: 1) a distinct (sessile) source, the maternal  
30 plant producing the fruits or the paternal tree acting as a source of pollen; 2) a  
31 distance component between source and target locations; and 3) a vector actually  
32 performing the movement entailing the dispersal event. While realized dispersal  
33 also depends upon stages subsequent to dissemination (e.g., successful germination  
34 and seedling establishment) Schupp (1995), the three previous components fully  
35 characterize the dispersal process per se. Therefore, plant movement differs in  
36 important natural history details from animal dispersal, yet both can be assessed  
37 within a common conceptual framework (e.g., Nathan, 2006). Characteristically,  
38 animal-assisted plant dispersal has three distinct, highly integrated, components  
39 missing in the process of animal dispersal: the properties of the source (parental)  
40 plant, that mediate in the foraging of the animal vector (pollinator or frugivore),  
41 the intrinsic properties of the propagule, and the functional characteristics of the  
42 animal vector who performs the movement (Nathan *et al.*, 2008a).

43 The movement of pollen and seeds by animals and its consequences have intrigued  
44 population geneticists and field ecologists since the infancy of both research disci-  
45 plines. Each has generated an impressive body of theoretical and empirical research  
46 through the past decades, yet advances have long been co-existing in ‘parallel

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47 worlds' and the great synergistic potential of population genetics and demography  
48 for the study of plant dispersal by animals remains little explored. Knowledge  
49 gaps still having the imprint of this conceptual disconnection include the idea of  
50 long distance dispersal, and the paradoxes of forest fragmentation effects on ge-  
51 netic diversity (Kramer *et al.*, 2008), survival and persistence of relict tree species  
52 (Hampe & Jump, 2011), rapid post-Pleistocene recolonization of vast continental  
53 areas in response to climate modification (Clark *et al.*, 1998; Clark, 1998), among  
54 other persisting issues. This conceptual isolation has been exacerbated by techni-  
55 cal difficulties for the robust characterization of dispersal events, especially those  
56 involving movement over long-distances (long-distance dispersal, LDD). LDD is a  
57 characteristically extreme event of propagule movement in any plant population,  
58 typically occurring with an extremely low probability but potentially reaching  
59 an extremely long distance. Some progress has recently been made through the  
60 fast-paced implementation of molecular tools in ecological research labs and the  
61 availability of cutting-edge technology for biotelemetry applications. But much of  
62 the population geneticist and ecologist communities remains unaware of the state  
63 of the art in each other and likely under-appreciates their potential to validate  
64 and enrich dispersal studies (Jones & Muller-Landau, 2008). In particular, LDD  
65 events remain difficult to assess, both technically- with serious methodological  
66 problems for its reliable estimation- and conceptually. Our aim here is to review  
67 the LDD concept with a specific emphasis on dispersal of plant propagules (seeds  
68 and pollen), providing an extended definition that might be helpful in the robust  
69 quantification of LDD events.

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70 Two main conceptual approaches have been used to assess dispersal (Fig. 1).  
71 The “forward” approach attempts to track the dispersal events away from the  
72 known sources, e.g., by tracking the movement patterns of frugivores as they leave  
73 fruiting plants after feeding (Fig. 1A). This is the main approach used in the  
74 movement ecology framework (Nathan *et al.*, 2008a), with extensive application  
75 to animal movement based on the use of advanced biotelemetry. The “backward”  
76 approach attempts to reconstruct the most likely source of a dispersed propagule  
77 by inferring the sources given the propagule delivery pattern, the fecundity of  
78 potential sources, and the dispersal function (Fig. 1B), i.e., by using an inverse  
79 modeling approach. The main technical challenge in Fig. 1A is to sample enough  
80 dispersal events away from the source to be able to fully characterize the tail  
81 (LDD events) of the dispersal function. In Fig. 1B, the main challenge is to have  
82 a robust sampling scheme with propagule collectors (e.g., seed traps) and a good  
83 characterization of the potential sources to derive robust estimates of the actual  
84 sources. Both approaches are limited logistically by the difficulties to sample the  
85 vast areas required to assess LDD events from the focal source population.

86 No explicit definition of what constitutes an LDD event exists. Previous ap-  
87 proaches (e.g., Nathan, 2006; Schurr *et al.*, 2009) include both absolute and  
88 proportional definitions to characterize LDD events. This means providing in-  
89 formation about the absolute distances moved by a given percentile of the events  
90 and/or providing data on the proportion of events exceeding a given distance  
91 threshold (Nathan *et al.*, 2008b). The exact proportional or absolute thresholds  
92 selected remain arbitrary, as no reference spatial frame is provided within the

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93 definition of LDD. This leaves the consideration of LDD as an extreme form of  
94 context-dependent phenomenon, strongly dependent upon the scale of the biolog-  
95 ical process studied (Kinlan *et al.*, 2005) and of the specific organism considered.  
96 For example, Kinlan *et al.* (2005) used a spatial reference frame to characterize  
97 LDD events of marine organisms, where sedentary adults and larvae differ enor-  
98 mously in the spatial scales of their dispersal (D'Aloia *et al.*, 2013). Therefore,  
99 any measure of extent and reach of LDD events requires reference to an explicit  
100 spatial frame or "local" scale (Kinlan *et al.*, 2005).

101 We aim at providing a general framework for the quantitative analysis of LDD  
102 events so that estimates of their frequency and extent could be comparable across  
103 different study systems. We argue that both demographic and genetic elements  
104 are needed for this framework, most likely requiring a combination of field-based  
105 movement data and genetic analyses. These elements can be overlaid on previous  
106 definitions based on absolute and proportional characterizations of LDD. We start  
107 with a definition of LDD events within a spatially-explicit mechanistic framework  
108 allowing an unambiguous meaning for setting long-distance thresholds. We then  
109 use a case study to assess differential contributions of animal frugivores performing  
110 LDD.

111 Long-distance dispersal is currently one of the most debated topics in dispersal  
112 ecology; it defines the connectedness within the network of local populations and  
113 the possibilities for range expansion and successful colonization events. We pro-  
114 pose a first demogenetically-based, operational definition of what a long-distance  
115 dispersal event actually is, and review existing empirical literature on distance



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116 thresholds from population and genetic perspectives. We also show how molecular  
117 tools have been used to identify the respective contributions of different animal  
118 species to the LDD portion of dispersal kernels of pollen and seeds by setting  
119 empirically-derived distance thresholds. Finally, we highlight potential applica-  
120 tions of molecular markers beyond the quantification of just the dispersal distances  
121 that prevails in current studies, e.g., experimental approaches to assess dispersal  
122 limitation and Janzen-Connell effects.

### 123 **LDD within a demo-genetic perspective: a taxonomy of dis-** 124 **persal events**

125 Here we propose an explicit definition of LDD and what constitutes a LDD event.  
126 Previous definitions of dispersal patterns emphasized only their distance compo-  
127 nents and characterized LDD events basically in terms of geographic distance be-  
128 tween a dispersed propagule (or an established early seedling) and its most likely  
129 maternal or paternal (in case of pollen) source. Absolute and proportional defini-  
130 tions for the LDD events have been proposed depending on arbitrary thresholds  
131 of either the distance beyond which a dispersal event is LDD or the proportion of  
132 events occurring beyond a specific distance (Nathan, 2005; Nathan *et al.*, 2008b).  
133 Thus, two key biological aspects of LDD events involve the transport of propa-  
134 gules outside a reference area: moving away from the source stand or population,  
135 and moving away from the area where relatives stand (Kinlan *et al.*, 2005). These  
136 two movements do not necessarily concur: a propagule may move over a very

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137 long distance yet still be disseminated within the reach of the neighborhood where  
 138 parental individuals mate. Within a demo-genetic framework it is easy to envision  
 139 a combination of situations concerning the spatial scale of the dispersal processes  
 140 (Table 1) and unambiguously define different types of LDD events. The idea that  
 141 dispersal occurs in reference to these two spatial reference frames, i.e., the popu-  
 142 lation or stand and the genetic neighborhood area, is motivated by the fact that  
 143 dispersal entails the movement of both an individual propagule (i.e., a pollen grain  
 144 or a seed) and a distinct set of genes (i.e., the male genotype in case of pollen, or  
 145 a seed genotype). Thus, dispersal entails simultaneous demographic and genetic  
 146 effects through recruitment of new individuals in the population and through con-  
 147 tributions to gene flow (Harper, 1977). When considered its combined influence  
 148 on demography and population genetics, the concept of LDD nicely bridges these  
 149 two paradigms embedded in the biological definition of population (Waples &  
 150 Gaggiotti, 2006).

151 Two important components of plant dispersal ecology concern the movement of  
 152 propagules away from the source population, a type of dispersal relevant to col-  
 153 onization ability and range expansion (Howe & Miriti, 2004), and the movement  
 154 away from the location of close relatives, i.e., a movement away from the genetic  
 155 neighborhood (Hardesty *et al.*, 2006; Jones & Muller-Landau, 2008). If we classify  
 156 dispersal events according to these two spatial frameworks (Table 1) we end up  
 157 with four distinct types of events depending on whether or not dispersed propagules  
 158 are disseminated within these reference areas. Setting the limits of a population  
 159 can be problematic (Waples & Gaggiotti, 2006) yet we can identify with relative

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160 ease the geographical limits of plant stands, patches, habitat spots or other types  
 161 of habitat or microhabitat discontinuities that determine landmark boundaries of  
 162 biological significance (see Kinlan *et al.*, 2005, for further discussion of boundaries  
 163 for dispersal). These "frontiers" set biological limits to what a LDD event is in  
 164 relation to the geographic limits of the source population. Most plants are dis-  
 165 tributed as clumped patches, discrete stands, or relatively isolated populations, so  
 166 we may distinguish between short-distance and long-distance dispersal events that  
 167 end up with dissemination within or beyond, respectively, the stand or population  
 168 geographic boundaries (Table 1,  $SSD_{loc}$  or  $LDD_{loc}$ ) (Figure 2).

169 A second consideration in terms of spatial boundaries, with effects on disper-  
 170 sal patterns, is the genetic neighborhood area  $N_e^b$ , i.e., the spatial extent includ-  
 171 ing a subset of panmictic individuals within a population (Wright, 1943, 1946).  
 172 Thus, the  $N_e^b$  area can be equal to the whole extent of the population whenever  
 173 the population is unstructured and there is evidence for random mating events  
 174 among all the individuals. However, most populations and stands of long-lived  
 175 trees show highly aggregated and clumped distributions (Seidler & Plotkin, 2006),  
 176 where relatively long distances may separate groups of individuals within the same  
 177 population. In these cases we might expect  $N_e^b$  area to be substantially smaller  
 178 than the total population area. Therefore, at least four possible scenarios exist  
 179 with distinct implications in terms of consequences for dispersal (Table 1). In the  
 180 case of dispersal events not extending beyond the geographic limits of the popu-  
 181 lation or reference area, actual LDD events may involve dissemination beyond a  
 182 reduced neighborhood area that is smaller than the geographic extent of the pop-

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ulation, originating local long-distance ( $LDD_{loc}$ ) dispersal events (Table 1, Fig. 2A). Actual short-distance dispersal would then involve those situations where the propagule is disseminated within *both* the population limits and the genetic neighborhood boundary ( $SDD_{loc}$ ). Along a similar reasoning, dispersal events outside the population limits will not necessarily convey LDD (Table 1, Fig. 2B): this is expected in cases where the genetic neighborhoods are extensive, going beyond the geographic limits of local populations, as in fig trees (Nason *et al.*, 1998), generating LDD events within the genetic neighborhood ( $LDD_{neigh}$ ). Finally, strict-sense LDD events would involve dissemination outside *both* the population limits and the genetic neighborhood boundary ( $LDD_{ss}$ ) (Table 1, Fig. 2A).

While both  $SDD_{loc}$  and  $LDD_{loc}$  can be crucial for assuring the local persistence of populations,  $LDD_{neigh}$  and  $LDD_{ss}$  would be extremely important contributors to the structuring of genetic pools, realized gene flow, and maintaining connectivity in metapopulation scenarios. We argue that both the demographic and the genetic references are relevant for a proper definition of LDD.

## Individual and Population Neighborhoods as Reference

Continuous populations can be modeled with the concepts of isolation by distance and neighborhood size (Wright, 1943, 1946). The former refers to the case that limited gene dispersal in continuous populations produces demes that are panmictic internally, but are isolated to some extent from adjacent demes. Each group of reproducing individuals is the neighborhood, defined as the population of a region

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in a continuum, from which the parents of individuals born near the center may be treated as if drawn at random (Wright, 1969). The importance and influence of the dispersal process in determining the size of the neighborhood is given by this equation, which shows how the spatial dispersion (pattern of spatial distribution) of the population influences the effective population size. This influence on the effective size is given by:

$$N_e^b = 4\pi\sigma\delta \quad (1)$$

where  $\delta$  is the density of adults per unit area and  $\sigma$  is the standard deviation of the distance between birth and breeding sites. This formulation is often called the neighborhood size and assumes a normal distribution of distances between parents and offspring (out in a perfect circular shape from the source). Thus, changes in the variance of dispersal distance can affect  $N_e^b$  (highly clumped populations will have reduced  $N_e^b$ ). This is the basic model of "Isolation by Distance" proposed by Wright (1943, 1946). Under this type of model, migration (gene flow) is given by the variance in dispersal, and not by the proportion of the population that is composed of migrants (denoted  $m$ ), as is the case with island models (Slatkin, 1985). With enough distance separating them, two plant individuals have a low probability of mating and can be considered members of distinct genetic populations even if they are not located in geographically distinct populations.

For plants, gene flow may be accomplished by both seeds and pollen, so the variance may be decomposed to account for different patterns of seed and pollen

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224 dispersal, and to take into account the mating system (outcrossing rate,  $t$ ). Thus,  
225 neighborhood size can be defined with the following equation (Crawford 1984) :

$$N_e^b = 4\pi(\sigma_s^2 + \frac{t\sigma_p^2}{2})\delta(1 + t) \quad (2)$$

226 where  $\sigma_s$  is the standard deviation of seed dispersal distance,  $\sigma_p$  is the standard  
227 deviation of pollen dispersal distance, and  $\delta$  is the density of potential parents.

228 Neighborhood size in plants can be estimated by marking pollen and seeds with  
229 fluorescent dyes, tags, or stable isotope enrichment (Carlo *et al.*, 2009). However,  
230 these methods do not measure effective pollen or seed movement, but they may  
231 be combined with genetic analysis to assess genetic identity and relatedness with  
232 hypervariable DNA markers (Levin, 1988; Nason *et al.*, 1998; Godoy & Jordano,  
233 2001) to achieve reliable estimates of both effective population size and neighbor-  
234 hood area.

235 The extent of neighborhood area in plants can be extremely variable, depending  
236 on life-history attributes such as life-span, spacing patterns, mating system, etc.  
237 Even a limited sample of available information (Table S1) highlights the fact that  
238 the size of neighborhood areas can in some cases exceed the geographic limits of  
239 local populations (Nason *et al.*, 1998). The size of neighborhood areas may en-  
240 compass at least four orders of magnitude,  $10^{-2} - 10^2$  km in radius, and include  
241 many individuals. Therefore, reference to this "genetic/evolutionary" paradigm  
242 and reference to the geographic boundaries (*sensu* Waples & Gaggiotti, 2006) may  
243 be instrumental to understand the actual role of LDD events in shaping the struc-

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244 turing of genetic pools and contributing to gene dispersal.

245 Whenever there is a large discrepancy between population area extent and  $N_e^b$   
 246 we might expect the frequency of  $LDD_{loc}$  and  $LDD_{neigh}$  differ enormously. For  
 247 example, relatively small  $N_e^b$  may rise the importance of  $LDD_{loc}$  in preserving  
 248 scenarios of panmixia within a local population, as most distant dispersal events  
 249 will disseminate seeds outside the neighborhood of maternal plants.

## 250 **Empirical analysis of contributions to LDD**

251 Empirical evaluation of differential contributions to the different forms of LDD  
 252 events outlined in Table 1 requires identification of source trees as well as assign-  
 253 ment of the dispersed propagules to specific vectors or functional groups of vectors  
 254 (Jordano *et al.*, 2007). Recently, DNA-barcoding techniques have been developed  
 255 and successfully applied to the identification of frugivore species contributing to  
 256 specific seed dispersal events whose source can be identified with genetic, direct  
 257 assignment techniques (González-Varo *et al.*, 2014). Otherwise, visual identifica-  
 258 tion can reliably assign the genotyped seeds to frugivore species groups based on  
 259 specific characteristics of scats and regurgitations (Jordano *et al.*, 2007).

260 We inferred the frugivore groups contributing dispersal events by visually iden-  
 261 tifying scats and regurgitations in seed traps and line transects (see Jordano  
 262 *et al.*, 2007, and Suppl. Mat. for additional details of methods). These frugivore  
 263 functional groups include up to 38 bird and 4 mammal species feeding on *P. ma-*  
 264 *haleb* fruits (Jordano & Schupp, 2000). Here, we differentiate four major frugivore

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265 groups: large carnivorous mammals (such as foxes, badgers, and stone martens);  
 266 two species of medium-sized frugivorous birds, mistle thrushes (*T. viscivorus*),  
 267 and carrion crows (*Corvus corone*); and a pool of small-sized frugivorous birds,  
 268 including warblers, redstarts, and robins (Jordano *et al.*, 2007).

269 To a large extent, short-distance dispersal events (strict-sense,  $SDD_{loc}$  events)  
 270 are contributed by small- and medium-sized (*Turdus*) frugivorous birds (Table 2).  
 271 Given the relatively reduced  $N_e^b$  area of *P. mahaleb* (Suppl. Mat. Table S1),  
 272  $< 1km^2$ , well below the extent of the local study population (Garcia *et al.*, 2007,  
 273 2005), we cannot estimate  $LDD_{neigh}$  events (Table 2), as all LDD events outside  
 274 the reference population occur, by definition, outside the  $N_e^b$  area. Larger fru-  
 275 givores such as corvids and the pigeon *Columba palumbus* contribute most LDD  
 276 events, and most immigrant seeds potentially dispersed from other populations  
 277 (Fig. S2). Notably, strict-sense long-distance dispersal ( $LDD_{ss}$ ) appears consis-  
 278 tently associated with large-bodied frugivores (Table 2), most likely associated  
 279 with a greater frequency of movements outside the local population (Fig. 4).

280 Empirically mapping of dispersal events for either pollen or seed disseminated by  
 281 animals may result in a complex pattern of different combinations of dispersal  
 282 events (Fig. S1), as animal movements are overlaid onto plant populations occu-  
 283 pying complex landscapes, resulting in different types of SDD and LDD events.



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## 284 Long-Distance Dispersal: the ecology of extreme events

285 Long-distance dispersal (LDD) is a major component of the population dynamics,  
286 genetic structure, and biogeographic history of plant species. It determines the  
287 colonization ability of new habitats and the possibilities for fragmented populations  
288 to sustain a cohesive metapopulation by immigration-emigration dynamics that  
289 rely on LDD events (Nathan *et al.*, 2008b; Schurr *et al.*, 2009). Yet our current  
290 understanding of the extent, frequency, and consequences of LDD is very limited.  
291 On one hand, theoretical models fail to predict accurately the behavior of the tail  
292 of the dispersal functions, and thus fail to predict very basic properties of LDD. On  
293 the other hand, we still have very limited documentation of actual LDD events in  
294 natural populations and we still see LDD as a sporadic, rarely far-reaching process  
295 still marked with the stamp of natural history curiosity.

296 Combining spatially-explicit references to the geographic population limits and the  
297 genetic neighborhood area extent ( $N_e^b$ ) helps avoiding some imprecision in setting  
298 distance thresholds to characterize LDD events (Jones & Muller-Landau, 2008).  
299 In addition, the framework outlined in Table 1 bridges the combined demographic  
300 and genetic effects of LDD events. When methods available to assign frugivore  
301 taxa to the analyzed dispersal events, as in the study case with *P. mahaleb*, a  
302 classification in the four categories of events is possible.

303 The frugivore assemblage of *P. mahaleb* is composed by a diversified set of animal  
304 species spanning a wide size range, ca. 12-14000 g in body mass. We might expect  
305 that this extreme variation translates in an ample pattern of foraging modes, move-

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ment distances, and fruit/seed processing (Jordano & Schupp, 2000). If the results for *P. mahaleb* are generalizable to other disperser assemblages, it seems that the functional roles of frugivore species in terms of contributions to LDD events are structured in two distinct groups: small-bodied frugivores, with substantial contributions to SDD events, and large-bodied species with a disproportionate contribution to LDD events. Both components of this sort of diplochorous (vander Wall & Longland, 2004) dispersal system are very frequent in fleshy-fruited plants with diversified frugivore assemblages (Galetti *et al.*, 2013). In such cases, small-bodied frugivores largely contribute the short-distance dispersal key to support *in situ* recruitment and population persistence. Yet the large-bodied frugivores distinctly contribute LDD events that sustain the connectivity of metapopulation scenarios (Urban & Keitt, 2001). As shown in Table 1, SDD and LDD events can be more complex when we consider the contributions to gene flow via seed and the consequences in terms of structure and spatial distributions of the genetic pools. For example, local, within-population, dispersal events may vary enormously in terms of genetic effects and local structuring of the genetic pools depending on whether they specifically contribute  $SDD_{loc}$  or instead,  $LDD_{loc}$ . Note that only the latter actually contribute erasing any form of local genetic structure by contributing to increased genetic neighborhoods.

A number of classic studies have demonstrated that the activity of large frugivores may also significantly contribute to SDD events and inefficient dispersal because of, i.e., territorial defence, short gut retention times relative to on-tree foraging, frequent revisitation of same trees and perches, etc., resulting in substantial SDD

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329 events (Pratt & Stiles, 1983; Pratt, 1984; Snow & Snow, 1984, 1988; Wheelwright,  
 330 1991). Yet these large-bodied frugivores are crucial for both  $LDD_{loc}$  and  $LDD_{ss}$ ,  
 331 given that extensive movement patterns and extremely large foraging ranges may  
 332 frequently contribute dissemination beyond distance thresholds defined with ei-  
 333 ther spatial landscape or genetic references. Recent analyses of the movement  
 334 ecology of large frugivores, coupled with results of their seed dispersal services  
 335 emphasize that LDD are by no means exceptional, either in terms of frequency  
 336 and extent (e.g., Westcott *et al.*, 2005; Bueno *et al.*, 2013; Morales *et al.*, 2013;  
 337 Carlo *et al.*, 2013). In addition, medium-sized birds such as thrushes (*Turdus* spp.)  
 338 can contribute substantial  $LDD_{loc}$  events, i.e., local LDD events contributing to  
 339 erase local population genetic structuring, effectively increasing the size of genetic  
 340 neighborhoods. In the case of *P. mahaleb* up to 55.49% of their dispersal events  
 341 are  $LDD_{loc}$  events. These birds are efficient seed dispersers of *P. mahaleb* and  
 342 other fleshy-fruited species (Snow & Snow, 1988; Jordano & Schupp, 2000; Carlo  
 343 *et al.*, 2013), also showing significant contributions of  $LDD_{ss}$  events.

344 As defined in our framework (Table 1), LDD, and in particular  $LDD_{ss}$  events are  
 345 a specific case of extreme events (García & Borda-de Água, 2017) consistently  
 346 associated with large-sized frugivores, yet including also medium-sized and highly  
 347 efficient frugivorous bird species. Robustly characterizing the expected frequencies  
 348 and extent of those extreme events would be crucial to properly assess the func-  
 349 tional role of frugivores and the full range of influences (demographic, genetic) in  
 350 plant populations.

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## 351 Challenges and future avenues for research

352 Pollen and seed dispersal in plants are essentially spatially-structured processes  
 353 for which the outcomes of interactions with dispersal vectors is intimately linked  
 354 to landscape features. Given this mechanistic link between the features of the  
 355 vector and the environments where its displacement occurs (Nathan *et al.*, 2008a),  
 356 consideration of landscape is key to understand the consequences of LDD events.  
 357 Yet these consequences hit two central aspects of plant life-histories: the demo-  
 358 graphic recruitment process (Harper, 1977), and the genetic signatures of pollen-  
 359 and seed-mediated gene flow in complex landscapes (Sork *et al.*, 1999). Recent  
 360 evidences point out that the selective extinction of large-bodied frugivores may  
 361 significantly impact plant populations dependent on frugivores both in terms of  
 362 recruitment (Traveset *et al.*, 2012; Pérez-Méndez *et al.*, 2015) and genetic con-  
 363 nectivity (Pérez-Méndez *et al.*, 2016). Frugivore downsizing represents a lasting  
 364 challenge for the collapse of seed dispersal processes where  $LDD_{ss}$  events are cru-  
 365 cial for population persistence and the cohesion of fragmented populations within  
 366 metapopulation scenarios.

367 We advocate (also see Jordano & Godoy, 2002; Nathan *et al.*, 2003; Jones &  
 368 Muller-Landau, 2008; Hardesty *et al.*, 2011) a combination of approaches includ-  
 369 ing large-scale biotelemetry to characterize animal movement, coupled with large-  
 370 scale genetic sampling of dispersed propagules, and demogenetic approaches that  
 371 combine both demographic and genetic research. A crucial aspect would be to  
 372 effectively associate the role of individual frugivore species to specific dispersal

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373 outcomes, by identifying the actual disperser contributing a dissemination event  
374 (González-Varo *et al.*, 2014) and simultaneously characterizing the source maternal  
375 plant (Jordano & Godoy, 2002).

376 The actual challenges to properly characterize the typologies of LDD events out-  
377 lined in Table 1 will probably persist. We need more efficient quantitative ap-  
378 proaches to assess these infrequent events, that occur over enormous spatial scales  
379 and that need to be documented with sample sizes sufficient to facilitate modeling  
380 efforts and robust statistical inferences. These are not trivial difficulties given the  
381 urgency to assess how forest loss, defaunation, genetic purging due to logging, etc.,  
382 alter plant populations.

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**Table 1:** Types of dispersal as a function of population area limits and genetic neighborhood limits. See Fig. 2 for a graphical representation of the four scenarios.

Genetic neighborhood limit	Population geographic limit	
	Within	Outside
Within	Local, short-distance dispersal, $SDD_{loc}$	Within neighborhood, long-distance dispersal, $LDD_{neigh}$
Outside	Local, long-distance dispersal, $LDD_{loc}$	Strict sense long-distance dispersal, $LDD_{ss}$

**Table 2:** Relative frequencies of *Prunus mahaleb* seed dispersal events for different frugivore groups according to population area limits and genetic neighborhood limits. See Fig. 2 for a graphical representation of the four scenarios.  $N = 655$  seeds (see Table 1 in Jordano *et al.*, 2007). Given that the estimated neighborhood size is smaller than population area,  $LDD_{neigh}$  would be zero.

Frugivore group	Within- population, within- neighborhood $SDD_{loc}$	Within- population, long-distance $LDD_{loc}$	Outside- population, within- neighborhood $LDD_{neigh}$	Strict-sense long-distance $LDD_{ss}$	$N$ seeds
Small-birds	0.7842	0.0171	0.00	0.1986	292
<i>Turdus</i>	0.2370	0.5549	0.00	0.2081	173
Large-birds	0.0435	0.3913	0.00	0.5652	23
Mammals	0.0120	0.2455	0.00	0.7425	167

# Figures

**Figure 1.** The two approaches used in analyses of dispersal processes in plants. A, the “forward” approach attempts to track the dispersal events away from the known sources, e.g., by tracking the movement patterns of frugivores as they leave fruiting plants after feeding. B, the “backward” approach attempts to reconstruct the most likely source of a dispersed propagule by inferring the sources given the propagule delivery pattern, the fecundity of potential sources, and the dispersal function. The main technical challenge in A is to sample enough dispersal events away from the source to be able to fully characterize the tail (long-distance dispersal, LDD, events) of the dispersal function. In B, the main challenge is to have a robust sampling scheme with propagule collectors (e.g., seed traps) and a good characterization of the potential sources to derive robust estimates of the actual sources with inverse-modeling techniques.

**Figure 2.** Schematic representation of different types of long-distance dispersal events in relation to the geographical limits of local populations (dashed lines) and the genetic neighborhood area  $N_e^b$  (grey area) of specific individual plants (squares). Dispersal events (arrows) can be classified depending on their actual incidence on propagule movement outside these spatially-explicit reference areas (Table 1). Strict-sense long-distance dispersal events ( $LDD_{ss}$ ) just include the LDD events that disseminate propagules out of *both* the population and genetic neighborhood boundaries. A, the neighborhood area is included within the geo-



414 graphic limits of the population, with some dispersal events potentially contribut-  
 415 ing local LDD; B, the neighborhood area is much larger than the geographic limits  
 416 of the population.

417

418 **Figure 3.** Empirical frequency distributions of seed dispersal events as a function  
 419 of dispersal distance by animal frugivores consuming *Prunus mahaleb* fruits. In  
 420 red, left (inset), frequencies of within-population dispersal events inferred from di-  
 421 rect assignment based on seed endocarp genotypes and maternal trees genotypes.  
 422 Larger frame, left, contributions of four functional frugivore groups (small birds,  
 423 medium- and large-sized birds, and mammals) to seed dissemination and propor-  
 424 tional contributions (right bar) to dispersal of the inferred immigrant seeds (i.e.,  
 425 those not matching any maternal tree in the study population) (Jordano *et al.*,  
 426 2007).

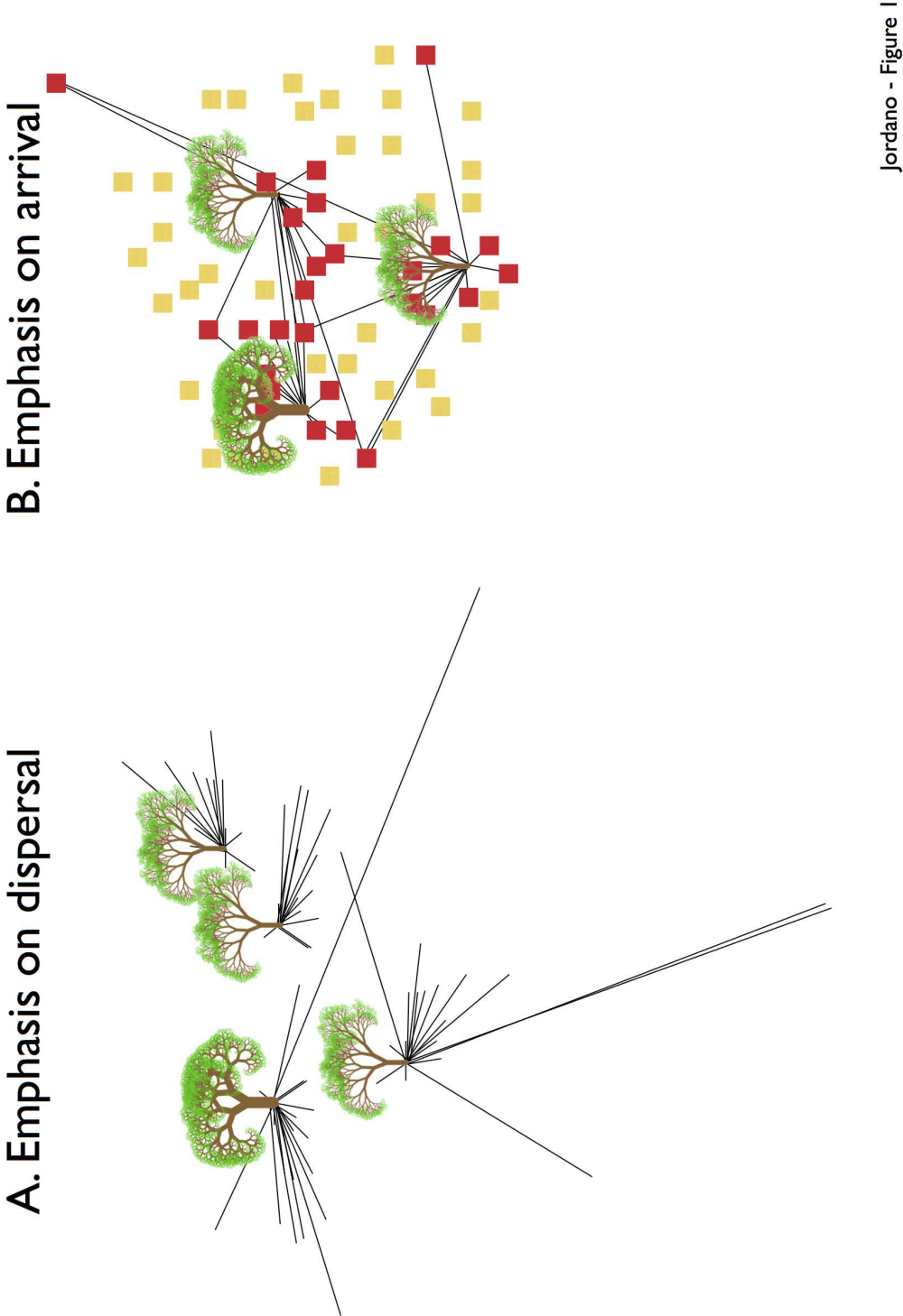
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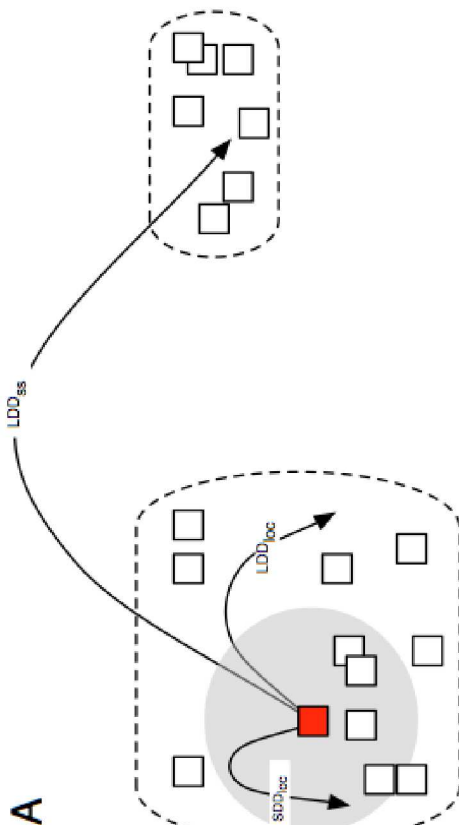
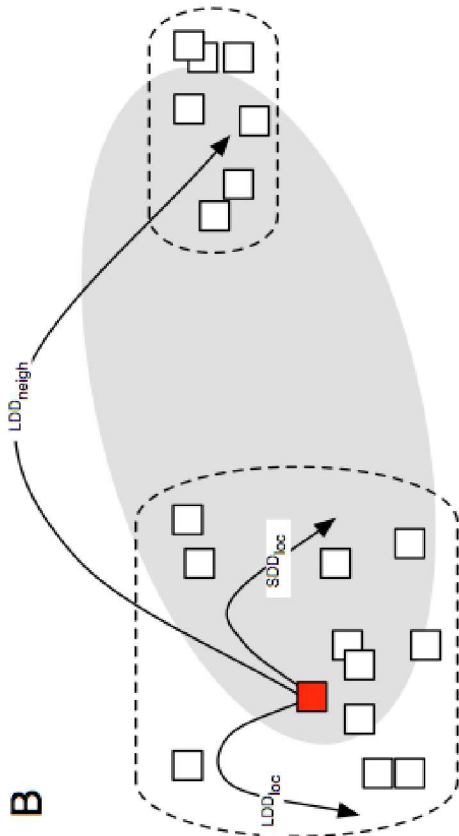
428 **Figure 4.** Differential contributions of functional groups of frugivores to the  
 429 four combinations of *Prunus mahaleb* seed dispersal events outlined in Table 1.  
 430 These result from dissemination within (yellow) or outside (blue) the population  
 431 geographic limits; within-population dispersal events can either be short-distance  
 432 ( $SDD_{loc}$ ) or local LDD ( $LDD_{loc}$ ) depending on the size of the genetic neighborhood.  
 433 Dispersal outside the local population can entail short-distance dispersal, if within  
 434 the genetic neighborhood area limits ( $SDD_{neigh}$ ) (yellow) or represent strict-sense  
 435 LDD ( $LDD_{ss}$ ) (blue).

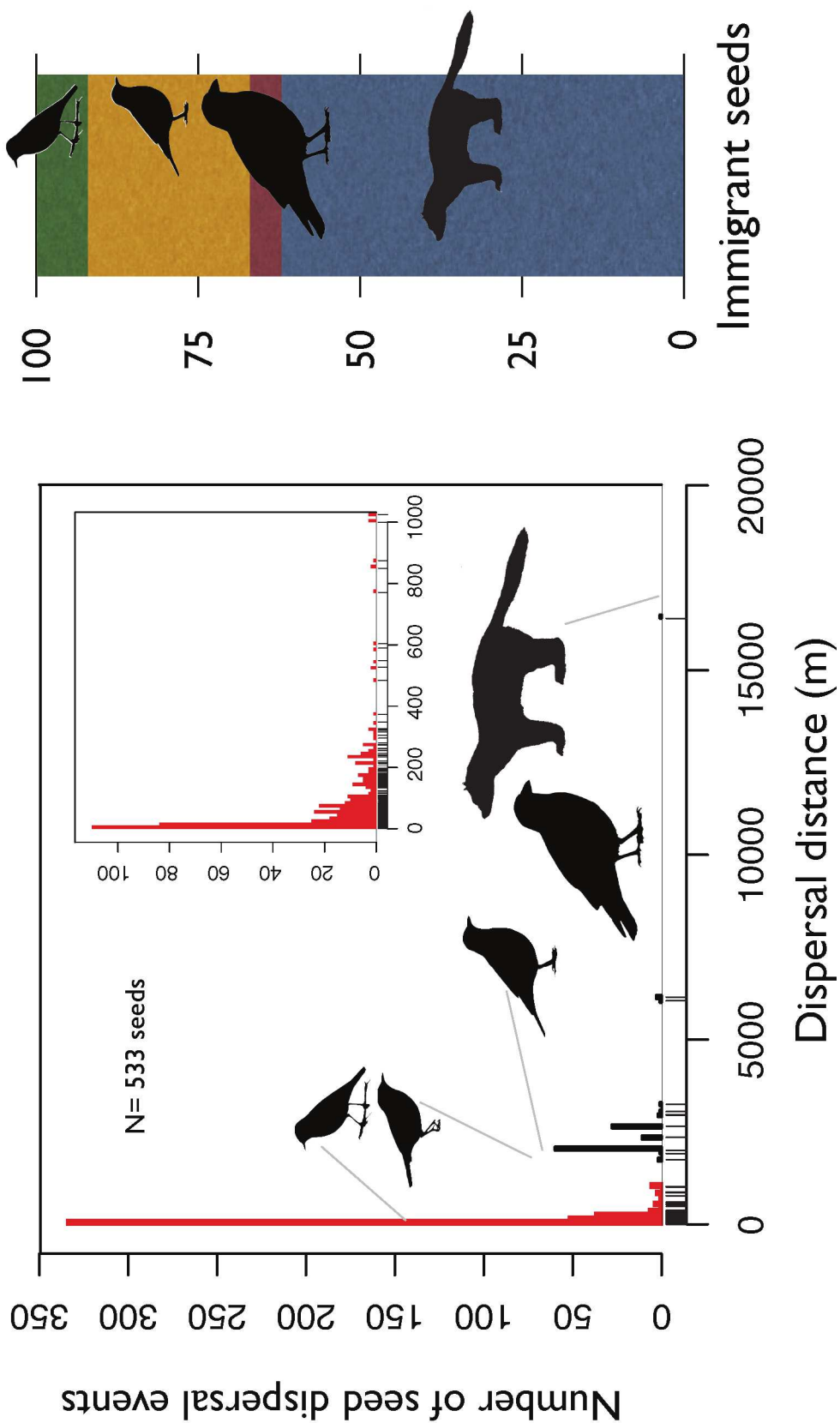
436

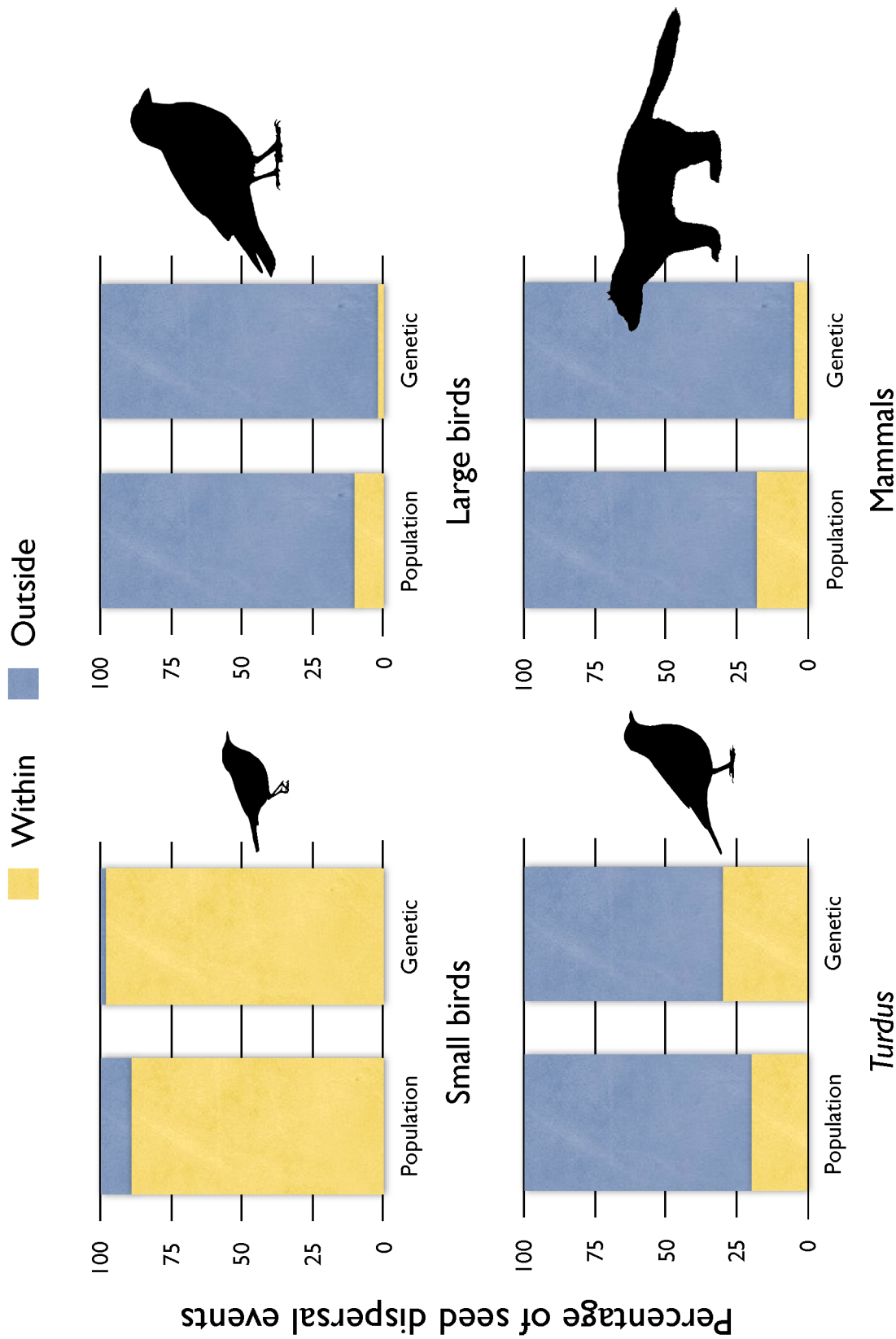
437 **Online Support Material and data accessiblity**

438 This review does not use new raw data, but includes some re-analyses of pre-  
439 viously published material. All the original data supporting the paper, R code,  
440 supplementary figures, and summaries of analytical protocols is available at the  
441 author's GitHub repository ([https://github.com/pedroj/MS\\_LDD](https://github.com/pedroj/MS_LDD)), with DOI:  
442 `#/zenodo.#`.









## Supplementary Material

### What is long-distance dispersal? And a taxonomy of dispersal events

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Sevilla, June 28, 2016

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**Key words:** \*\*\*

**Manuscript information:** \*\* Words; \*\* Chars; \*\* Pages, \* Figures; \* Tables.

# 1 Methods

2 **Species and Study Site.** The tree species we use as a case study to illustrate  
 3 different types of dispersal events, *Prunus mahaleb* (L.) (Rosaceae), is a shrub or  
 4 small tree that produces fleshy fruits that are consumed by frugivores, who disperse  
 5 seeds after regurgitating or defecating them. This species is frequently visited  
 6 during July to mid-August by small- and medium-sized birds and carnivorous  
 7 mammals that include fruits in their diets during late summer to winter (Jordano  
 8 & Schupp, 2000). *P. mahaleb* occurs in a patchy distribution at the regional scale,  
 9 with relatively isolated populations consisting of dozens to hundreds of trees. Our  
 10 study population included a total of 196 adult reproductive trees distributed over  
 11 an area of 26 ha in patches of variable density. Other populations within 20 km  
 12 exist as scattered patches of 10–150 trees, with some containing  $\geq 1,000$  trees. The  
 13 nearest population is 1.5 km away. Additional information on the study population  
 14 and description of methodological approaches is reported by Jordano *et al.* (2007)  
 15 and Garcia *et al.* (2009) and references therein.

16 **Sampling dispersed seeds.** To estimate the relative contribution of each dis-  
 17 persal vector to the different categories of dispersal events defined in Table 1,  
 18 we first collected dispersed seeds, following different sampling schemes according  
 19 to the functional group of dispersal vector. We used this grouping of frugivores  
 20 giving the difficulties of resolving the identification of scats, pellets and regurgi-  
 21 tated seeds down to species level just based on visual cues. We differentiated four  
 22 major frugivore types: large carnivorous mammals (such as foxes, badgers, and  
 23 stone martens); two species of medium- and large-sized frugivorous birds, mistle  
 24 thrushes (*T. viscivorus*), and carrion crows (*C. corone*); and a pool of small-sized  
 25 frugivorous birds, including warblers, redstarts, and robins (Jordano *et al.*, 2007).

26 Seeds were collected in 1997–1999 and 2003–2005. The sampling schemes are  
 27 described in detail elsewhere (Jordano *et al.*, 2007; Garcia *et al.*, 2009) and include  
 28 a combination of seed traps and direct sampling of mammal feces along fixed  
 29 transects. We haphazardly collected 130 samples of mammal feces during the  
 30 *P. mahaleb* fruit ripening period and recorded their location relative to potential



31 source trees. Overall, we genotyped 167 seeds from 20 fecal samples. Most samples  
32 were from red fox (*Vulpes vulpes*) and stone marten (*Martes foina*); some ( 10  
33 samples) were from badger (*Meles meles*) (Jordano *et al.*, 2007).

34 In addition we sampled directly the pellets of large corvids (*Corvus corone*) and  
35 from *Turdus viscivorus*, the latter by direct sampling beneath pine trees and scats  
36 from seed traps (see Jordano *et al.*, 2007, for details). Finally, a seed sample di-  
37 rectly from seed traps included seeds dispersed by small- and medium-sized passer-  
38 ines, such as *Phoenicurus ochruros*, *Turdus merula*, *Erithacus rubecula*, *Sylvia com-*  
39 *munis*, *Sylvia atricapilla*, etc. (Jordano *et al.*, 2007). The total seed sample thus  
40 consisted of seed endocarps collected from the seed traps (mostly small passerines)  
41 ( $n=465$ ), mammal scats ( $n=167$ ), and *C. corone* pellets ( $n=23$ ) (see Table 1 in  
42 Jordano *et al.*, 2007).

43 **Seed genotyping.** We used material described in Jordano *et al.* (2007), and  
44 genotyping methods described in detail in previous work (Godoy & Jordano, 2001;  
45 Garcia *et al.*, 2007, 2009). Briefly, we used a set of 10 polymorphic microsatellite  
46 markers (simple DNA sequence repeats) (Godoy & Jordano, 2001) to obtain the  
47 multilocus genotypes of both of the adult trees (candidate source trees from the  
48 study population) and the sample of seed endocarps. Given that all adult trees  
49 in the population had a distinct multilocus genotype, an unambiguous assignment  
50 of each seed to its source tree could be made. When a full match between the  
51 endocarp genotype and any of the adult-tree genotypes in the population was not  
52 possible, we assumed that the seed came from another population. To assess the  
53 effect of genotyping errors, we reexamined the exclusion of genotypes due to a single  
54 locus mismatch, two loci mismatches, etc. At the analysis level, any exclusion of  
55 identity between a seed and a potential mother tree based on mismatches of only  
56 one or two loci was rechecked. We used GIMLET software (Valière, 2002) to find  
57 the matching adult multilocus genotype for each endocarp with eight or more  
58 loci successfully typed. Because each seed belonged to one of the four groups of  
59 dispersers, we could thus derive the relative contribution of each frugivore group  
60 to different classes of seed dispersal events and to seed immigration.

61 **Contribution of dispersal vectors to types of dispersal events.** We con-  
 62 sidered each dispersed seed as an independent replicate, because each represented  
 63 a dispersal event from the perspective of plant population genetics, i.e., an in-  
 64 dependent "arrival" event resulting from the dispersal process mediated by the  
 65 frugivore.

66 Once the maternal source tree of each individual seed was identified (or its prove-  
 67 nance from outside the study population determined) we assessed the dispersal  
 68 distance and grouped the seeds separately as coming from trees located within  
 69 or outside the population. In addition, for seeds originating from local trees we  
 70 determined whether dispersal distances were  $\geq 45$  m to sort out  $LDD_{loc}$  dispersal  
 71 events from  $SDD_{loc}$  events. All the events involving immigrant seeds were con-  
 72 sidered  $LDD_{ss}$  by definition, given that the neighborhood size was very reduced  
 73 (radius= 0.045 km) relative to the geographic limits of the study population (max-  
 74 imum length for a within-population dispersal event: 1220 m)(Garcia *et al.*, 2009).  
 75 Along this reasoning,  $LDD_{neigh}$  events were considered non-existent in this partic-  
 76 ular case study given that neighborhood size area was smaller than the population  
 77 area.

Table S1. Summary of neighborhood area sizes and estimated neighborhood radius for tree species with different combinations of dispersal modes. Data from Nason *et al.* (1998); Garcia *et al.* (2005, 2007) and present study.

Species	Pollinator	Seed disperser	Density ( $ha^{-1}$ )	Breeding unit ( $km^2$ )	Radius (km)
<i>Ficus dugandii</i>	Fig wasp	Vertebrates	0.004	631.7	14.2
<i>Ficus obtusifolia</i>	Fig wasp	Vertebrates	0.072	105.9	5.8
<i>Prunus mahaleb</i>	Bees, flies	Vertebrates	0.003	0.87	0.042
<i>Frangula alnus</i>	Bees, flies	Vertebrates	0.0004	0.45	0.013
<i>Astrocaryum mexicanum</i>	Beetle	Vertebrates	1364.0	0.011	0.06
<i>Calophyllum longifolium</i>	Bees	Vertebrates	0.28	1.241	0.629
<i>Platypodium elegans</i>	Bees	Wind	0.78	0.866	0.525
<i>Cedrus atlantica</i>	Wind	Wind	61.7	0.151	0.22
<i>Frazinus americana</i>	Wind	Wind	24.7	0.008	0.05
<i>Pseudotsuga menziesii</i>	Wind	Wind	25.0	0.078	0.158

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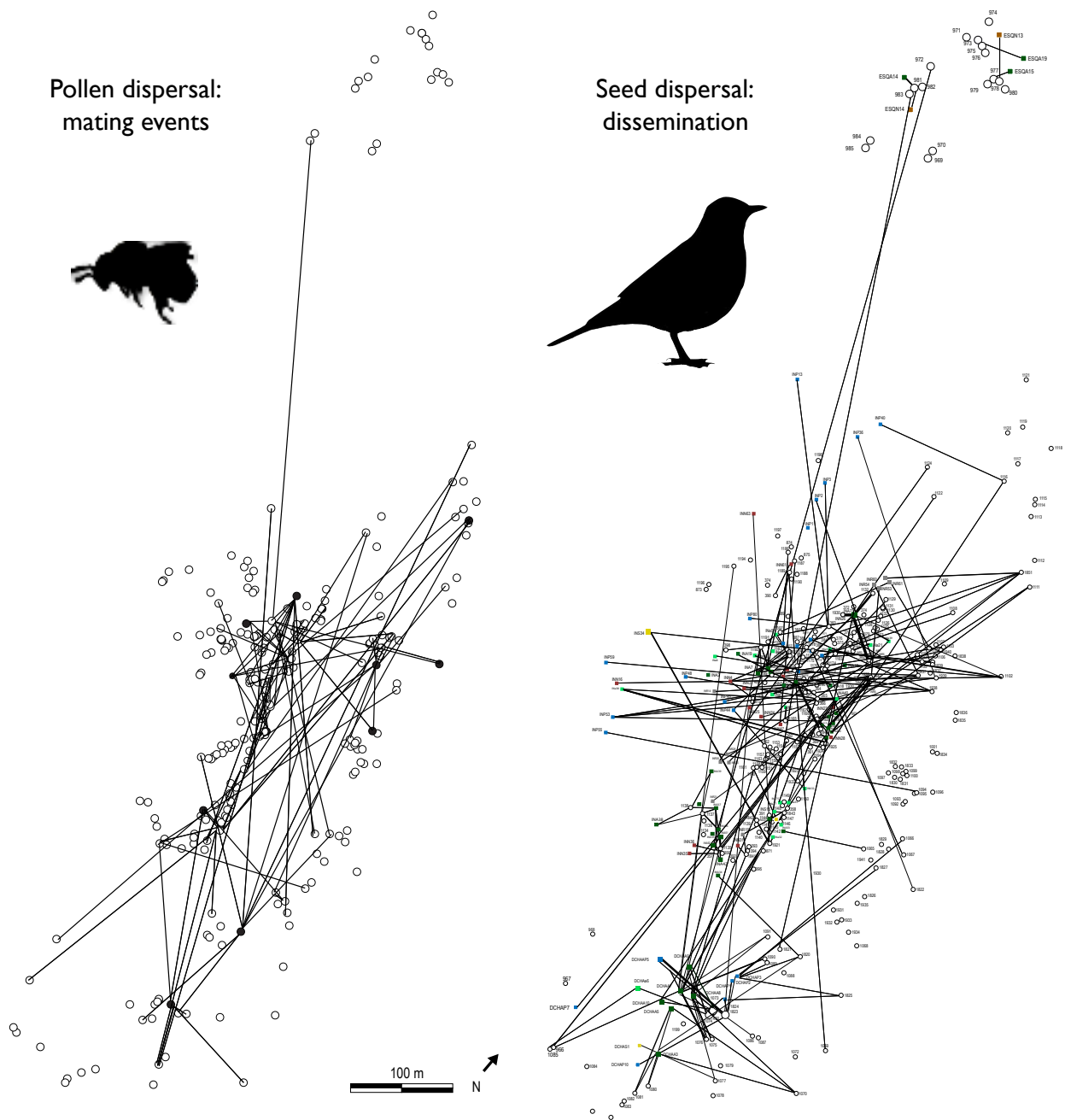


Figure S1. Dispersal events for pollen (left) and seeds (right) traced for *Prunus mahaleb* trees (white dots). All the adult, reproductive, trees in the population are mapped. Lines indicate mating events of pollen dispersal among trees (left) or seed dissemination events from source fruiting trees to seed traps (squares; right). Line thickness is proportional to the number of events recorded.

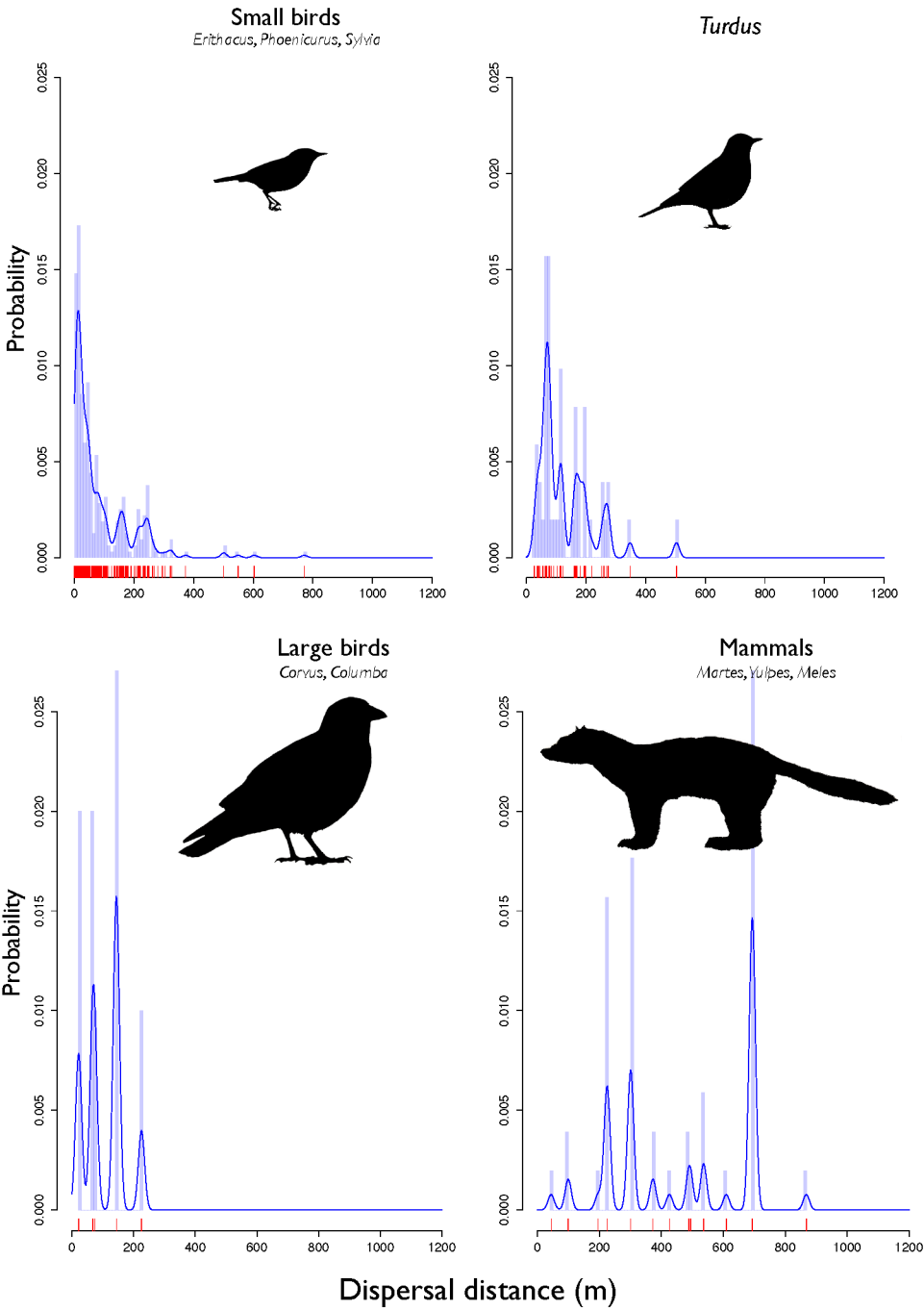


Figure S2. Differential contributions of functional groups of frugivores to the short- ( $SDD_{loc}$ ) and long-distance ( $LDD_{loc}$ ) local seed dispersal events for *Prunus mahaleb*.