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### Short communication

### Adapting the steepness parameter from stock–recruit curves for use in spatially explicit models

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### **ABSTRACT**

To inform the design of MPA networks and ensure that they will meet stated goals, spatially explicit metapopulation models are often used to simulate the response of fished species to MPA implementation. Typically, such models are simply spatial extensions of traditional, nonspatial population models used in fisheries management. A common assumption used in making this transition is that R (0), the slope at the origin of the nonspatial, population-wide egg–recruit relationship (often termed the steepness or compensation ratio), can be used to estimate  $\alpha$ , the slope at the origin of the small-scale settler–recruit relationship used in spatially explicit models. This assumption is not always correct. In particular, the value of R (0) often implicitly accounts for a variety of processes spanning the egg–recruit transition, including larval mortality and advection away from suitable habitat. If a spatial model accounts for some of those loss processes explicitly, such as by using an oceanographically realistic dispersal matrix, it becomes necessary to adjust the estimate of  $\alpha$  upwards to avoid double-counting those losses. Here I present a simple correction involving the dominant eigenvalue of the dispersal matrix that adjusts the value of R (0) to avoid this error. Applying this correction factor ensures that a spatially explicit model will predict population collapse at the same level of fishing implied by a large-scale estimate of R'(0).

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### **1. Introduction**

As marine protected areas (MPAs) become a more common tool for marine conservation and fisheries management ([Lubchenco et](#page-4-0) [al., 2003; Leslie, 2005; Lester et al., 2009\),](#page-4-0) there is increasing interest in the use of spatially explicit metapopulation models to forecast the effects of MPAs on fished populations (reviewed by [Gerber et](#page-4-0) [al., 2003; Pelletier and Mahévas, 2005; Botsford et al., 2008, 2009\).](#page-4-0) Such models can be used in a strategic context, to obtain general relationships between MPA design and population dynamics (e.g., [Botsford et al., 2001\)](#page-4-0) or in a tactical context, to project the population consequences of proposed MPAs in a particular location (e.g., [Meester et al., 2004; Little et al., 2007; Walters et al., 2007; Kaplan](#page-4-0) [et al., 2009; White et al., in press\).](#page-4-0)

The use of tactical population dynamic models for MPA design can be especially valuable ([Pelletier et al., 2008\).](#page-4-0) While strategic modeling efforts have produced general guidelines for MPA design ([Botsford et al., 2001; Gaines et al., 2003; Neubert, 2003; Kaplan and](#page-4-0) [Botsford, 2005; Kaplan, 2006; McGilliard and Hilborn, 2008\),](#page-4-0) the success of a particular MPA or MPA network will be sensitive to the details of habitat distribution, the spatial configuration ofMPAs, lar-

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val connectivity, adult movement, and fishing fleet behavior in that geographical location ([Botsford et al., 2008; Pelletier et al., 2008\).](#page-4-0) Thus site-specific models will be useful for projecting MPA effects when one or more key assumptions of more general strategic models are violated. Furthermore, spatially explicit model predictions should be invaluable in an adaptive management setting. In that case, model projections can be compared to subsequent empirical observations of MPA effects to determine whether MPAs have had the desired effect on populations of interest ([Walters, 1997;](#page-4-0) [Pelletier et al., 2008\).](#page-4-0)

The models used for this type of analysis are typically spatially explicit extensions of nonspatial population models developed for conventional fisheries management (e.g., [Kaplan et al., 2006, 2009;](#page-4-0) [Walters et al., 2007; White et al., in press;](#page-4-0) reviewed by [Pelletier](#page-4-0) [and Mahévas, 2005; Pelletier et al., 2008\).](#page-4-0) Here I identify and propose a solution for a crucial oversight that is often made when making the transition from nonspatial population models to spatial metapopulation models.

### **2. Theory**

For many marine species, population dynamics can be effectively summarized by the relationship between egg production and subsequent recruitment ([Fig. 1;](#page-1-0) [Sissenwine and Shepherd, 1987;](#page-4-0) [Botsford, 2005; Botsford and Hastings, 2006\).](#page-4-0) The saturating nature

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**Fig. 1.** Typical form of the egg–recruit relationship in marine populations. The relationship between egg production and subsequent recruitment is saturating because of post-settlement density-dependent mortality. The equilibrium density of recruits can be found at the intersection of the egg–recruit curve and a line with slope 1/FLEP; several representative examples are shown. The dashed line shows the slope at the origin of the egg–recruit curve, R (0); if 1/FLEP > R (0), the equilibrium recruit density is zero and the population collapses. Here,  $R'(0)$  = 1/0.35, so the population is not persistent for the FLEP = 0.2 case. This curve describes the large-scale relationship represented by nonspatial fishery models. For a spatial model, a similar curve would describe the relationship between larval settler density and subsequent recruit density.

of the curve in Fig. 1 reflects density-dependent resource competition among juveniles. The equilibrium density of recruits is found at the intersection of the egg–recruit curve with a line of slope 1/(lifetime egg production) drawn through the origin [\(Botsford,](#page-4-0) [2005\).](#page-4-0) The value of lifetime egg production (LEP) reflects all postrecruitment processes, including growth, mortality, harvest, and fecundity, integrated over the average lifespan of a new recruit (LEP is essentially equivalent to eggs per recruit, EPR, or spawning stock biomass per recruit, SSB/R, both of which are commonly used in the fisheries literature). Fishing reduces LEP from its natural, unfished maximum, thus increasing 1/LEP and shifting the equilibrium recruit density to the left along the egg–recruit curve. If 1/LEP exceeds the slope at the origin of the egg–recruit curve, termed R (0), the equilibrium density is zero and the stock collapses due to overfishing. That is, the population is persistent if LEP > 1/R (0). This relationship is the basis for the use of biological reference points derived from LEP in conventional fisheries management [\(Goodyear, 1993; Mace and Sissenwine, 1993\),](#page-4-0) and most nonspatial models used in stock assessments and other fisheries contexts incorporate some version of this framework [\(Hilborn and](#page-4-0) [Walters, 1992; Martell et al., 2008\).](#page-4-0)When estimating R (0) it is common practice to scale both LEP and recruitment by their respective maximum values, so that the horizontal axis becomes FLEP, the fraction of unfished LEP ([O'Farrell and Botsford, 2005\),](#page-4-0) and the persistence threshold is FLEP = 1/R (0). This formulation of R (0) is also referred to as the compensation ratio because it is the ratio of recruit survival in the unfished state to survival at near-zero population densities [\(Goodyear, 1980\).](#page-4-0) For convenience the slope can also be parameterized in terms of steepness,  $h$ ;  $R'(0)$  = 4  $h/(1-h)$  [\(Hilborn](#page-4-0) [and Walters, 1992\).](#page-4-0) Regardless of the terminology, the slope of the egg–recruit curve is a fundamental population parameter, and considerable effort has been devoted to estimating its value for various fished populations (e.g., [Myers et al., 1999; Dorn, 2002\).](#page-4-0)

In order to represent MPA effects in any tactical situation, it is necessary to move to a model that is explicitly spatial. In making the transition from nonspatial to spatial models, one must make two major adjustments to the basic model framework outlined above. First, connectivity among locations must be represented in a spatially explicit way, such as using a dispersal matrix ([Botsford et al.,](#page-4-0) [2008, 2009\).](#page-4-0) By contrast, nonspatial models implicitly assume that all portions of a population are equally well connected via some sort of a larval pool. Second, it is necessary to assume that the density dependent process represented by the saturating egg–recruit curve (Fig. 1) is spatially distributed, so that a similar curve describes the density-dependent survival of settlers within each model cell. Given these two adjustments, a simple example of a spatially explicit model would be:

$$
S_{i,t} = \sum_{j=1}^{n} D_{ji} N_{j,t} \phi
$$
  
\n
$$
R_{i,t} = f_i(S_{i,t}) = \frac{\alpha_i}{1 + \beta_i S_{i,t}} S_{i,t}
$$
  
\n
$$
N_{i,t+1} = R_{i,t} + N_{i,t} e^{-(M+F_i)}
$$
\n(1)

where  $S_{i,t}$  is the density of settlers in cell *i* (out of *n* cells) at time t,  $R_{i,t}$  is recruit density, and  $N_{i,t}$  is adult density.  $D_{ii}$  is an element of the dispersal kernel and gives the probability of dispersal from cell  $j$  to  $i$ .  $\phi$  is per-capita fecundity; M is natural mortality,  $F_i$  is the fishing mortality rate in cell *i*, and function  $f_i(S)$  is a Beverton–Holt function with initial slope  $\alpha_i$  and asymptotic maximum  $\alpha_i/\beta_i$ . The density-dependent Beverton–Holt parameter  $\beta_i$  may vary over space, reflecting variation in habitat availability or predator density (e.g., [Osenberg et al., 2002; White, 2008\).](#page-4-0) The Beverton–Holt slope  $\alpha_i$  may also vary over space, though there has been little empirical attention to this possibility, and it is typically assumed that it takes on a constant value  $\alpha$ , as in the nonspatial version. I will make the same assumption here, unless otherwise noted.

More complex, age-structured versions of Eq. (1) are commonly used (e.g.,[Walters et al., 2007\),](#page-4-0) and [Kaplan et al. \(2006\)](#page-4-0) showed that the steady-state equilibrium for such models can be found rapidly by iterating this system of equations:

$$
S_i = \sum_{j=1}^{n} D_{ji} R_j \text{FLEP}_j
$$
  
\n
$$
R_i = f_i(S_i) = \frac{\alpha}{1 + \beta_i S_i} S_i
$$
\n(2)

where the effects of fishing, natural post-settlement mortality, and age-dependent fecundity are now encapsulated by the value of FLEP<sub>i</sub> in each cell *i*. The formulation given in Eq.  $(2)$  makes the parallel between the nonspatial and spatial models quite clear, because population persistence in Eq. (2) depends on the value of  $FLEP_i$ (and its spatial distribution) relative to  $\alpha$ , just as persistence in the nonspatial case depends on the value of FLEP relative to R (0). Consequently, it is standard practice to parameterize  $\alpha$ , the slope of the Beverton–Holt settler–recruit relationship in Eq. (2), using an estimate of R (0) derived from the large-scale, nonspatial stock–recruit or egg–recruit relationship ([Kaplan et al., 2006, 2009; Little et al.,](#page-4-0) [2007; Walters et al., 2007; McGilliard and Hilborn, 2008\).](#page-4-0) However, this approximation may be biased in some cases.

Consider the rationale for describing population dynamics in terms of the egg–recruit relationship. It is exceedingly difficult to observe and measure larval movement, survival, and settlement, and there are virtually no data on these processes for most species. By contrast, it is more straightforward to measure egg production and recruitment over multiple years and estimate the slope at the origin of the egg–recruit relationship (assuming the egg production data extend sufficiently close to zero). Therefore it is possible to obtain an empirical estimate for  $R'(0)$  and thus for the value of FLEP that leads to population collapse. However, it is important to be mindful of the suite of processes that are subsumed within the egg–recruit relationship: given X eggs,  $R(X)$  will survival the larval

<span id="page-2-0"></span>period, avoid advection into open water, return to suitable habitat, and successfully recruit to the adult population. Thus one could decompose R (0) into its component processes:

$$
R'(0) = r_1 \, r_2 \, r_3 \, \dots \, r_n \tag{3}
$$

where the *n* values of  $r_i$  each represent the probability of surviving one of the series of processes (larval mortality, advection, finding suitable habitat, settlement, etc.) spanning the egg–recruit transition.

Within a spatial metapopulation model, it is possible to explicitly represent some of the processes implicitly contained within R (0) in Eq. (3). For example, consider a rocky reef fish population along a coastline containing both rocky- and soft-bottom habitat. It is reasonable to expect that some of that species' larvae disperse to non-habitat (i.e., soft-bottom) locations, where they do not survive. In a nonspatial model, that larval loss is one of the processes  $r_i$  represented by  $R'(0)$  in Eq. (3). In a spatial model, that loss could be represented explicitly by the larval dispersal matrix (the  $n \times n$ matrix **D** of dispersal probabilities  $D_{ii}$ , as in Eqs. [\(1\)–\(2\)\),](#page-1-0) which will specify the fraction of larvae that are lost to non-habitat locations. Thus it would be improper to use  $R'(0)$  as an estimate of  $\alpha,$ because that would effectively double-count process  $r_i$ . Instead, one would ideally use  $\alpha$  =  $R'(0)/r_i$ . Depending on the complexity of the method used to estimate **D**, the spatial model could include explicitly a range of the processes implied by Eq. (3), including offshore advection and larval mortality, and the value of  $\alpha$  would need to be corrected to account for each of these.

As a practical matter, we lack independent estimates of the probabilities  $r_i$ , so it is difficult to apply the desired correction to  $R'(0)$ . Rather the only value that has empirical support is R (0) itself, which has been derived from observations of the egg–recruit relationship of an actual population. However, it is reasonable to expect that as estimates of the dispersal kernel become more realistic (e.g., moving from an idealized, one-dimensional dispersal kernel to a dispersal matrix estimated from the output of a numerical circulation model) and account for more of the processes implicitly described by R'(0), the value of  $\alpha$  should be reduced so as not to double-count those processes in the spatial population model. I now propose a method to accomplish this and demonstrate its validity.

#### **3. Methods**

The key empirical result that should be preserved in the spatial population model is that the population collapses if  $FLEP < 1/R'(0)$ . If one considers population dynamics at low density (i.e., near the point of collapse), it is reasonable to ignore density-dependent processes and use a linear approximation to the nonspatial model, so that  $R_{t+1}$  =  $R'(0) \times R_t \times$  FLEP (e.g., [Hastings and Botsford, 2006\).](#page-4-0) Similarly, a linearized version of the spatial model can be written using matrix notation as

$$
\mathbf{R}_{t+1} = \mathbf{A} \cdot [\mathbf{D} \times (\mathbf{R}_t \cdot \mathbf{L})] \tag{4}
$$

where **A** is an  $n \times 1$  vector of the slope  $\alpha_i$  at each location, **R** is an  $n \times 1$  vector of the recruit density at each location, **D** is an  $n \times n$  matrix of dispersal probabilities  $D_{ii}$ , and **L** is an  $n \times 1$  vector of FLEP<sub>i</sub> at each location;  $\times$  represents matrix multiplication and · represents elementwise (Hadamard) multiplication. Making the assumption that  $\alpha$  and FLEP are constant across space (i.e., scalars), representing the scenario implied by the nonspatial model, Eq. (4) becomes

$$
\mathbf{R}_{t+1} = \alpha \mathbf{D} \times \mathbf{R}_t FLEP \tag{5}
$$

Defining matrix  $C = \alpha \times D \times FLEP$ , then the dynamics are  $\mathbf{R}_{t+1} = \mathbf{C} \times \mathbf{R}_t$ . Because **C** has only non-negative entries, the Perron–Frobenius theorem applies and the population will persist (i.e.,  $\mathbf{R}_t$  will increase over time rather than decreasing towards zero) if  $\lambda_c$ , the dominant eigenvalue of **C**, is greater than 1 ([Caswell, 2001; Hastings and Botsford, 2006\).](#page-4-0) Equivalently,  $\lambda_{\text{D}}$ , the dominant eigenvalue of **D**, must be greater than  $1/(\alpha FLEP)$ , and the population does not persist if  $FLEP < 1/(\alpha \lambda_D)$ . Therefore, in order to preserve the result that the population is not persistent if FLEP <  $1/R'(0)$ , one must parameterize the slope of the settler–recruit function to be

$$
\alpha = \frac{R'(0)}{\lambda_D}.\tag{6}
$$

This correction ensures that any larval loss explicitly accounted for in **D** (such as larval mortality, advection offshore, or dispersal to non-habitat, or any other process implied by Eq. (3)) is not implicitly accounted for by  $\alpha$ . For this correction to account for dispersal to non-habitat, **D** must represent the failure to settle in non-habitat as a dispersal probability of zero. The magnitude of the correction in Eq. (6) will depend on how many of the suite of possible processes  $r_i$  are explicitly accounted for in **D**. If no larval loss processes are represented by **D** (e.g., if **D** consists of a dispersal kernel that integrates to one along an infinite coastline with homogenous habitat; [Botsford et al., 2001\),](#page-4-0) then  $\lambda_{\mathbf{D}} = 1$  and  $\alpha = R'(0)$ . Note that it should be possible to adjust this correction factor for the case in which  $\alpha$  is known to vary spatially (as implied by vector **A** in Eq. (4)), but the connection to a large-scale aggregate estimate of  $R'(0)$  is less clear and I do not pursue that special case here.

To demonstrate the use of the correction in Eq. (6), I simulated the dynamics of population occupying a one-dimensional coastline with heterogeneous habitat, using the model given in Eq. [\(2\). T](#page-1-0)he coastline consisted of spatial units that were classified as either suitable habitat or non-habitat. Larval dispersal among cells was modeled using a Gaussian dispersal kernel, so that the probability of dispersal from cell *j* to cell *i*,  $D_{ji}$ , was a function of the distance between  $i$  and  $j$  and given by a normal distribution with a mean of zero and a standard deviation, d, that defined the mean dispersal distance in one direction ([Largier, 2003\).](#page-4-0) Larvae were assumed to die if they dispersed to non-habitat cells, a process that was represented by setting  $D_{ii} = 0$  for all non-habitat cells *i*. The dispersal matrix **D** thus accounted for some larval loss that would be implicitly included in R (0) in a nonspatial model. This is a relatively simple example intended for illustrative purposes (although it similar to the representation of **D** used in several recent tactical MPA models; [Kaplan et al., 2006, 2009; White et al., in press\).](#page-4-0) In a more sophisticated setting, **D** might be estimated using output from a numerical circulation model (e.g., [Paris et al., 2007\),](#page-4-0) and more larval loss processes (the  $r_i$  in Eq. (3)) would be represented explicitly.

Coastlines with a range of habitat heterogeneities were represented using a spatial domain with a total of 20 linear units of which a fraction p were a contiguous string of habitat cells and the remainder were non-habitat cells (i.e., 12 habitat cells followed by 8 non-habitat cells would be a  $p = 60\%$  coastline). Values of  $p$ ranged from 60 to 100%, which is similar to the range of rocky reef habitat coverage used in a one-dimensional model of the California coast [\(Kaplan et al., 2009\).](#page-4-0) To avoid edge effects the coastline was made circular. Modeled species had dispersal distances of  $d = 0.5$ , 1, 5, and 10 spatial units. All species were assumed to have a persistence threshold of  $1/R'(0)$  = 0.35. This corresponds to a Goodyear compensation ratio of  $\kappa$  = 1/0.35 = 2.86, and a steepness of h = 0.42, similar to estimates of steepness for several eastern Pacific rock-fishes [\(Dorn, 2002\).](#page-4-0) In other words, this is an estimate of  $R'(0)$  that one might obtain from typical fisheries data.

For each combination of dispersal distance d and level of habitat coverage, p, I determined the minimum value of FLEP for which the population was persistent. This was done using the dispersal-

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**Fig. 2.** Coast-wide value of FLEP (fraction of unfished lifetime egg production) at which a spatially explicit population model predicts population collapse (defined as nonzero density of recruits in at least one model cell at equilibrium). Models were run for species with a range of dispersal distances on coastlines with a range of habitat heterogeneity. Habitat density describes the proportion of the coastline that was suitable settlement habitat. Model species all had a nonspatial, coast-wide persistence threshold of  $1/R'(0)$  = 0.35. Actual persistence thresholds in the spatial model were calculated without the proposed correction to  $\alpha$ , the slope at the origin of the settler–recruit curve. When the proposed correction was applied to  $\alpha$ , all model runs matched the targeted threshold of 0.35, regardless of dispersal distance (not shown).

per-recruit method of [Kaplan et al. \(2006\)](#page-4-0) to find the equilibrium density of recruits in each cell, **R**. Persistence was defined as at least one nonzero element of **R** at equilibrium. I determined the persistence threshold using both the commonly used approximation  $\alpha$  = R'(0) and the corrected version from Eq. [\(5\).](#page-2-0)

#### **4. Results and discussion**

When R (0) = 1/0.35 (the nonspatial persistence threshold) was used as a direct estimate of  $\alpha$ , the simulation model indicated (erroneously) that the FLEP required for population persistence was greater than 0.35 whenever the coastline had less than 100% habitat coverage (Fig. 2). Furthermore, the increase in the minimum FLEP threshold estimated by the simulation model was much greater for longer dispersal distances. This phenomenon is a consequence of a nonzero fraction of spawned larvae effectively dying when they dispersed to non-habitat cells. For short dispersal distances, most larvae settled in the cells where they were spawned, and there was little effect of the non-habitat cells. As dispersal distances increased, larger proportions of larvae spawned in each cell were lost to non-habitat cells, and the model indicated that greater larval production (FLEP) was required for persistence. By contrast, when the corrected estimate of  $\alpha$  from Eq. [\(5\)](#page-2-0) was used, the persistence threshold was always the correct value: FLEP = 0.35.

These model results reveal that if 1/R (0) had been estimated (nonspatially) as 0.35 for a population with spatially heterogeneous habitat (i.e., less than 100% of the coastline is covered with suitable habitat), a corresponding spatial model would predict that the population would collapse even for values of FLEP > 0.35. Thus, without the proposed correction, the spatial analogue of a nonspatial model would produce strikingly different predictions regarding population persistence. Specifically, species with longer dispersal distances would be erroneously predicted to be more vulnerable to fishing than shorter distance dispersers, especially along coastlines with patchy habitat distributions. Following from this one could also expect biased predictions regarding the level

of FLEP corresponding to maximum sustainable yield or other quantities.

It is worthwhile to consider the possible effects of error in estimating  $\lambda_{\bf p}$ . Even sophisticated representations of **D**, such as from numerical ocean circulation models, may introduce unexpected errors into estimates of dispersal, and thus population persistence. For example, one might generally expect  $\lambda_{\bf D}$  derived from circulation models to overestimate the loss of larvae due to physical advection because such models often poorly resolve extreme nearshore areas where larvae may be retained ([Largier, 2003\)](#page-4-0) and may not perfectly represent larval behaviors that can be crucial to retention and onshore transport ([Paris et al., 2007\).](#page-4-0) The predictions of such models are also sensitive to poorly known quantities such as larval mortality rates, although it is unclear whether typical estimates of larval mortality are biased in a particular direction. However, if larval losses were overestimated, the value of  $\lambda_{\bf D}$  would be erroneously high, producing lower estimates of the minimum value of FLEP needed for population persistence in simulation models. Large downward errors in  $\lambda_{\mathbf{D}}$  could cause population models to predict that a population could support erroneously high levels of fishing (low FLEP), so the correction factor should be used with that caution in mind.

It is important to note that the correction proposed here is appropriate only when R (0) has been empirically estimated in a large-scale, nonspatial context by analyzing a population-wide egg–recruit or stock–recruit relationship (e.g., [Myers et al., 1999;](#page-4-0) [Dorn, 2002\).](#page-4-0) Alternatively, if  $\alpha$  were estimated directly from a settler–recruit relationship measured at a small spatial scale comparable to the individual cells in spatial model, no correction would be necessary because the estimate of the slope parameter would not implicitly include larval loss processes. While direct estimation of  $\alpha$  is possible when data are available, such as for some coral reef species (e.g., [White, 2008\),](#page-4-0) the assumption that  $\alpha$ =R'(0) has been the norm in most fishery applications [\(Little](#page-4-0) [et al., 2007; Walters et al., 2007; Kaplan et al., 2009\).](#page-4-0) As such, future fisheries studies should employ the correction factor applied here (e.g., [White et al., in press\),](#page-4-0) especially as more sophisticated representations of larval connectivity, larval mortality, and other processes become increasingly available and can provide explicit representations of the various processes in Eq. [\(3\)](#page-2-0) ([Botsford et al.,](#page-4-0) [2009\).](#page-4-0)

In light of the results presented here, re-examination of some prior model results may be called for. In particular, spatially explicit models of coastlines with heterogeneous habitat that directly parameterized  $\alpha$  from nonspatial estimates of  $R'(0)$  may have somewhat underestimated recruit survival and overestimated the persistence threshold, especially for widely dispersing species (e.g., [Walters et al., 2007; Kaplan et al., 2009\).](#page-4-0) That said, the general result presented by [Kaplan et al. \(2009\)](#page-4-0) remains entirely correct: given a constant value of  $\alpha$  and heterogeneous settlement habitat, longer distance dispersers require greater FLEP for persistence. The caveat is that such results should be interpreted as representing the case in which similar values of  $\alpha$  have been estimated at small scales for both long- and short-distance dispersers. If, on the other hand, similar values of R (0) were estimated for longand short-distance dispersers, then the correction factor should be applied to  $\alpha$  to ensure that a spatial model recaptures the same persistence threshold [i.e.,  $1/R'(0)$ ] evident in the natural population. Unfortunately, as [Kaplan et al. \(2009\)](#page-4-0) noted, both largeand small-scale estimates of this crucial demographic parameter are sorely lacking. Given the importance of  $\alpha$  to population persistence and conservation planning, additional research effort to estimate its value for key species would be welcome. In the meantime, the procedure proposed here should ensure that largescale estimates are not misused in their application to small-scale problems.

#### <span id="page-4-0"></span>**Acknowledgements**

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