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Designing spatially-explicit reserve networks in the presence of mandatory sites

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ABSTRACT

In the selection of reserve networks there are special sites whose ecologic, strategic or morphologic values dictate their inclusion. The existence of regional rare or confined-distribution species is one among other reasons that often determines the existence of such mandatory sites. Moreover, quite often these mandatory sites are located far apart. Although several methods have been proposed to accommodate structural connectivity in reserve selection, they were not devised to deal specifically with such mandatory sites. Those that encourage aggregation of sites by means of criteria incorporated in the objective function do not seem suitable to acquire consistent connectivity levels in the presence of mandatory sites. Methods that enforce “full connectivity” tend to produce long and narrow solutions, which results in efficiency deficits and biological unsuitability, as they force the selection of more sites of less quality to ensure connectivity. Hence specific methods to select ecological reserves when mandatory sites exist are needed. Here we discuss and propose a 0–1 linear programming model to deal with this issue. The model was applied in two data sets of forest breeding birds and butterflies. Its solutions and computational performances are discussed.

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1. Introduction

In a world of a changing climate and increased human-directed impacts on ecosystems it urges to implement effective measures to protect biodiversity. Reserves should provide representative samples of biodiversity and combine additional biological considerations (Araújo et al., 2002) with socio-economic ones (Williams et al., 2003). Thus, limited resources should be used efficiently, harboring the maximum diversity, or any other valued conservation feature, with minimum cost or area (Pressey et al., 1993; Margules and Pressey, 2000; Rodri-

gues et al., 2000). There are multiple methodological issues to consider in the selection and establishment of reserve networks. One issue of concern is the spatial arrangement of protected sites (Diamond, 1975; Margules et al., 1982; Pressey et al., 1997; Margules and Pressey, 2000) which should exhibit high levels of connectivity (Collinge, 1996; Tischendorf and Fahrig, 2000; Calabrese and Fagan, 2004).

Fragmentation as the opposite of connectivity, has impact on biodiversity, increasing isolation of habitats, endangering species and modifying population dynamics (Zidema et al., 1996; Miller and Calle, 2000; Moilanen and Hanski, 2001;

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Malcolm and ReVelle, 2002). It may cause negative effects on species richness (Mace et al., 1998) by reducing the probability of successful dispersal and establishment of populations (Brokaw, 1998), by limiting the capacity of a patch of habitat to sustain resident populations and, or by enhancing vulnerability of small fragmented populations to stochastic events (Kapos et al., 2000) (but see, Araújo et al., 2004 for a discussion on possible benefits of scattered areas on climate change).

Connectivity has been understood as functional or structural according to whether ecological functions or only inter-site configurations are considered (Tischendorf and Fahrig, 2000; Calabrese and Fagan, 2004).

Functional connectivity explicitly accounts for species' specific responses to habitat, where structure and quality of both the matrix and the reserve network influence the conservation value of selection units (e.g., Cabeza and Moilanen, 2001; Moilanen and Cabeza, 2002; Cabeza, 2003; Westphal and Possingham, 2003; Cabeza et al., 2004; Moilanen, 2005; Williams et al., 2005; Moilanen and Wintle, 2006; Van Teeffelen et al., 2006). It can be interpreted as an indicator of the dispersive aptitudes of populations for the establishment of genetic, demographic and energetic fluxes along the landscape, which are relevant for their persistence (Hanski, 1999; Macdonald and Johnson, 2001). Reserve selection methods implementing this type of connectivity should be established coupled with multi-representation targets to interface with the spatial population dynamics (Pressey et al., 2003; Malcolm and ReVelle, 2005).

Structural connectivity is a spatial feature which only regards to the patterns of distribution of sites independently of any species' specific dispersal ability (Opdam et al., 2003). The persistence of biological units and ecosystem processes can benefit from structural connectivity (Lande, 1988; Frank and Wissel, 1998; Hanski and Ovaskainen, 2000). In particular, aggregation and compactness are likely to reduce edge effects (enhanced disturbance or predation, invasive species, changes in abiotic conditions, see, Gaston et al., 2002).

Several methods have been proposed to accommodate structural connectivity in reserve selection. Some of these formulations include cost minimization options together with constraints forcing the existence of buffer zones surrounding certain selected sites (Williams and ReVelle, 1998; Clemens et al., 1999); the maximization of the number of adjacent pairs of sites (Nalle et al., 2002); enforcement of proximity between pair-sites, with the requirement that the sites representing a species will not be farther apart than a stated distance (Williams, 2006); minimization of the distances between pairs of sites to be included in the network (Nicholls and Margules, 1993; Briers, 2002; Önal and Briers, 2002), the summed distance between all pairs of sites (Briers, 2002; Nalle et al., 2002), the maximum distance between sites (Önal and Briers, 2002), the boundary length, a measure of compactness, of a reserve network (Fischer and Church, 2003, 2005; Önal and Briers, 2003), or a combination of boundary length and total area (Possingham et al., 2000; McDonnell et al., 2002). All these models treat connectivity as a quantified target incorporated somehow in the objective function. Stricter proposals by Williams (2002), Cerdeira et al. (2005), Cerdeira and Pinto (2005), Önal and Briers (2005, 2006), Fuller et al. (2006) seek to identify "fully connected" reserves (i.e., consisting of a unique con-

nected cluster) of minimum size, satisfying the species representations requirements.

Functional and structural responses may differ (With and King, 1997; Pimm and Lawton, 1998) as functional solutions may not be structural connected, and vice versa. Yet, there are situations where the use of reserve selection methods based on structural connectivity may lead to networks that are functionally well connected. For example, when one wants to protect a large set of species belonging to the same functional group (i.e., with similar habitat response mechanisms), general assumptions can be made to circumvent the lack of information on effective ecological aptitudes of individual species, providing the habitats where they are more likely to disperse. Accordingly, when functional connectivity is intended but no practical approach is available, structural connectivity may be used, supplying robust solutions in terms of biological value.

The objective of this study is to develop a model for selecting reserve networks, which incorporates structural connectivity meant to operate in situations where special sites considered as mandatory site exist. Mandatory sites are commonly present in the management of ecological reserves. This follows, among other reasons, from being highly irreplaceable for the protection of species (cf, Pressey et al., 1994), being occupied by source populations, being refuge areas where species can survive extreme environmental conditions, or being central or peripheral in respect to the species' spatial distribution (Gaston et al., 2002). Although, the inclusion of mandatory sites seems the least of the problems, as the selection process has no option to drop them out, the spatial configuration of the resulting reserves will be strongly conditioned by their presence. The existence of mandatory sites, particularly when distant from each other, may deteriorate the performance of existent approaches which account for structural connectivity to identify spatially-coherent reserve networks. Indeed, the "fully connected" models (Williams, 2002; Cerdeira et al., 2005; Cerdeira and Pinto, 2005; Önal and Briers, 2005, 2006; Fuller et al., 2006) will outcome long and narrow spatial structures. As a result one loses efficiency (Pressey et al., 1994) and biological value by forcing the selection of more sites of less quality (Williams, 1998; Woodruffe and Ginsberg, 1998). Methods that search for efficient connected solutions by means of criteria incorporated in the objective function also do not seem suitable to acquire consistent connectivity levels in the presence of mandatory sites. For example, if mandatory sites would be quite apart, the minimum diameter reserve model of Önal and Briers (2002) would probably select the remaining sites somewhere on the convex hull defined by the mandatory sites. If minimization of the summed distances between all pairs of selected sites (e.g., Briers, 2002; Nalle et al., 2002) was applied, the most probable solutions would configure clusters of selected sites equidistant from the mandatory sites, leaving them isolated and vulnerable. Models that seek boundary-length minimization (e.g., Fischer and Church, 2003, 2005; Önal and Briers, 2003) do not take special attention to the mandatory sites, and clusters of the remaining selected sites would probably be formed somewhere in the focal space.

It thus seems to be important to develop specific methods that explicitly account for the existence and location of these

mandatory sites to induce spatial coherence and enhance the efficiency on the resulting reserve networks.

Our proposal is based on the idea that, for spatially-coherence, it may be realistic to let mandatory sites act like independent “attractive centres” allowing aggregation of different clusters around them. Ideally, it would be desirable to find efficient networks where fragmentation is confined to a number of clusters limited by the number of mandatory sites. This may reverse edge effects, encouraging the buffering and shielding of mandatory sites, which by their special character may be considered vulnerable.

We present and discuss a 0–1 linear model that goes in this direction. An application with two data sets is performed and reports on computational experiments to access the aptitude of the model are given.

2. Materials and methods

2.1. Data

To access the ability of the model we worked with two data sets. One data set (data from Standley et al., 1996) represents the distribution (i.e., presence/absence records) of 118 species of forest breeding birds in the Berkshire’s County, UK, on a grid map consisting of 391 (2×2 km) eligible parcels. The other set (data from Sawford, 1987) represents the distribution of 45 species of butterflies within 496 (2×2 km cells) eligible sites from Hertfordshire’s County, UK.

We ranked the species according to their increasing number of occurrences in the landscape to determine a set of rare species (top 25%). This resulted in 30 rare species of forest breeding birds and 12 rare species of butterflies. The most frequent of the rare forest breeding birds occurs in 36 sites (9.2% of study area), and the most frequent rare butterfly species is presented in 14 sites (2.82% of study area). We assigned single representation targets (i.e., protection of at least one population) for the common (non-rare) species, and larger representation targets for the rare species as described below.

Mandatory sites result from a number of different reasons. However, in our computational experiments only those sites that become irreplaceable for species to be represented according to their targets are mandatory.

2.2. A first approach to deal with mandatory sites

We aim to develop a method to select sites satisfying species representation targets, and which accounts for connectivity around the mandatory sites.

Ensuring species representation targets by means of integer linear programming can be straightly settled with

$$\sum_{i \in V_s} x_i \geq t_s, \quad \text{for every species } s \quad (1)$$

$$x_i \in \{0, 1\}, \quad \text{for every site } i \in V \quad (2)$$

where V is the set of all candidate sites, $V_s \subset V$ is the set of sites where species s is represented, $t_s \geq 1$ is the specific target representation required for species s , and the 0–1 variable x_i indicates whether site i is selected ($x_i = 1$), or not ($x_i = 0$).

To guarantee that the solutions include all the mandatory sites the equations

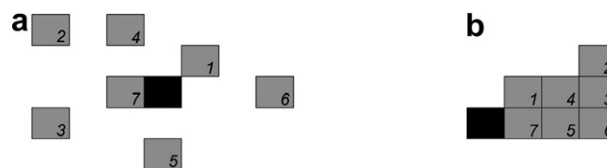


Fig. 1 – A fragmented (a); and an aggregated/connected (b) hypothetical configuration of a reserve system, each consisting of one mandatory site (dark square) and 7 other sites numbered 1–7 (gray squares). Both present the same value under the objective function (4).

$$x_i = 1, \quad \text{for every mandatory site } i \quad (3)$$

are added.

If maximum efficiency disregarding the spatial aspects was intended, the objective function would be $\min \sum_{i \in V} x_i$ and the optimal solutions would have the minimum number of sites. When $t_s = 1$ this is the well known set covering problem (Cocks and Baird, 1989).

A reasonable approach to enhance some level of connectivity when dealing with mandatory sites is to consider each one as an “attractive centre” for the remaining sites that will be selected to represent species. A simple procedure in this direction consists in minimizing the sum of distances from the selected sites to their nearest mandatory site. The resulting model is (1)–(3) with the objective function

$$\min \sum_{i \in V} D_i x_i \quad (4)$$

where D_i is the distance from site i to its nearest mandatory site.

This model certainly encourages the selection of sites around the mandatory sites. However, no other spatial relationship between sites is taken into account. For example, despite being considerably different as far as aggregation is concerned, the objective function (4) retrieves the same value for the two configurations in Fig. 1.

2.3. The proposed mandatory-based model

If clustering of sites is important, as it happens when one intends to avoid edge effects, we would like the model to be able to distinguish the more aggregated configuration in Fig. 1b from the one in Fig. 1a. Therefore, we devised a way to give the model enough flexibility to differentiate between these patterns, turning those which are less fragmented more appealing. This was achieved with an objective function which associates to each site i the distance to the nearest selected site somewhere “in between” i and its nearest mandatory site. (The meaning of “in between” a site and its nearest mandatory site will be discussed later.)

To illustrate this idea consider the configurations in Fig. 2. The objective function (4) weights the set of sites in Fig. 2a as the sum of their distances to their nearest mandatory sites. Our suggestion is to assign to this set a weight equal to the sum of the distances corresponding to the arcs in Fig. 2b. The arc originating from site i links i to its nearest selected site “in between” i and its nearest mandatory site (Fig. 2b).

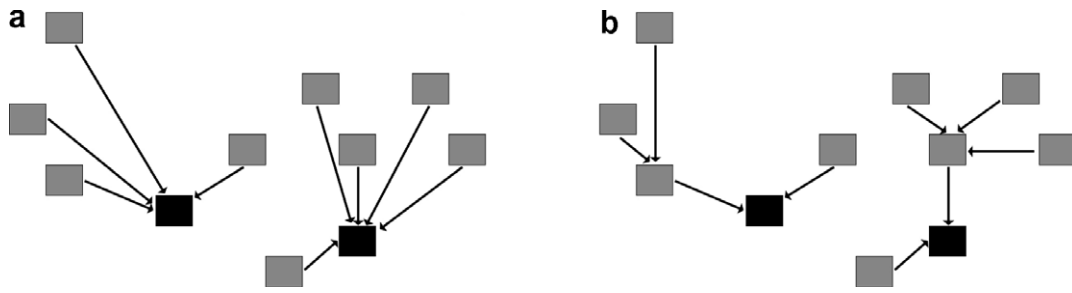


Fig. 2 – Illustration of different spatial layouts of the objective function (4) (a) and (9) with d_i as in (10) (b). The first one is related to the minimization of the summed distance to mandatory sites (distance-to-mandatory metric), the second one with the minimization of the summed distance to the nearest neighbor site (mandatory-based metric). Dark squares represent mandatory sites, gray squares represent selected sites, edges' length refers to distances.

Let H be the set of all mandatory sites. For each site $i \in V \setminus H$, let $h(i)$ be its nearest mandatory site (if there are more than one choose any one of them), and let $V(i)$ denote the set of sites “in between” i and $h(i)$. Several possibilities for $V(i)$ can be envisaged. In our computational experiments we defined $V(i)$ to be the set of sites different from i in the rectangle having i and $h(i)$ as opposite vertices. (Another possibility could be $V(i) = \{j: \max\{d(i,j), d(j,h_i)\} < D_i\} \cup \{h(i)\}$, where $d(u,v)$ is the distance between sites u and v .)

We aim to introduce in the model (1)–(3) new variables that, for each chosen site i , identify the selected site j in $V(i)$ which is closest to i .

For this purpose we consider the variables y_i^j satisfying the constraints

$$\sum_{j \in V(i)} y_i^j = x_i, \quad \text{for every site } i \in V \setminus H \quad (5)$$

$$y_i^j \leq x_j, \quad \text{for every site } i \in V \setminus H \text{ and } j \in V(i) \quad (6)$$

$$y_i^j \in \{0, 1\}, \quad \text{for every site } i \in V \setminus H \text{ and } j \in V(i) \quad (7)$$

In the presence of (7), each Eq. (5) ensures that, when site i is selected (i.e., $x_i = 1$) there will be exactly one site $j \in V(i)$ for which y_i^j will be equal to 1 and, in case i is not selected (i.e., $x_i = 0$), for every j in $V(i)$, y_i^j will be equal to 0.

Inequalities (6) restrict sites j in $V(i)$ for which y_i^j can take value equal to 1, to those sites that have been selected (i.e., $x_j = 1$).

When $x_i = 1$, to guarantee that the unique site j in $V(i)$ for which $y_i^j = 1$ will be the one closest to i , define

$$d_i = \sum_{j \in V(i)} d(i,j) y_i^j, \quad \text{for every site } i \in V \setminus H \quad (8)$$

and let

$$\min \sum_{i \in V \setminus H} d_i \quad (9)$$

be the objective function.

Indeed, if in any solution $y_i^j = 1$ and $x_k = 1$, for some $k \in V(i)$ such that $d(i,k) < d(i,j)$, then setting $y_i^k = 1$ and $y_i^j = 0$ would decrease d_i and consequently the value of the objective function.

With this model, contrarily to the previous one, the choice of a site depends on the spatial distribution of other selected sites and not only on the location of its nearest mandatory site. When a site i is chosen it will play, in some sense, the role of a mandatory site making the sites which are close to i more

attractive for selection. Although in general this is a desirable feature to promote the aggregation of the chosen sites, if the distance D_i , from i to $h(i)$, is large this can contribute to the formation of clusters far from every mandatory site.

In addition, the model does not explicitly enhance the search for highly efficient solutions. As an example, consider four consecutive sites on a vertical or horizontal line of a grid, and suppose that one of the extreme sites of that segment is a mandatory sites. From these four sites only the two extreme ones in the line segment contributed to the objective value (9) with three units of distance. The remaining sites inflate the cost and are not considered in the model's objective.

These drawbacks can be overcome by taking as the objective function a convex combination of the objective functions of the two previous models (4) and (9) linked with (8). Such function will account, not only for the distance between a site and other selected sites, but also for the distance between that site and its nearest mandatory site. This amounts to replace the definition (8) of d_i by

$$d_i = \sum_{j \in V(i)} (\alpha d(i,j) + \beta D_i) y_i^j, \quad \text{for every site } i \in V \setminus H \quad (10)$$

with $\alpha, \beta \geq 0$, $\alpha + \beta = 1$.

The 0–1 linear formulation for the resulting model is therefore (9), (1), (2), (3), (5), (6), (10) and, interestingly, instead of (7) stating that every variable y_i^j must be 0 or 1, it can be proved that only the non-negative constraints

$$y_i^j \geq 0, \quad \text{for every site } i \in V \setminus H \text{ and } j \in V(i) \quad (11)$$

should be added. Indeed, take any solution x, y of the above model with $y_i^1, y_i^2, \dots, y_i^k > 0$ summing 1. If j_s is a site, among j_1, j_2, \dots, j_k , for which the minimum value of $d(i, j_1), d(i, j_2), \dots, d(i, j_k)$ is attained, then the value of (9) will not increase and no constraint will be violated by letting $y_i^s = 1$ and $y_i^l = 0$, for every other $l = 1, 2, \dots, k$ different from s . This simplification speeds up the computational procedure.

This model permits to balance clustering and proximity around the mandatory sites. Clustering is enhanced by increasing the values of the parameter α . The weights assigned to β regulates levels of scattering of sites within the neighbourhood of mandatory sites.

Computational tests were performed on a computer with an Intel Pentium IV, 3.20 GHz processor and 504 MB RAM. CPLEX 9.0 was used to solve the integer programming problems.

3. Results

We carried out several computational experiments with the forest breeding birds and the butterflies data sets with different representation targets for the rare species. Here we report results obtained requiring at least three sites for each rare species or, in case the species occurs in less than three sites, all the sites where the species is represented.

To provide a benchmark for efficiency, the solutions from the new developed mandatory-based (MB) model are compared with those of maximum efficiency (ME), in which species' representation requirements and inclusion of all mandatory sites are accomplished within the minimum number of sites. Fig. 3 shows the ME and the MB solutions obtained for each data set, and Table 1 describes some of their properties. Besides giving the number of sites, some measures are displayed to evaluate their spatial configurations. The boundary/area ratio was used as a measure of compactness. To assess the proximity of the selected sites from their nearest mandatory sites, the sum and the average of the distances from each site and its nearest mandatory site were computed. To analyse the performance with respect to the metric developed within the MB model, the value of (8) (the sum of distances of the edges that link each selected site to its nearest neighbour) is given. This metric can somehow rate the structural connectivity of the outcomes. Since this value depends on the number of selected sites, we also present the result of dividing the metric by the number of selected sites. We refer to these

two values as the MB metric and the average MB metric, respectively.

The representation targets used for rare species have determined the existence of 10 and 11 mandatory sites, which are obligatory for the achievement of bird and butterfly species' representation, respectively.

ME solutions, shown in Fig. 3, consist of 23 and 20 sites scattered over the study area, and fail to guarantee a reasonable level of protection by buffering effects of close-by selected sites.

The MB model was developed to promote buffering around mandatory sites. For breeding birds protection 30 sites were selected (Fig. 3) which is an increase on reserve size when compared with the ME solution. However (see Table 1), this additional number of sites decreases the boundary/area ratio index of compactness (1.60 vs. 1.91), better countering edge effects. The overall distance of distances to mandatory sites is 85.90 km (less 46% that the minimum set representation solution). When averaged by the number of sites selected this reduction passes to 65%. Curiously, for butterfly species' the MB model has delivered a solution with 20 sites to protect, equaling the ME solution (Fig. 3). The values of the spatial descriptors for the ME and MB solutions compare similarly as for the forest breeding birds (Table 1), which again indicates a better spatial coherence of the later. The differences between these values are mainly due to the rearrangement of three distant isolated sites (18, 54 and 279) of the ME solution (Fig. 3). The boundary/area ratio decreases from 1.90 of the ME solution to 1.65 of the MB solution. The sum of distances to

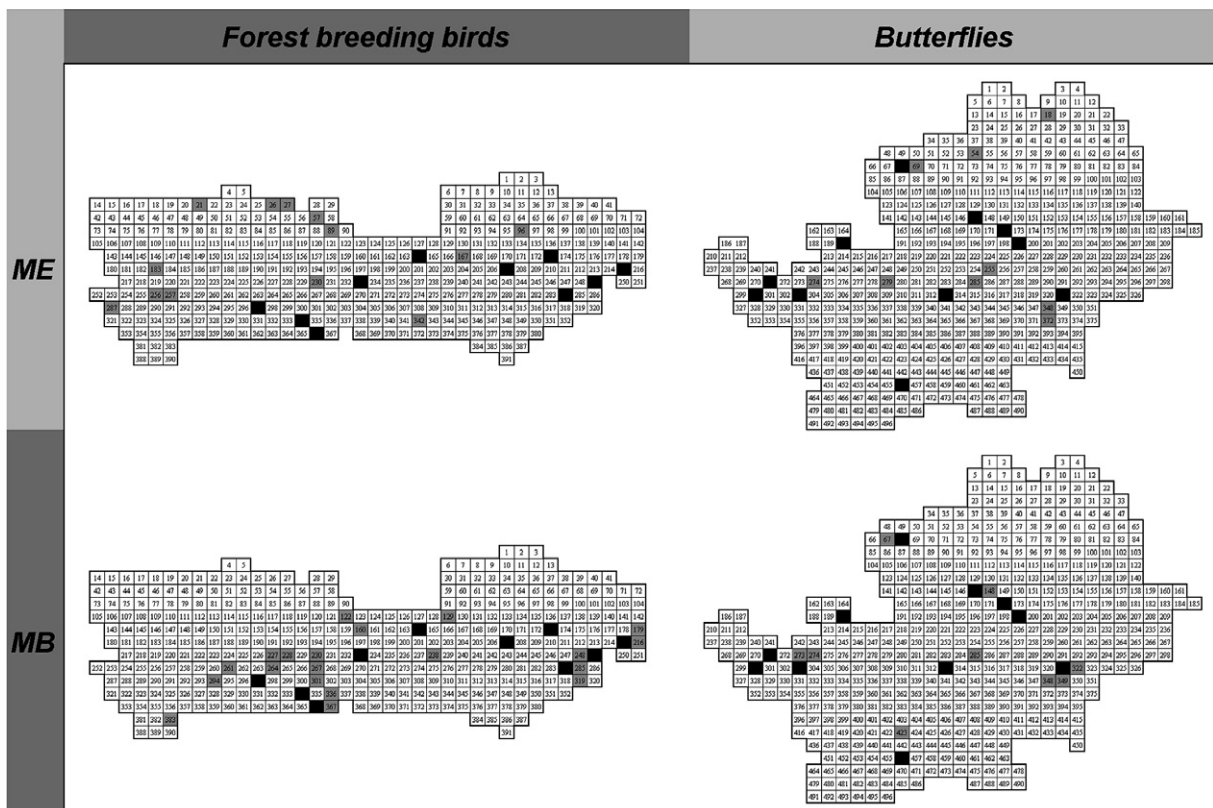


Fig. 3 – Selected grid cells under two tested models (MS: minimum set; MB: mandatory-based) applied over the forest breeding birds' and butterflies' data sets. Black cells indicate mandatory sites and gray cells other selected sites.

Table 1 – Morphometric and spatial descriptors of the solutions produced by the two tested models (ME model and MB model) applied on forest breeding birds' and butterflies' data sets

	Forest breeding birds		Butterflies	
	Solution ME	Solution MB	Solution ME	Solution MB
No. sites	23	30	20	20
No. mandatory	10		11	
Mandatory sites	104;173;207;215;233;249;294;334;365		68;147;172;100;100;271;300;313;321;450	
Boundary area (km ⁻¹)	1.91	1.60	1.90	1.65
DM (km)	159.44	85.90	59.48	24.13
Averaged DM (km/site)	12.26	4.30	6.61	2.68
MB (km)	172.74	109.21	61.48	28.13
Averaged MB (km/site)	13.29	5.46	6.83	3.12
CPU time (s)	0.02	0.84	0.03	0.08

No. sites: number of selected sites; No. mandatory: number of mandatory sites; mandatory sites: enumeration of the mandatory sites; boundary/area length: ratio between the outside perimeter of the reserve network and its area; DM: summed distance to mandatory sites (see Fig. 2a); averaged DM: averaged distance to mandatory sites, DM/No.sites; MB: mandatory-based metric: distance from each selected site to its closest neighbour (see Fig. 2b); averaged MB: averaged mandatory-based metric, MB/No.sites; CPU time: computational time.

mandatory sites is 59.48 km and 24.13 km for the ME and the MB solutions, respectively. The averages show the same proportion, since both solutions have the same number of sites.

With respect to the MB metric, the MB and the ME solutions applied over the breeding birds data set score 109.21 km and 172.74 km, respectively. This indicates that an improvement on proximity between sites was accomplished. One third of the sites of the MB solution are selected in a small region defined by the rectangle with cells 226 and 367 as opposite vertices (Fig. 3). This means that several sites were chosen close together, thus contributing to reduce the value of (8). An accumulation of selections also occurs in the right-hand side near the three mandatory sites 215, 249, 284. All mandatory sites, but 173 and 209, seem to be somehow reasonable protected by nearby sites. The averaged MB metric gives mean distance per site of 5.46 km (less 59% than ME solution), showing a better individual-site performance with respect to structural connectivity. Similarly, the ME and MB butterflies networks presents values for MB metric of 61.48 km and 28.13 km, respectively, and average MB metric values of 6.83 km/site and 3.12 km/site (Table 1).

ME models produced for both data sets have run very quickly, spending 0.02 s and 0.03 s. While the MB solution for the butterfly species' network was achieved within 0.08 s, the breeding birds' MB solution required 0.84 s, which is about 40 times more than the computational time needed to get the ME solution (Table 1). This is still, however, quite acceptable when applied to such a medium-sized data set.

4. Discussion

Here we show that when explicitly accounting for the existence of mandatory sites, the proposed MB model can be a suitable tool to produce reserve networks designed to face edge effects and nearby matrix deregulations, among other stressors. This may bring a greater expectation of conservation success when planning for reserve selection.

A strong point of the MB approach resides on the ability to accommodate three attributes comprised within reserve

selection (efficiency, inter-site distance, and protection of important sites), in a simple linear mathematical description. This representation seems to allow effective computations for at least medium-sized data sets.

The MB model is especially relevant for species exhibiting a metapopulation structure, which seem to be the case of many butterfly species (Thomas and Hanski, 1997; Hill et al., 2001) and forest birds (Hinsley et al., 1995; Fahrig, 2002). Their persistence resides in balance between extinctions and colonizations, which turns species difficult to persist if their populations are fragmented. Moreover, the high ecological value of source areas (i.e., where immigration fluxes guarantee most of the species' survival, Hanski and Ovaskainen, 2000), make those special sites potential candidates to be considered as mandatory.

Despite its positive aspects, several concerns regarding the MB model should be pointed out.

First, it could be argued that since the model incorporates the distance from each site to its nearest predetermined mandatory site, a network with one or a few remote sites may be preferred to an alternative with several tightly packed sites far from the mandatory site. This problem may be circumvented by tuning the α and β parameters in (10). Increasing α one can accent the distance between sites. Increasing β significance is given to the proximity to the nearest mandatory site. To judge on the differences between solutions, sensitivity analysis can be performed. Varying levels of aggregation and proximity stakeholders intervene on the selection process, allowing the guidance to more conceivable solutions.

A second aspect concerns an issue that arises upstream on the conservation planning process which is the identification of the mandatory sites (Pressey et al., 1993). While the assumption of the pre-designation of these areas may be conceivable (e.g., "gap analysis", and the extension of existent reserve networks, Scott et al., 1993), locating "prioritized" areas, i.e., irreplaceable areas, may be itself a difficult task (Pressey et al., 1994). Indeed, choices can be grounded on a variety of factors such as location relative to sites already "reserved", cost, condition, and the occurrence of special features like rare species, distinctive landscapes or recreational opportuni-

ties. Each choice alters the representation of features, their assemblage patterns and therefore, the potential contribution of all the “unreserved” sites. If mandatory status for site i is assigned, two separated approaches are conceived regarding the MB model “protocol”: (1) explicitly acting as a mandatory site of the MB model, i.e., making $x_i = 1$ and adding i to the list H of mandatory sites; or (2) forcing i to present by means of $x_i = 1$ but not including i in H , and therefore not being designated to act as an attractive area for the selection of other neighbor sites. Both approaches are expected to retrieve different solutions, and their viability is somehow linked with the protection status we want to give to each specific mandatory site. Once again we emphasize the aptitude of the model to deal with this issue, by allowing some degree of freedom for choices and assumptions.

The third issue relates to the identification of sites that should serve as the nucleus of an optimal cluster, which may be a complex problem. According to Shafer (1999), priority sites may not necessarily serve as nucleus of clusters. In our model these attractive nucleus are identified with the mandatory sites. In point 2 of the previous comment, we explain how the MB model can handle this situation. It may also be desirable that certain non-mandatory sites perform the role of “attractors”. This can be easily achieved by including these sites in H .

5. Conclusions

The optimal solution may not necessarily be the ultimate plan selected by the resource manager. However, it provides the baseline of what can be accomplished at different investment levels against which alternative selections meeting additional objectives can be compared.

The present model is particularly useful to be applied on fragmented landscapes for which information about species specific response to fragmentation is not available. It is not intended to be the final answer along the implementation step of conservation planning. For the establishment of reserves suitable for the long-term persistence of biodiversity many elements, including those resulting from deep knowledge of the region, should be considered. Many land managers are either unaware of the methods, or perhaps more often, unaware of how they can be used to get the most from their local expert knowledge. Nevertheless, we trust that the outcomes of the model can provide a valuable basis to assist stakeholders in conservation planning. Hence, people will appreciate that models are just a tool for getting the most out of the assumptions on a quantitative way. This kind of decision support management makes area selection easily accessible and widespread, improving the chances of preserving the most of biodiversity.

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