



Distribution patterns of biodiversity and the design of a representative reserve network in Portugal

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Abstract. Representativeness is a desirable property of conservation networks. In this paper an attempt is made to assess the efficiency of current conservation networks in Portugal in representing vertebrates (reptiles and amphibians) and plants (gymnosperms, pteridophytes and bryophytes). It was found that whilst the protected areas do not sample all species in the database they provide a better result than choosing areas at random. For the goal of maximizing representation of taxa per unit area hotspots and complementarity performed better. A pattern of over-representation of vertebrates in relation to lower plants was discovered among selected conservation areas in Portugal suggesting that charismatic organisms with large home ranges may not always be the most appropriate surrogates for biodiversity when representativeness is sought. When

trying to fill the gaps in current protected areas with additional areas only complementarity performed better than choosing areas at random. Both rarity and richness hotspots gave worse results. Opportunistic administrative criteria such as supplementing the PAS with other conservation areas (CORINE Biotopes) without taking into account their contribution to a representation goal was nearly half as good as choosing areas at random. The results recall for the need of explicit goals and accountable methods in area selection for conservation and reinforce the role of complementarity for finding additional areas to protected areas when limited resources are available for 'in situ' conservation.

Key words. Biodiversity, complementarity, gap analysis, hotspots, Portugal, representativeness.

INTRODUCTION

Area selection for biodiversity conservation is concerned with representation and persistence of target attributes within sets of areas. Two major representation problems arise in planning conservation area networks.

The first is that not all groups of organisms can be included within data for area selection procedures. The use of one group to infer patterns for other groups is widely accepted, but there remains the question of 'which ones?' In Europe (and most of the world) this has been done by focusing conservation efforts on more charismatic groups such as terrestrial vertebrates and

flowering plants and expecting these to represent the 'interests' of other less charismatic organisms. But do such groups act as good indicators for the other groups? The predictive ability of some groups has been demonstrated by some studies (e.g. ICBP, 1992; Pearson & Cassola, 1992; Gaston & David, 1994; Beccaloni & Gaston, 1995; Williams & Gaston, 1998; Williams *et al.*, in press) but discouraged by others (e.g. Prendergast *et al.*, 1993; Lawton *et al.*, 1994; Williams & Gaston, 1994; Gaston *et al.*, 1995; Prendergast & Eversham, 1997).

The second problem is that the total area available for conservation is limited. In a world designed by conservationists, parks and reserves should be as many and as large as the requirements for persistence of wild populations in their environments would require. However, the resources allocated for conservation are limited, neither is the conservationist's view of the world unquestionable in a society of multiple (often conflicting) interests. For that reason, conservation

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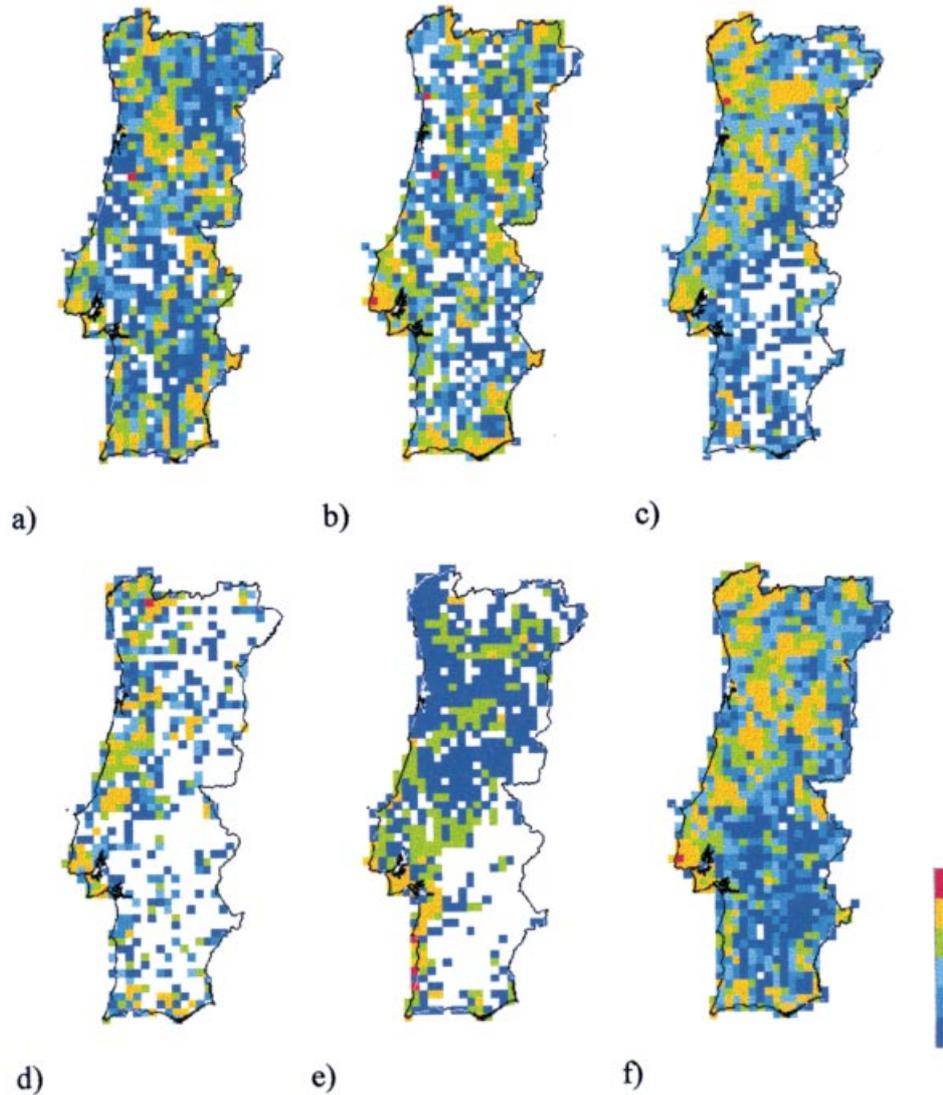


Fig. 1. Species richness for five groups of animals and plants in Portugal and combined map of richness for all groups: (a) amphibians, seventeen spp., max. richness in a grid cell 15; (b) reptiles, twenty-six spp., max. richness in a grid cell 17; (c) pteridophytes, sixty-six spp., max. richness in a grid cell 32; (d) bryophytes, ninety spp., max. richness in a grid cell 34; (e) gymnosperms, nine spp., max. richness in a grid cell 5; (f) combined map of richness, 208 spp., max. richness in a grid cell 82. Records are located on 993 UTM 10 by 10-km grid cells. Richness scores were divided into six colour-scale classes of approximately equal size by number of grid cells, with maximum scores shown in red and minimum in blue, with white for zero scores.

policies should be carefully targeted in order to optimize the total area available for conservation and the representation of taxa within this area (e.g. Vane-Wright *et al.*, 1991; Pressey *et al.*, 1993; Church *et al.*, 1996). Even if limiting thresholds of land availability are

not made explicit, it is likely that once a conservation network is set up it becomes increasingly difficult to add new areas to the whole set.

In this paper an attempt is made to address these problems in the context of *in situ* conservation in

Portugal using distribution data for some vertebrates (reptiles and amphibians) and plants (gymnosperms, pteridophytes and bryophytes). The efficiency of the current Portuguese protected areas system to represent all selected taxa is tested against a null model and compared to other conservation scenarios using hotspots and complementarity. Different procedures to find additional areas for the conservation of unrepresented taxa are investigated and discussed. Possible biases in the representation of different taxa are explored. Three questions in particular are asked.

- (1) How well does the current Portuguese protected areas system (PAS) represent various groups of plants and animals? How does it compare to choosing areas at random, for hotspots, or for complementarity?
- (2) Are all groups equally well represented? Is there any particular bias towards favouring particular groups at expenses of others?
- (3) How well do hotspots and complementarity perform when applied to fill the gaps of representation in the current conservation networks in Portugal?

THE DATA

Distribution data

Analyses are based on distribution data for selected vertebrates (amphibians and reptiles) and plants (gymnosperms, pteridophytes and bryophytes) (Fig. 1). The data were compiled from published atlases (Franco & Rocha Afonso, 1982; Oliveira & Crespo, 1989; Casas *et al.*, 1985/89/92) and additional records obtained from continuing digital database projects. These included (1) the commercial 'Nature Database', which puts together published and unpublished data on vertebrate and plant distributions at a national scale; and (2) the University of Évora 'UNIBA database' (Miles, in press), which is part of a regional biological records centre project. Presence data was referenced onto 993 UTM 10 by 10-km grid cells. Distribution data represented 208 species including seventeen amphibians, twenty-six reptiles, sixty-six pteridophytes, nine gymnosperms and ninety bryophytes. The median of the number of records per species across taxa was 178 for the amphibians, 80 for the reptiles, 37 for the gymnosperms, 22 for the pteridophytes and 10 for the bryophytes. Overall, this included a total of 15,039 records. In Portugal, there are no published atlases for

other vertebrates (except for birds, but at a non-UTM compatible grid) or higher plants. Digital databases are beginning to compile distribution data on a UTM 10 by 10-km grid for other groups, but data sets are still very incomplete.

Conservation areas

Two kinds of conservation areas were considered: (1) protected areas classified under the Portuguese legislation (PAS); and (2) areas designated under the European CORINE (Co-ordination of Information on the Environment) Biotope project. The first set of areas was selected using a progressive process of designation, which started in 1971 and is still undergoing. Lobby groups such as environmental NGO's and academic researchers substantially influenced the choice of the areas. Following Pressey (1994) and Pressey & Tully (1994) these areas may have been selected in an *ad hoc* fashion because criteria for selection were not explicit and reserves located depending on political constraints of the moment. The CORINE areas include sites considered by the EU worthy of conservation. The selection of these areas was supported by a set of formal criteria, which were made explicit before the evaluation of areas was carried out. These include choosing sites with the presence of vulnerable habitats, with high richness for a particular taxonomic group and high richness for a syntaxon of phytosociological unit (Heywood, 1995). Terrestrial vertebrates and flowering plants were the favoured surrogates for biodiversity.

Boundaries of protected areas and Corine biotopes were extracted from a vector map and transferred to a raster format of 10 by 10-km grid cells. Only squares with at least one third of their area covered by protected areas or classified Corine biotopes were considered. For squares lying on the border with either Spain or the ocean, full representation was considered regardless of the proportion of the grid covered.

METHODS

Gaps in representation

The efficiency of current conservation networks was assessed using a procedure similar to gap analysis (Scott *et al.*, 1993; Kiester *et al.*, 1996). In the U.S., gap analysis has been associated with attempts to map land cover types and predict distribution of vertebrates so

as to identify which remain underrepresented in areas managed primarily for biodiversity. Other interpretations of the concept may see gap analysis as a simple overlay procedure 'seeking to identify gaps in biological reserve networks that may be filled through the establishment of new reserves' (Biggs *et al.*, 1990). Outside the U.S., examples of this simplified type of gap analysis can be seen from Australia (Pressey & Tully, 1994), Europe (Castro Parga *et al.*, 1996; Moreno *et al.*, 1996; Williams *et al.*, 1996), New Zealand (Linzey & Harvey, 1995) and South America (Fjeldså & Rahbek, 1997). In this paper four steps were followed: (1) map surrogate attributes to biodiversity, i.e. vertebrate and plant species; (2) map conservation networks, i.e. protected areas and EU CORINE network areas; (3) identify gaps in representation by overlaying the maps obtained in 1 and 2; (4) explore additional areas to complement current conservation areas using quantitative area selection methods such as hotspots of richness, hotspots of rarity and complementary areas.

Quantitative area selection methods

Three different types of methods were contrasted: hotspots of richness, hotspots of rarity and complementary areas. Hotspots were originally used for seeking areas world-wide with exceptional concentrations of species richness, narrow endemics, and areas facing exceptional degrees of threat (Myers, 1988, 1990). Subsequently the term has been used in the narrower sense by listing, for example top 5% of areas of exceptional richness (e.g. Prendergast *et al.*, 1993; Curnutt *et al.*, 1994; Williams *et al.*, 1996) or recommending those areas with many species of restricted range size (ICBP, 1992; Williams *et al.*, 1996). In this paper hotspots were calculated for richness (sum of species occurrence records in each grid cell) and range-size rarity hotspots (calculated for all species in a grid cell as the sum of each species' inverse number of grid-cell records = $\sum (1/c_i)$, $i: c_i \neq 0$, $1 \leq i \leq n$, where c_i is the number of grid cells occupied by species i).

Complementarity is a more direct approach to the problem of representation and may be defined as the extent to which an area, or set of areas, contributes unrepresented attributes to an existing set of areas (Vane-Wright *et al.*, 1991). To find complementary area sets, heuristic techniques have often been used (e.g. Kirkpatrick, 1983; Ackery & Vane-Wright, 1984; Margules *et al.*, 1998; Pressey & Nicholls, 1989; Rebelo & Siegfried, 1990; Vane-Wright *et al.*, 1991; Bedward

et al., 1992; Pressey & Tully, 1994; Saetersdal *et al.*, 1993; Kershaw *et al.*, 1994; Williams *et al.*, 1996; Pressey *et al.*, 1997). These methods find near-optimal combinations of areas to a given representation goal (Csuti *et al.*, 1997). Two representation problems have been formalized: (1) minimum area set solutions—seeks representation of attributes a given number of times in a near minimum number of areas; (2) maximum area coverage solutions (e.g. Church *et al.*, 1996)—seeks to maximize representation of attributes in a given fixed limit for area or cost. In this paper I used an adapted version of the Margules *et al.* (1988) near-minimum set algorithm to choose areas to represent all taxa a given number of times (e.g. to select all taxa at least once). Changes to the original algorithm included (i) two additional levels of tie-breaking, (ii) a test to reject any areas that in hindsight are redundant, and (iii) a final re-ordering of areas to provide an approximate solution for 'maximum-coverage' problems (see Williams *et al.*, in press for details).

Random areas

In order to assess the efficiency of conservation networks for representing biodiversity, their performance was compared against an equivalent number of areas chosen at random. This was achieved by simulating random choices of areas where species have been recorded. Simulations were repeated 1000 times to estimate the average number of species that would be expected to be represented by chance. A simple test was made by comparing conservation networks to results of random choices at the top 5% of scores among these 1000 trials (Williams *et al.*, in press). This is a guide to the maximum number of species that might be expected to be represented by chance, so deviations from this model may be interpreted as a test for significant differences in efficiency for different conservation networks. This is an improvement over some earlier tests based on random choices (e.g. Rebelo & Siegfried, 1992; Saetersdal *et al.*, 1993; Williams & Humphries, 1993) which made additional assumptions about the expected frequency distribution of the representation scores.

All analysis were carried out using WORLDMAP 4 (Williams, 1996), software package designed to explore patterns of diversity, rarity and their implications for area selection.

Table 1. An assessment of the efficiency of the current PAS in Portugal in terms of area required for representing all taxa. Included are a random selection (1000 simulations) of areas with the same number of grid cells as for the PAS, the top 8.9% of the species richness and range-size rarity hotspots, and the minimum set required to represent all species once (complementarity). It is also shown the minimum set required to represent all species four times.

	No. areas	% Taxa
1. Protected areas (PAS)	85	89
2. Random selection, 5% upper tail	85	80
3. Hotspots richness	85	98
4. Hotspots rarity	85	99
5. Complementarity, 1 representation	27	100
6. Complementarity, 4 representations	88	100

RESULTS

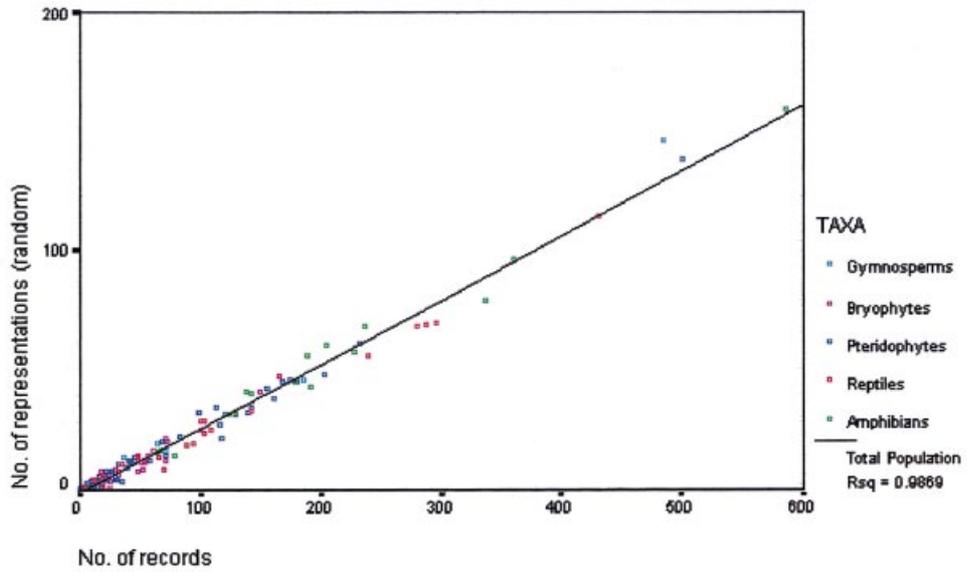
Question 1. How well does the current Portuguese protected areas system (PAS) represent various groups of plants and animals? How does it compare to choosing areas at random, for hotspots, or for complementarity

The total number of grid cells occupied by the PAS is eighty-five (8.7% of the grid cells); 11% of the taxa in the database are not represented within the current system of protected areas in Portugal (Table 1, row 1). It was found that the performance of the PAS in representing all taxa is significantly better than choosing areas randomly (Table 1, row 2). A comparison of the performance of the PAS with the results of applying area selection techniques such as richness and rarity hotspots and complementarity areas to the data set is shown in Table 1 (rows 3, 4, and 5). Given the goal of representing all species at least once the existing PAS was the least successful followed by richness hotspots, rarity hotspots and complementarity. Given a goal of four representations for all species, complementarity was able to define an alternative network for full representation with 88 areas (Table 1, row 6). This represents an increase in number of only three areas compared to the 85 areas of the PAS, which was unable to fulfil the goal of one representation.

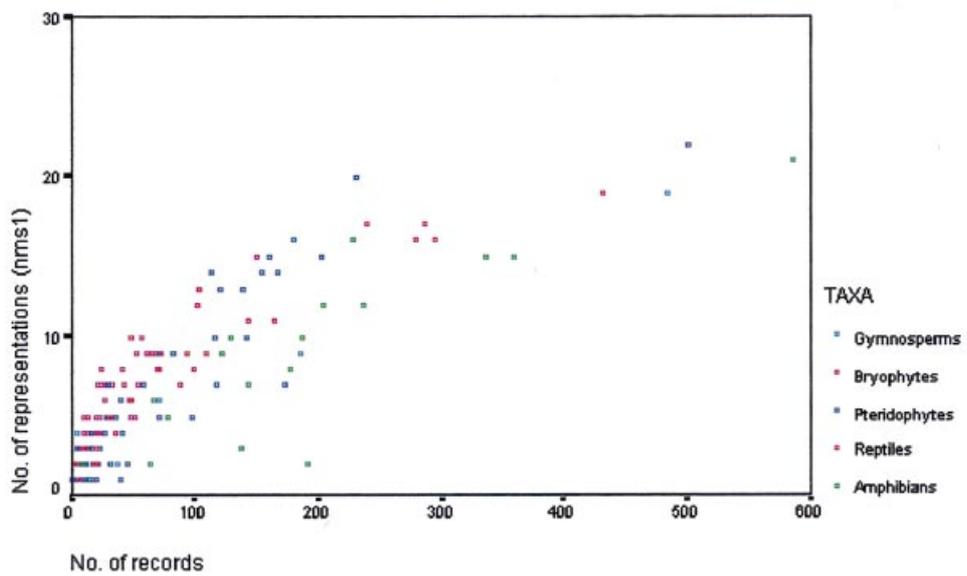
Question 2. Are all groups equally well represented? Is there any particular bias towards favouring particular groups at expenses of others?

If areas were chosen at random one would expect a close correlation between species representation and their frequency distribution. As in Fig. 2a common species would be proportionally more represented than rare species ($R_{sq}=0.99$). If areas were selected to favour rare species this curve would tend to deviate from a linear relationship and approximate to an asymptote, i.e. rare species should be proportionally more represented than common species. This is what happens when selecting areas using Margules *et al.* (1988) near-minimum set algorithm to select all species at least once (Fig. 2b). Intuitively that is what is expected for most conservation policies. Figure 2c shows how patterns of representation of organisms in the PAS relate to the number of records. In particular, there is an over-representation of rare species. No taxonomic bias is obvious from clumping of points in this figure. In contrast, the relationship between the number of representations of organisms in the PAS + CORINE network and the number of records (Fig. 2d) is close to what would be expected by chance (Fig. 2a). However, examining the residuals a taxonomic bias seems to appear. Amphibians and reptiles are over-represented in comparison to bryophytes and pteridophytes. Gymnosperms seem to follow a random pattern with no clear bias in representation.

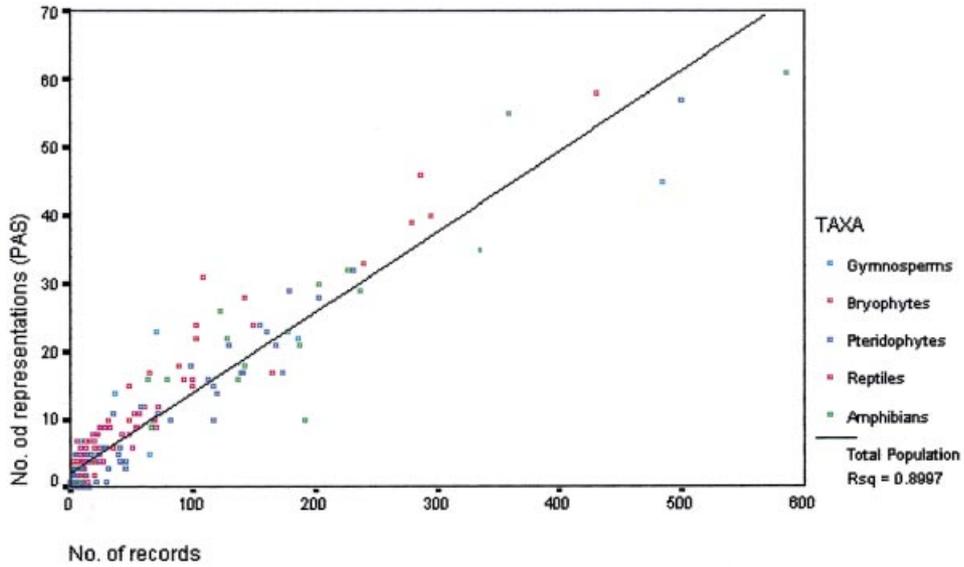
This general pattern of over-representation of terrestrial vertebrates over lower plants is also apparent from the taxa that fail to be represented in conservation networks (Fig. 3). For example, in the PAS all reptiles, amphibians and gymnosperms are represented at least once. Gaps of representation (Appendix) are found only for pteridophytes (eight species missing out of sixty-six species in the database) and bryophytes (fourteen species missing out of ninety species in the database). Amongst the unrepresented bryophytes thirteen are Red Data Book species (Sérgio *et al.*, 1994): one extinct; five vulnerable; and seven rare. Criteria to classify species as extinct may, in some cases, over-estimate the real number of extinctions (Diamond, 1987) since they rely on the definition of some arbitrary threshold for when the taxon was last recorded. In this case species not recorded after 1950 were considered extinct (Sérgio *et al.*, 1994). No national or Iberian Red data list is available for



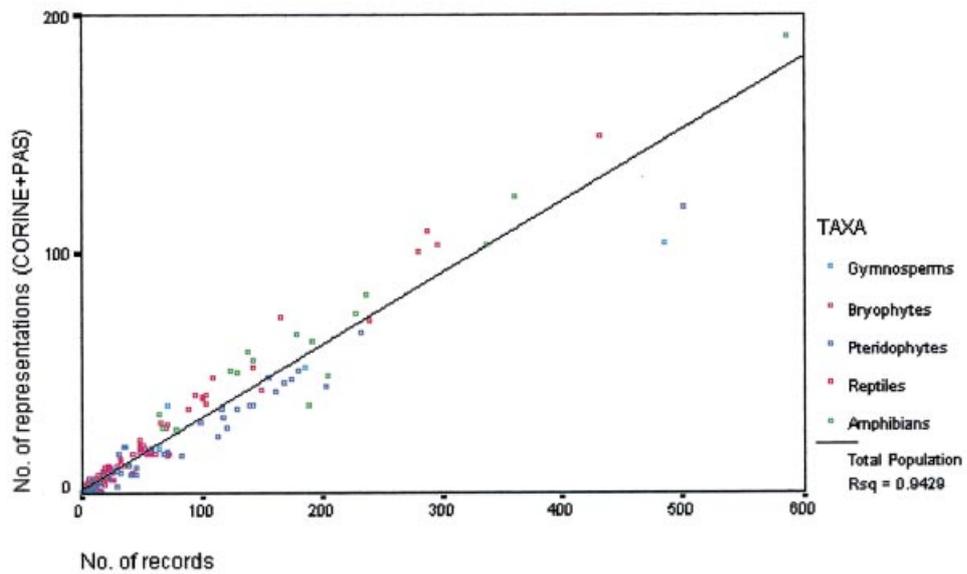
a)



b)



c)



d)

Fig. 2. Relationship between the number of represented species and their frequency in the data: (a) when areas are chosen at random; (b) when areas are chosen for the one-representation goal using the near-minimum set algorithm; (c) for the protected areas system in Portugal; (d) for the CORINE Biotopes network.

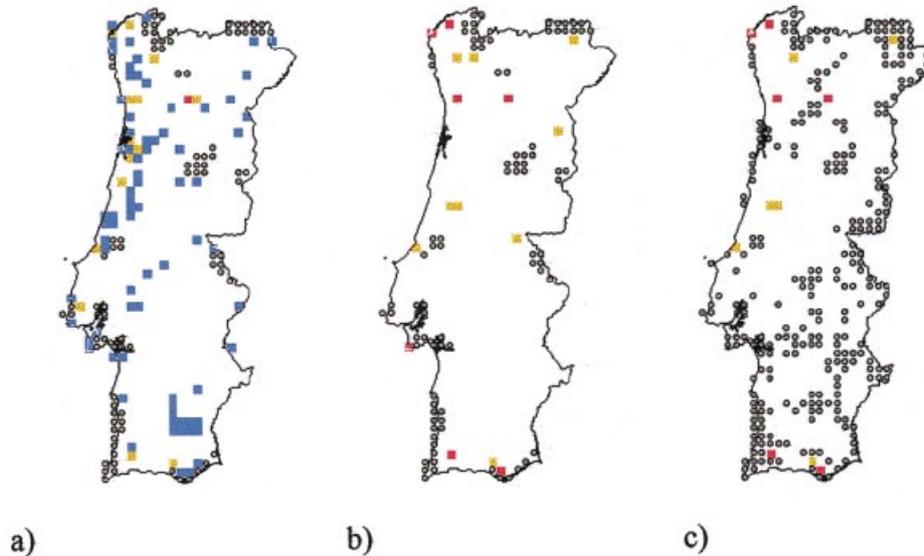


Fig. 3. Gaps in representation of selected taxa in conservation networks: (a) shows the protected areas system (PAS) in Portugal (grey spots) and the richness in all species that remain unrepresented (nineteen spp.); (b) shows the near-minimum set of additional areas (sixteen) needed to represent all taxa at least once; (c) shows the overlay of areas from the PAS + CORINE network (grey spots) and near-minimum set of additional (twelve) needed to represent all taxa at least once (thirteen spp. unrepresented). Red spots are irreplaceable areas. Orange spots are flexible areas from among alternatives.

pteridophytes so that similar analysis cannot be performed for this group. Overall 27% of the known Red Data species in the database were not represented within the PAS. Considering the broader conservation network that results from combining the current PAS with the EU Corine Biotopes Network, only five pteridophytes and two bryophytes are added (Appendix). Amongst the fifteen species that were still not represented within this wider conservation network, one is considered extinct, five are considered vulnerable and five are considered rare.

Question 3. How well do hotspots and complementarity perform when applied to fill the gaps of representation in the current conservation networks in Portugal?

Starting from the existing network of conservation areas in Portugal (PAS), where should we select next? A straightforward approach would be to include other priority areas identified outside the national conservation network by other official bodies such as the EU (e.g. the Corine Biotope Network). This would fit in clearly with the spirit of the Earth Summit

Convention on Biological Diversity (UNEP, 1994), in particular with respect to article 6 which states that national strategies for biological conservation should adapt 'existing strategies, plans or programmes which shall reflect, inter alia, the measures set out in the Convention'. With this in mind, the implications of selecting an extra one hundred and ninety-one grid cells from the Corine network to add to the existing eighty-five PAS areas can be tested against choosing additional areas at random.

Results show that, despite an increase of 325% in the area under conservation management, only 3% more species from the database would be included if the Corine network were considered along with the PAS (Table 2, row 1; Fig. 3). This is no more efficient than choosing areas at random (Table 2, rows 2 and 3), which would sample all species with a mean increment of 114% grid cells to the current PAS (5% upper tail would require an increment of 82% grid cells). Both richness and rarity hotspots gave very similar results to each other (Table 2, rows 4 and 5). They were more efficient than supplementing the PAS with the Corine network but not significantly better than choosing areas at random. If,

Table 2. Alternative scenarios for finding additional areas to the PAS, number of areas required and % of taxa represented

	No. areas	% Taxa
1. PAS + Corine	276	93
3. PAS + random selection (5% upper tail)	155	100
4. PAS + richness hotspots	161	100
5. PAS + rarity hotspots	160	100
6. PAS + complementarity, 1 representation	101	100

instead, complementarity were explicitly pursued to complement the current PAS an increment of sixteen areas (19%) would be needed to represent all remaining taxa in the database (22%) at least once (Table 2, row 6; Fig. 3).

DISCUSSION

The current protected areas system (PAS) in Portugal is insufficient to represent all biodiversity in even this partial database; 11% of the total species are not included within the eighty-five grid cells of the PAS. This is, nevertheless, significantly better than choosing areas at random. However intuitive this may be it is not a universal pattern. For example, Rebelo & Siegfried (1992) found that existing reserves in the Cape Floristic Region, in South Africa, did not contain more Proteaceae species than areas selected at random. Araújo & Sérgio (in press) found a similar pattern looking at the degree of representation for nearly 1000 species of plants and animals in the areas proposed for the EU NATURA 2000 network in Portugal. Not surprisingly, methods explicitly tailored to deal with representation problems (hotspots and complementarity) were more efficient than the PAS to represent the taxa. Within these, complementarity was the most efficient approach (see Kiester *et al.*, 1996; Williams *et al.*, 1996; Williams *et al.*, in press for similar results) being able to represent all taxa, four times, with nearly the same area as the PAS.

Low representation of biodiversity is in itself not sufficient for a claim of inadequacy of a protected areas system to be made. Some degree of apparent inefficiency in representation is inevitable when selection criteria other than representation are included. For example, if a requirement for persistence of populations is included

and the size of the areas increased, then there might be an inevitable redundancy in the set (e.g. Pressey & Logan, 1998). This recalls to the SLOSS (single large or several small) debate (Diamond, 1975; Simberloff & Abele, 1982) where it was demonstrated that an atomization of small reserves would contain more species than a single large reserve of equal total area (Simberloff & Abele, 1982). Portugal is the European Union's Mediterranean country where protected areas have larger average size (23,305 ha) followed by Spain (19,747), Italy (13,226) and Greece (9294) (WCMC, http://www.wcmc.org.uk/protected_areas/data/). Therefore it is not surprising to find sub-optimality in representation.

The question that follows is whether the pattern of under-representation among taxa is random or is consistently biased towards particular groups of organisms. The analyses showed that terrestrial vertebrates (amphibians and reptiles) were, generally, over-represented in relation to lower plants (bryophytes and pteridophytes). This feature was particularly striking with the combined set of PAS plus CORINE biotopes. In the PAS, 16% of the bryophytes and 12% of the pteridophytes were found to be unrepresented. All these bryophytes were listed as threatened in the Iberian Red List (Sérgio *et al.*, 1994). Overall this accounted for 27% of the species in the database known to be threatened. Adding the CORINE areas to the PAS increased the number of grid cells by 189 but represented only seven more species (out of twenty-two unrepresented in the PAS). This level of representation is nearly half as good as it would be expected by choosing additional areas at random.

These results illustrate some of the main disadvantages of making *ad hoc* choices (Pressey, 1994; Pressey & Tully, 1994). One is the bias towards some particular feature of conservation interest at expenses of others. Second is that *ad hoc* choices may not be cost-effective given limited resources and conservation goals. Third is that since *ad hoc* reservations do not establish explicit representation goals, it is impossible to evaluate whether goals have been attained or not. Surprisingly, however, the PAS is more efficient than the CORINE areas to represent the taxa in the database. This is surprising because whilst the first set of areas was selected in an *ad-hoc* fashion (i.e. without explicit criteria for reservation and subject to various political pressures) the second was selected using a formal set of evaluation criteria. The poor performance of the CORINE biotypes to sample lower plants can be explained partly by selecting areas based on

information for charismatic taxa such as vertebrates (specially threatened birds and mammals) and higher plants. Part of the justification for using these organisms as surrogates for biodiversity conservation comes from the belief that they can act as 'umbrellas' for other organisms (e.g. Furness & Greenwood, 1993). It is expected that selecting areas for wide-ranging taxa will provide areas to conserve other groups of organisms (e.g. Tracy & Brussard, 1994). These results suggest that this might not always be the case and that particular care should be paid to the choice of biodiversity surrogates. Similar results were obtained by Franklin (1994) who showed that a single species strategy for the Northern spotted owl (*Strix occidentalis caurina*) was insufficient to conserve aquatic ecosystems, some other vertebrates, and forest successional stages not used by the owl. Indeed, Oliver *et al.* (1998) suggested that if a representative reserve network is sought it might be more appropriate to consider surrogates that exhibit high levels of spatial turnover (small range sizes) rather than 'umbrella species' with large home ranges.

If new conservation areas are to be designated to complement the current protected areas in Portugal, explicit procedures and clear goals should be defined in order to maximize the representation of biodiversity. A first question is whether *in situ* conservation should be proactive or be 'firefighting' reactively as particular species become endangered (Groves, 1992). If the latter approach is preferred it is legitimate to concentrate efforts on areas selected for threatened species regardless of their performance as surrogates for other taxa. Alternatively, if a proactive approach is preferred particular care must be given to the choice of biodiversity surrogates so that maximum representation is achieved within the scope of limited resources available for conservation. Opportunistic administrative criteria can be counterproductive for the selection of new areas for conservation, because large quantities of land may be set aside with only minimum increments of value added. Traditional gap analysis sought to find additional areas to add to conservation networks by selecting hotspots (but see Kierster *et al.*, 1996). In this study this method was found to be less efficient than choosing additional areas at random. This result may be due both to the poor congruence between patterns of distribution of the various groups (Fig. 1) and to the small range size of the unrepresented species (median = 2 records), which appear to be scattered (Fig. 3). As expected, complementarity was the most efficient way to find

combinations of areas to supplement the existing PAS and fill 'gaps' in species representation (an increment of only 19% grid cells to include all species at least once). Although complementary area set methods are not panaceas to solve all area selection problems, they may be particularly useful when used as extensions of gap analysis and as *post-hoc* procedures to evaluate the efficiency of current selections.

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APPENDIX. Unrepresented taxa in the Protected Areas System (PAS) and CORINE Biotopes network, number of records in the database and Red Data Book status (NA, Not Applicable; NT, Not Threatened; R, Rare; V, Vulnerable; Ex, Extinct).

Taxa	Represented in PAS?	Represented in CORINE?	Number of records	Red Data Book status
Pteridophytes				
<i>Lycopodiella cernua</i>	No	No	1	NA
<i>Equisetum palustre</i>	No	Yes	16	NA
<i>Cheilanthes guanchica</i>	No	Yes	1	NA
<i>Marsilea batardae</i>	No	Yes	15	NA
<i>Marsilea quadrifolia</i>	No	Yes	12	NA
<i>Pilularia globulifera</i>	No	Yes	15	NA
<i>Ophioglossum azoricum</i>	No	Yes	6	NA
<i>Ophioglossum polyphyllum</i>	No	No	1	NA
Bryophytes				
<i>Coscinodon cribosus</i>	No	Yes	3	R
<i>Ephemerum recurvifolium</i>	No	No	3	V
<i>Grimmia pitardii</i>	No	No	2	V
<i>Acaulon fontiquerum</i>	No	Yes	1	R
<i>Acaulon triquetrum</i>	No	No	1	V
<i>Barbula ehrebergii</i>	No	No	2	V
<i>Campylostelium strictum</i>	No	No	13	R
<i>Ephemerum sessile</i>	No	No	8	R
<i>Ephemerum stellatum</i>	No	No	2	R
<i>Frullania muscicola</i>	No	No	1	NT
<i>Marupella profunda</i>	No	No	2	R
<i>Mnium stellare</i>	No	No	2	V
<i>Preissia quadrata</i>	No	No	1	Ex
<i>Sphagnum papillosum</i>	No	No	4	R