Nature reserve selection in the Transvaal, South Africa: what data should we be using?

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Iterative reserve selection algorithms were applied to two mammal databases, generalized to sixteenth degree grid squares, for the Transvaal region of South Africa. Based on primary point data, 24 grid squares are required to represent all species at least once, while only 13 grid squares are required when based on distribution map data; only two of these grid squares are common to both analyses. As the number of representations per species is increased from one to five, the number of selected grid squares increased to 86 and 71 or 72 respectively, with only 17 of these common to both analyses. These differences in the selection of sites are further reflected in the degree of congruence between selected grid squares and existing conservation areas which is on average 63.3% for grid squares selected from the primary database and only 42.5% for those selected from the distribution map database. These results emphasize the importance of quality data input when evaluating regional reserve networks. Highly generalized distribution map data sets, on the one hand, are extrapolations of limited data sets and contain non-quantifiable levels of false-positives which could have significant implications if used for establishing regional reserve networks. On the other hand, although there are problems associated with the establishment of primary diversity databases, namely data currency and uneven and non-random sampling (leading to false negatives), they remain our most reliable option for assigning conservation value.

Keywords: reserve selection; databases; mammals; South Africa

Introduction

The importance of conserving maximum biological diversity has become a central issue in conservation biology and critical decisions concerning where biodiversity should be permanently protected are being made. Moreover, nature conservation has only recently become recognized as a form of land use (Margules and Usher, 1981), competing for limited land resources with forestry, agriculture, urban and industrial development. Consequently, the need for reserve networks to be as representative of biodiversity as possible is widely emphasized (Austin and Margules, 1986; Margules and Nicholls, 1987; Margules, 1989; Pressey *et al.*, 1994a). In addition, issues such as the location and adequacy of existing reserve networks in encompassing regional biodiversity urgently need to be addressed (McKenzie *et al.*, 1989). These are two pertinent considerations since the majority of reserves were originally allocated largely on an opportunistic, species-specific and *ad hoc* basis (Gotmark *et al.*, 1986; Pressey *et al.*, 1993), resulting in an uneven representation of biological diversity in many regional reserve networks.

Despite there being over 8600 major protected areas (meeting IUCN management

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criteria) by 1992, this only represents 5% of the world's total land surface (McNeely, 1994). An additional 40 000 conservation areas not falling within recognized IUCN categories bring this area to over 12.2 million square kilometres, or approximately 8.2% of the world's land surface (McNeely, 1994). In South Africa, 5.8% of the land area has been set aside for official conservation (Siegfried and Brown, 1992), with almost half of this area falling within the Kruger National Park. South Africa is therefore still well below the internationally accepted target set by the IUCN, namely that every country should have at least 10% of its land surface under formal protection (IUCN, 1980). This figure also falls short of the 10% total area currently designated as protected areas in Sub-Saharan Africa (McNeely, 1994). The required figure of 10% is however scale-dependent, and the adequacy of a reserve network cannot merely be assessed by the 'sums' argument of the amount of land area that it covers; rather, it depends on the extent to which the reserve network samples the range of indigenous biodiversity (Pressey and Nicholls, 1991). Quality, not quantity, orientated reserve selection methods are thus required to select the 'best' available options.

It is widely believed that in the face of limited resources for the acquisition of additional conservation areas and competition from other forms of land use, the identification and prioritization of potential conservation areas will maximize the effectiveness of conservation actions. This is facilitated by systematic and explicit reserve selection procedures. Developments, particularly in Australia, have emphasized systematic iterative procedures for selecting representative reserve systems (Kirkpatrick, 1983; Margules *et al.*, 1988; Pressey and Nicholls, 1989; Bedward *et al.*, 1992a; Pressey *et al.*, 1994b; Rebelo and Siegfried, 1992; Nicholls and Margules, 1993) as an alternative to the conventional weighting of evaluation criteria and ranking of conservation sites (Margules and Usher, 1981). Such iterative algorithms are based on different criteria, including species richness, taxonomic diversity, ecological redundancy and red data books (Rebelo, 1994).

A prerequisite for the development of reserve selection methods is the development of a database for conservation evaluation (Margules, 1989; Bedward *et al.*, 1992a). Ideally such a database would contain information on the geographical distribution, abundance and habitat requirements of all species within the region of concern (Pressey, 1990). However, in reality, a worldwide constraint is the very incomplete knowledge of species and subspecific taxa (Pressey *et al.*, 1994a) and a general lack of long-term empirical data necessary for determining conservation priorities. With limited monetary resources for large-scale surveys, sampling of a subset of candidate sites becomes the principal information database on which reserve selection has to be based. This has resulted in reserve selection utilizing probabilistic presence/absence data (Margules and Nicholls, 1987; Cocks and Baird, 1989). Although the existence of many years of census data, over various seasons, increases the probability of sampling and detecting rare species (Gotmark *et al.*, 1986), reserve networks are often designed in terms of expected, as opposed to actual or absolute, appearances of species or communities.

This study involves evaluating mammalian diversity patterns in the Transvaal, South Africa. Here we compare the implications of selecting conservation areas based upon 'estimated extent of occurrence', taken from published distribution maps, and those based on actual species records, or primary point data. We are concerned with only one of the number of possible criteria for reserve selection, namely the absolute species richness approach.

Materials and methods

For the purposes of this paper, the study area is defined as the borders of the old Transvaal Province within the Republic of South Africa, an area covering approximately 286 000 km^2 and 23% of the RSA (Fig. 1). Large numbers of faunal surveys have been conducted in the Transvaal resulting in large quantities of readily available data. The point database used in this analysis is thus based on primary data collections and species lists of the Transvaal Museum, United States National Museum African Mammal Collection, Transvaal Chief Directorate of Nature and Environmental Conservation, National Parks Board (specifically the Kruger National Park), the South African Defence Force, KaNgwane Parks, Rautenbach (1982) and other published and unpublished records.

Specimen records in the form of point locations were recorded as such while grid references were assigned to the centre of the grid. This was generalized to 474 sixteenth degree (15′ × 15′) grid squares covering the Transvaal by giving each record within a specific grid square the coordinates of the centre point of that particular grid square. The minimum data set used is therefore the presence or absence of species at different locations. The possibility of large locational errors for specimen records was recognized and the raw point data rigorously checked to minimize the chance of records falling within incorrect grid squares. The accuracy of future evaluations could be improved by using the
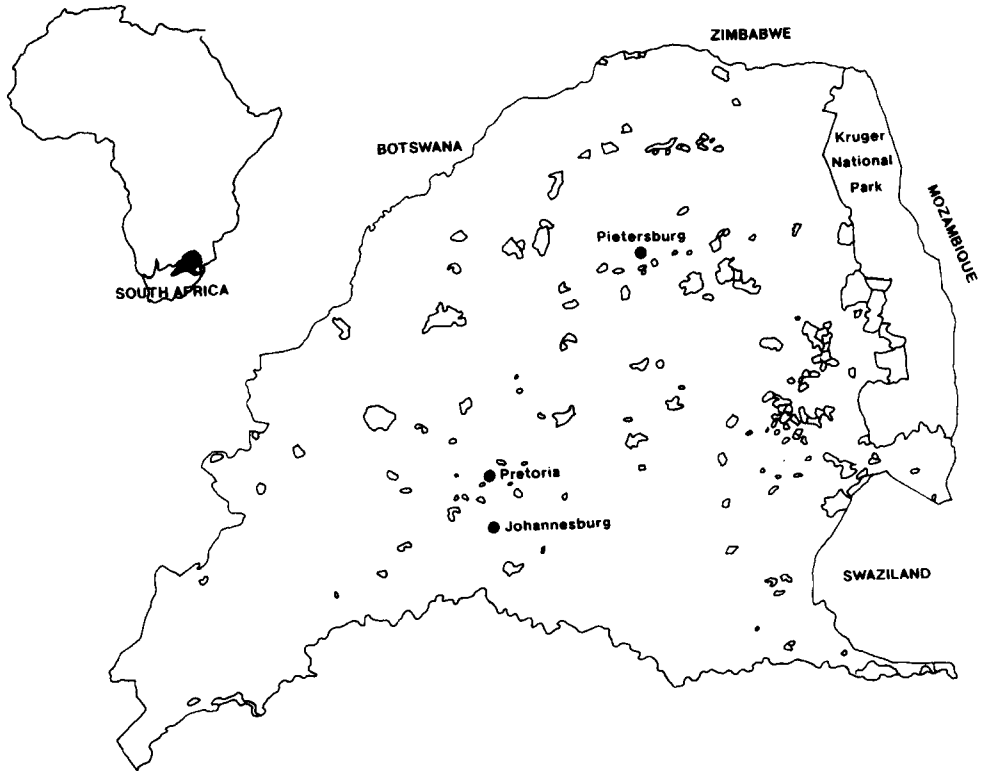

Figure 1. Map of Transvaal Province, South Africa showing major National Parks, nature reserves and cities.

Global Positioning System (GPS) technology during surveys. The distribution map database is similarly based on the presence or absence of species in sixteenth degree grid squares extracted from published distribution maps in Skinner and Smithers (1990). All mammals naturally occurring in the Transvaal have been considered, including the insectivores and bats which are frequently omitted from other analyses (e.g. Crowe, 1990; Siegfried and Brown, 1992).

The iterative algorithms developed by Margules *et al.* (1988) and Nicholls and Margules (1993) were used for selecting representative reserve networks. Here the minimum number of grid squares required to represent each species is determined by first selecting those sites containing the least frequently represented, or rarest, species. Subsequent stepwise iterations select those grids which add the next rarest species, taking into consideration those species found in sites already selected. This may be termed the 'unconstrained' selection routine as it does not take distance between selected sites into consideration (Margules *et al.*, 1988). In the 'adjacency constrained' routine (Nicholls and Margules, 1993), selection rules are as for the unconstrained algorithm, except that priority is given to those cells that are closest to the initial selection areas, where there is such a choice. Thus an attempt is made to select groups of sites as opposed to single isolated sites as determined by the unconstrained analysis. As the relative efficiency of the adjacency constraint may be influenced by its position within the set of selection rules, adjacency was invoked after rule 2 in these analyses.

The results of the presence/absence based adjacency constrained and unconstrained algorithms were compared for one to five representations of each species, where this was possible, for both the distribution and point data sets. Results of the reserve selection algorithms were graphically displayed using the Geographic Information System REGIS™ (Automated Methods, Verwoerdburg, South Africa).

The efficiency of the approach in representing all species one to five times was calculated using the formula of Pressey and Nicholls (1989): $E = 1 - (X/T)$, where X is the number of sites selected and T is the total number of sites considered. Values closest to 1 represent greatest efficiency. Here efficiency refers to the ability of a set of selected sites to represent regional biodiversity in the least number of available sites. However it does not necessarily achieve 'optimality' (Underhill, 1994) and could be referred to as 'relative efficiency', adequately describing the principle of efficiency as described by Margules *et al.* (1994) and Pressey *et al.* (1994b) and enabling comparison of the results of the two techniques used here.

Results

The iterative algorithm analyses show that a wide scatter of grid squares are required for minimum representation of all mammal species within the Transvaal. Figures. 2a and 2c show the scatter of sites required for representation of all species one or five times based on primary point data, and using the adjacency constrained selection routine. The increase in the number of selected grid squares from 24 to 86 is evident as the number of representations per species is increased from one to five. This geographical scatter of sites differs marginally from those selected by the unconstrained algorithm, sharing 21 of 24 selected sites for single representations and 83 of 86 sites chosen for five representations (Table 1). The adjacency constrained algorithm selected far fewer grid squares for the
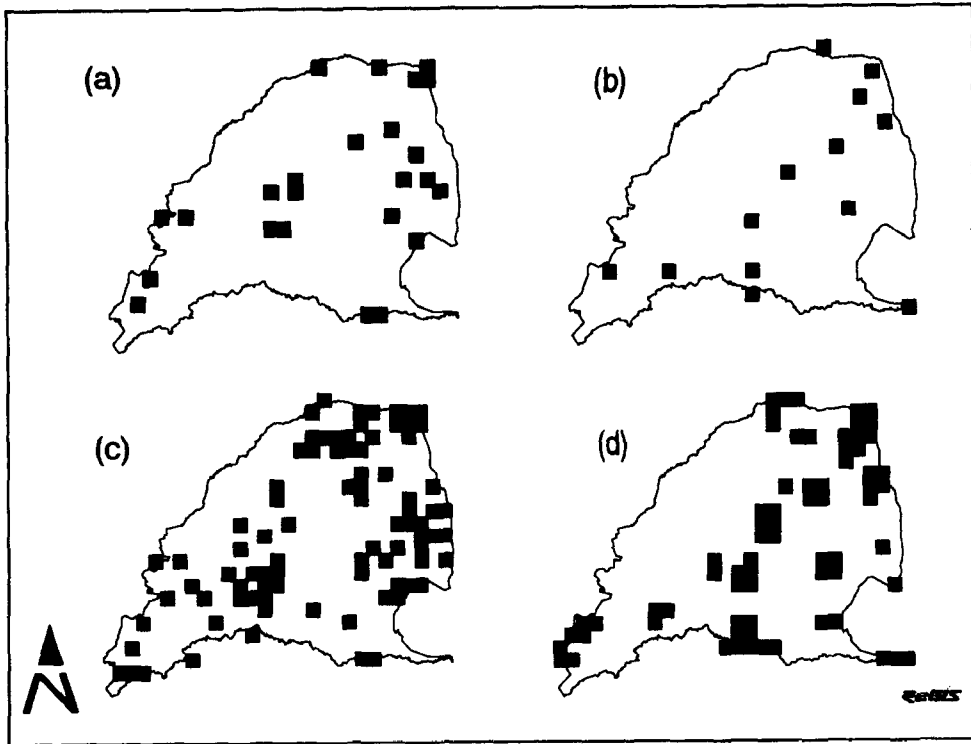
Figure 2. Sixteenth degree grid square networks selected by the iterative adjacency constrained reserve selection algorithm. Grid squares required to represent each species in the point database (a) and distribution map database (b) at least once; and grid squares selected to represent each species in the point database (c) and distribution map database (d) at least five times.

representation of mammal species one or five times based on the distribution map database (13 and 71 respectively; Figs. 2b and 2d). Once again the positions of the selected sites for single representation are similar to those selected by the unconstrained routine (Table 1). However, only 55.6% of sites selected by the two algorithms for five representations per species based on the distribution map database were shared (Table 1).

Reserve site selection based on the point data versus distribution map data for single representations of all species resulted in almost twice the number of grid squares being selected (24 versus 13; Table 2). As the number of representations per species was increased from one to five, the number of grid squares selected for both data sets increased accordingly, irrespective of which algorithm was used (i.e. unconstrained versus adjacency constrained). However, the adjacency constrained solution was found to be slightly more efficient than the unconstrained solution for the distribution map data set, resulting in marginally fewer sites being selected in the case of three, four or five required representations per species (Table 2). It should however be noted that the effect of shifting the position of the adjacency rule within the algorithm might affect the positions of selected grid squares as well as the relative efficiencies of the two algorithms (in prep).

Figure 3 illustrates the geographical positions of selected grid squares based on the two data sets for one and five representations respectively. The selection of grid squares to represent all mammal species at least once results in the sharing of only two sites (Fig. 3a),

Table 1. Comparison of the number of selected and shared grid squares as determined by the unconstrained (Uncons) and adjacency constrained (Constr) reserve selections for both the primary point and distribution map databases. Results for 1 and 5 representations of each species in the reserve network are shown.

Database	No. of Reps	Algorithm		No. shared	% shared
		Uncons	Constr		
Points	1×	24	24	21	87.5
	5×	86	86	83	96.5
Maps	1×	13	13	11	84.6
	5×	72	71	40	55.6

while the attempted representation of all species at least five times results in the sharing of only 17 of the total of 157 grid squares selected by the two analyses (Fig. 3b).

A further point of dissimilarity between the results of the grid square selection based on these two data sets is reflected in the number of species inadequately represented one to five times in the selected grid square networks. Inadequate representation here is due to insufficient occurrences of taxa in either or both of the two databases. Based on point data, and requiring only single representations of species, all species may be successfully represented in the selected network (Table 2). However, from two to five representations per species 14, 23, 32 and 37 species respectively are inadequately represented in the selected networks based on available point data. In contrast, all species may be successfully represented one to four times in the selected network when based on distribution map data, and only once five representations are required do seven species fall short of this target (Table 2). Thus, theoretically, 100% of all mammal species occurring in the data bases may be represented at least once in 24 grid squares based on point data, or in only 13 grid squares if based on distribution maps. However, if at least five representations of all species is considered then 86 grid squares are required to represent 81.5% of species using the point data base while 96.4% of all species will be adequately represented in 71 grid squares if based on distribution map data (Table 2). These deviations from 100% (namely 81.5% and 96.4% respectively) reflect the occurrences of certain taxa in less than the five required grid squares.

The percentage areas of selected grid squares, for both primary point and distribution map databases, falling within existing nature reserves are detailed in Table 3. The number of selected grid squares which fall completely outside of the existing reserve network varies from 33.33% (for squares selected for single representations based on point data) to 62.5% (for squares selected for five representations using the unconstrained algorithm and based upon the distribution map database; Table 3). Conversely, congruence between the selected set of sites and the existing conservation areas in the Transvaal varies from 66.66% to 37.5%. Congruence here is estimated by the percentage of selected grid squares which have >25% of their area dedicated to conservation (National Park, Provincial Nature Reserve or private game reserve).

Table 2. Results of unconstrained (Uncons) and adjacency constrained (Constr) reserve selections for both the primary point and distribution map databases. Results for 1 to 5 representations of each species in the reserve network are shown. GS refers to the number of sixteenth degree grid squares selected, A represents percentage total area required by the proposed reserve network, E indicates the efficiency of the selection algorithm, S represents percentage successful representation of all species in the databases, N reflects the number of species inadequately represented in the selected reserve configurations

Algorithm	No. of Reps	Point database					Map database				
		GS	A	E	S	N	GS	A	E	S	N
Uncons	1×	24	5.06	0.95	100	0	13	2.74	0.97	100	0
Constr	1×	24	5.06	0.95	100	0	13	2.74	0.97	100	0
Uncons	2×	40	8.44	0.92	93.0	14	27	5.70	0.94	100	0
Constr	2×	40	8.44	0.92	93.0	14	27	5.70	0.94	100	0
Uncons	3×	58	12.24	0.88	88.5	23	43	9.07	0.91	100	0
Constr	3×	58	12.24	0.88	88.5	23	42	8.86	0.91	100	0
Uncons	4×	72	15.19	0.85	84.0	32	61	12.87	0.87	100	0
Constr	4×	73	15.40	0.85	84.0	32	60	12.66	0.87	100	0
Uncons	5×	86	18.14	0.82	81.5	37	72	15.19	0.85	96.4	7
Constr	5×	86	18.14	0.82	81.5	37	71	14.98	0.85	96.4	7

Discussion

Based on the general spatial distribution of grid squares chosen by the reserve selection algorithm, it becomes obvious that the location of selected sites within the Transvaal differ markedly depending on the database used (Fig. 3). Furthermore, grid square selection for five representations of all species results in the sharing of only 17 of the total of 157 selected grid squares by the two analyses (Fig. 3b). Fourteen of these fall within existing conservation areas, seven of them are contained within the Kruger National Park. The latter is the largest reserve within the Transvaal and encompasses extensive biotic, particularly mammalian, diversity and represents the most valuable component of the existing reserve network. It is therefore of utmost importance to quantify correctly the Kruger National Park's contribution to sampling overall regional biodiversity beyond mere large mammal diversity.

The northeastern Transvaal is implicated by the reserve selection algorithms as being of value for a regional reserve network (Figs 2 and 3). Although these areas possibly would not feature strongly in a broader scale reserve network, the protection of marginal species at the southern limits of their distribution in the northern Transvaal, may be justified here by the fact that they possibly enjoy limited protection elsewhere in Africa (Rainbird, 1993).
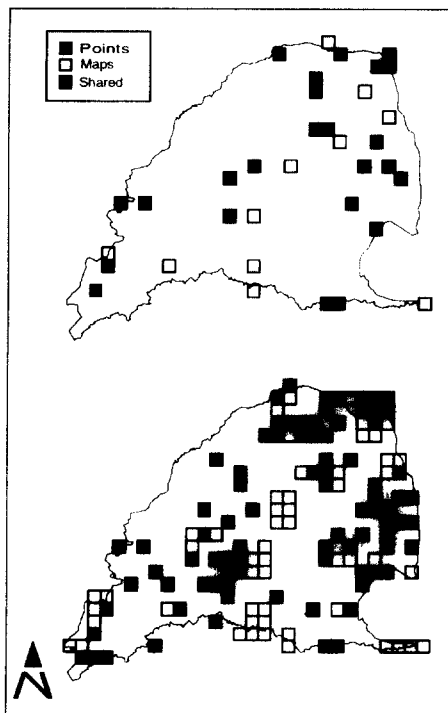

Figure 3. Degree of concordance between sixteenth degree grid square networks selected by the iterative adjacency constrained reserve selection algorithm based on point and distribution map databases for one (a) and five (b) representations.

These areas have also been implicated as important conservation sites for the protection of 66 large mammal species in greater South Africa (Rainbird, 1993) and South African snakes (Lombard *et al.*, in press).

The efficiency of the iterative approach used here varied from 0.95 to 0.82 for the point data analyses and from 0.97 to 0.85 for the distribution map data (Table 2). The efficient choice of reserve networks is an important consideration in view of the need to defend reserve proposals in competition with other land uses (Pressey *et al.*, 1994b; Margules and Nicholls, in press). Although the algorithm used here is a relatively efficient, although possibly 'greedy and suboptimal' (Underhill, 1994) method of protected area selection, a reserve network containing long-term viable populations of species may require many more sites and a large proportion of the total area (Bedward *et al.*, 1992a). The inclusion of minimum viable populations in a reserve network is essential; however, available data do not allow quantitative representation goals such as species abundances and population sizes to be addresed. Nevertheless, the qualitative determination of reserve configurations to represent all species at least one to five times represents a very crude and simplistic but preliminary attempt to include multiple species' populations in such a network. This is based on the assumption that localities determined from point data do in fact harbour viable populations of the species in question. The interrelation of species' local abundances and overall range size (Brown, 1984; Gaston and Lawton, 1990; Lawton, 1993) may become an important issue here; species with larger geographic ranges may be more abundant locally than more narrow range species while population densities may be greater at the centre of the species' geographic range, declining towards the outer edges (Brown, 1984). These observations, potentially, have significant impacts on the value of determining conservation sites where all parts of species' ranges are given equal weight. Although this is applicable to both distribution map and primary survey data, conservation areas based on distribution maps in particular may be more useful if they can be combined with a probability function which quantifies the probability of finding a species at a particular distance from the centre of its estimated range. Survey data on the other hand represents actual species occurrences and marginal and/or isolated occurrences could be removed from the database by omitting those grid squares which do not have immediate

Table 3. Number of selected grid squares with their approximate percentage areas falling within existing nature reserves. This is based on grid squares selected by the unconstrained (Uncons) and adjacency constrained (Constr) reserve selections for both the primary point and distribution map databases. Results for 1 and 5 representations of each species in the reserve network are shown

Database	Algorithm	No. of Reps	Approximate % area covered					Total No.
			0	25	50	75	100	
Points	Uncons	1×	8	9	5	1	1	24
	Constr	1×	8	8	3	3	2	24
	Uncons	5×	31	33	11	2	9	86
	Constr	5×	38	28	11	0	9	86
Maps	Uncons	1×	8	2	0	1	2	13
	Constr	1×	6	3	1	1	2	13
	Uncons	5×	45	10	5	4	8	72
	Constr	5×	42	13	5	2	9	71

adjacent or diagonal grid square neighbours (Lombard *et al.*, in press), although this will be greatly influenced by the size of the grid squares.

Use of the adjacency constrained algorithm is in agreement with the general consensus that larger contiguous reserves are better than many smaller isolated ones (Burkey, 1989) although such a scatter of sites should best accommodate the spatial distribution of species (Burgman, 1988). Although criteria such as flexibility, associated irreplaceability, and reserve design (Margules *et al.*, 1991) are not taken into account here this analysis satisfies the commonly used intrinsic value criteria of conservation value, namely diversity, rarity and representativeness (Margules and Usher, 1981; Margules *et al.*, 1991; Austin and Margules, 1986).

Comparison of selected sites, as determined by these selection algorithms for the primary point database, and the existing conservation network in the region, show that over half (56–67%) of the identified grid squares have at least 25% of their areas represented in reserved areas (Table 3). Based on these results, it would appear that the existing network of conservation areas represents 66.7% of these hypothetically selected sites. The equivalent figure is far lower for sites determined from the distribution map database where only between 38 and 54% of selected sites fall within existing protected areas (Table 3). This difference may be an artifact of biased primary data collecting within current nature reserve boundaries. Additionally, the principle of flexibility in reserve selection procedures will identify additional potential reserve network options attaining the same or slightly reduced efficiency in terms of land area (Pressey *et al.*, 1994a) and will in all probability change these currently observed percentages of overlap between selected sites and current conservation areas. The 'ideal world' specific sites selected here may therefore not necessarily be core priority areas and may well change on consideration of 'real world' constraints such as taking current reserve networks and the associated redundancy into account, inclusion of other taxonomic groups, reserve design, vulnerability and viability of species populations and reserve sites, land availability and costs. This may be overcome to some extent by including estimates of the irreplaceability of sites into the iterative procedure (Pressey *et al.*, 1994a).

There are thus many complexities associated with the determination of conservation priorities and the identification of conservation sites are complicated by the fact that areas selected by different approaches do not necessarily coincide. Distribution patterns may vary within and amongst different groups of taxa (but see Gaston and Hudson, 1994) while conservation approaches based solely on protecting the maximum number of taxa, or rare and endangered species, have several limitations, including the use of only a single set of organisms (mammals in this instance) for evaluation. Centres of endemism, speciation and biogeographical refugia also need to be identified. Ideally, these would include patterns common to major taxonomic groupings and not be restricted to a single group.

Aside from the multitude of available diversity indices and reserve selection algorithms currently available, the importance of what data input to use is critical. As a result of inadequate primary distribution data and insufficient environmental correlates, representing interpolated data (see Margules and Nicholls, 1987; Margules and Stein, 1989), biologists often resort to using published distribution maps for conservation planning purposes (e.g. Crowe, 1990; Siegfried and Brown, 1992; Rainbird, 1993; Turpie and Crowe, 1994). It is our contention that such an approach is dangerous and could have significant negative implications should such preliminary findings be implemented uncritically since such maps are invariably extrapolations of limited data sets and as such

do not reflect actual geographically explicit species' distributions. These should be treated with caution when used for determining regional or national protected area networks.

On the other hand, there are also problems associated with a mammalian diversity database based on primary point survey data. It is influenced by the need to represent biotic distributions at a certain level of precision and resolution (Bedward *et al.*, 1992b), while the choice of scale used is constrained by the spatial and temporal resolution of available data. An important drawback and limitation of the data is the effects of data currency and sampling or survey bias. These factors could lead to conservation priorities being determined and based on outdated species occurrences and/or false absence records simply due to non- or under-surveying of particular areas. Obviously, the more recent and comprehensive the primary survey data, the more reliable and effective the determination of site conservation value (Margules and Nicholls, 1987; Margules *et al.*, 1991; Bedward *et al.*, 1992a), irrespective of which particular reserve selection procedure is used. This highlights the immediate and urgent need for comprehensive surveys to be conducted on a national scale to refine and produce more robust distribution data sets for all taxa which may then be used for definitive selection of areas of significance for the protection of biodiversity.

The regional conservation needs at any point in space or time should be expressed in terms of a range of conditions extending from the most ideal (regardless of whether or not it is feasible) to the point of unacceptability. Within this range, compromises will be reached and optimum land allocations determined using the ideal as a starting point. It is therefore very important to estimate these extremes with reasonable confidence and allow for flexibility (Pressey *et al.*, 1993; Pressey *et al.*, 1994a) and compromise in determining the spatial arrangement of reserves; some achieving the goal of representativeness without a cost, while others may carry a cost, such as increased land area, but still achieve the required conservation goal. In this way, reasonable compromises can be reached with competing landuses.

Nevertheless, the real problem revolves around data input. Should we accept and tolerate a higher degree of false-positives (as represented by the overestimates of distribution maps) or false-negatives (found in the less well surveyed grid squares of the point data base)? It is our contention that basing conservation priorities on data containing false-positives leads to high levels of uncertainty, as there is no means of estimating how many of the species estimated to be protected are in fact protected. However, reserve selection based on actual species records, although requiring a greater number of reserved grid squares, enables far greater confidence in the probability of protecting species in the chosen sites. In other words, although protected area selection based on primary data is less efficient in the number of grid squares required for conservation, requiring greater land area, it is the most reliable data for making such choices.

Conclusions

Although the rapidity of land use change requires short-term solutions which increase the likelihood that regional reserve networks encompass maximum biological diversity, a sound strategy for the long term protection of biodiversity requires reliable quantitative information on the spatio-temporal variation in this diversity and poor data input cannot be compensated for by the most sophisticated analysis and modelling tools. Our results show the discrepancies and problems associated with basing conservation priorities on

highly generalized probabilistic distribution map data rather than on primary point data. These decrease our confidence in protected area networks based on such maps where extrapolations of limited data sets are used to design reserve systems in terms of possible expected, as opposed to actual appearances of species. Thus, decisions need to be made with the best information that is available at present, and although there are some caveats in the point data, this represents our most reliable option.

It is clear that the ability to update, manipulate and query information is essential, and making data more accessible will enable development planners, conservation managers, organizations and government bodies involved in environmental decision-making to make more informed decisions. It is hoped that the problems highlighted in this study will contribute towards the establishment of a national biodiversity inventory and database for sound environmental conservation and resources management (Van Jaarsveld and Lombard, 1995).

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