

CHAPTER 3

Assessment techniques for biodiversity surrogates

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*B. Reyers*¹ and A.S. van Jaarsveld^{1,2}*

¹ *Conservation Planning Unit*

Department of Zoology & Entomology

and

² *Centre for Environmental Studies*

University of Pretoria

Pretoria, 0002

South Africa

* To whom correspondence should be addressed

Conservation Planning Unit

Department of Zoology & Entomology

University of Pretoria

Pretoria, 0002

Tel: (012) 420 4396

Fax: (012) 420 3210

E-mail: breyers@zoology.up.ac.za

Abstract

The use and evaluation of indicator taxa as surrogates for unsurveyed species in the identification of sites important to conservation is a widely researched field. However, support for the use of indicator taxa in reserve selection is often varied and conflicting. We consider that these discrepancies in the levels of support for different indicator approaches are often a result of the assessment techniques employed. Our results appear to confirm the assumption that the assessment technique influences the level of support for indicator taxa as biodiversity surrogates. Because the techniques examine different aspects of indicator approaches, we recommend consideration of final goals and standardisation of techniques before the implementation of indicator-based approaches in conservation planning.

The plight of biodiversity as well as the inadequacy of existing protected areas are well established and much cited facts in conservation biology.¹⁻⁷ Existing reserve networks were proclaimed primarily on an *ad hoc* basis and usually contain land with either a low potential for economic and political conflict or a high potential for recreation and tourism.^{1,3,8-10} There is therefore a widely recognised need for the systematic establishment of protected areas for effective *in situ* species conservation.¹¹⁻¹⁶ This realisation has led to the development of systematic, explicit procedures for the selection of representative reserve networks.^{14,17-19} These procedures rely on a suitable database of geographical areas of land or water, such as sample sites, grid cells or catchments, containing features of species, habitat types, communities or environments.²⁰ Frequently, as is the case in this study, the database contains grid cells and unique occurrences of species within those grid cells.^{1,6,16,21-24}

Sets of grid cells or reserve networks with a high biodiversity or conservation value can then be identified and selected from this database by a variety of reserve selection procedures. These procedures identify various types of reserve networks which can include richness hotspots (grid cells of high species richness),²¹ rarity hotspots (grid cells with high numbers of rare species)⁶ and complementary sets of grid cells.¹⁴ Complementary sets are grid cells selected by an iterative algorithm, which proceeds in a step wise fashion adding on grid cells that contain species most complementary (so far unrepresented) to species in grid cells already selected. These algorithms may be either richness-based (initially selecting the richest grid cell)^{11,23,25} or rarity-based (initially selecting the grid cell with the rarest species)¹⁴ and then proceed to add grid cells in a complementary fashion until a specific representation target is achieved.

However, the species distribution data used in these reserve selection procedures are often of poor quality, inadequately surveyed and of uncertain taxonomy.^{21,25-28} Although it is argued that high quality biodiversity inventories for the selection of representative reserve systems will be more cost efficient in the long run,²⁹ the resources and time required to conduct these regional biodiversity inventories are usually unavailable. Thus the use of substitute or surrogate biodiversity measures in reserve selection procedures is often recommended. These surrogate measures can be surveyed in a more cost and time efficient manner and include broad-scale environmental measures (e.g. climate or vegetation data), higher taxa (e.g. genera or families) or indicator taxa.^{26,30-40} Indicator taxa are groups with a sound taxonomy that have been well surveyed in the region (e.g. birds, butterflies). It is then assumed that patterns of species richness, endemism and rarity in these taxa are indicative of similar patterns in unsurveyed taxa within the region.^{26,27,41} Thus by selecting sites for the conservation of indicator taxa (e.g. birds), unsurveyed taxa within the region will also be conserved. This indicator-based surrogacy approach has been widely used in several countries to identify sites of conservation importance.^{6,21,22,27,42} However, the assumptions of indicator taxa reflecting regional biodiversity patterns require rigorous testing before reserve networks selected from indicator distribution data can be successfully implemented in practice.

Several assessments of the value of surrogate indicator taxa in reserve selection have been carried out with widely differing results.^{6,21,24,25,43,44} Three main types of assessments have been applied in these studies. First, several authors have used the degree of spatial overlap between reserve networks based on different indicator taxa as a measure of the success of these indicator-based networks in including sites of conservation importance for other taxa.^{21-23,25,44} Two measures of spatial overlap exist in the conservation biology literature:

$$(a) \text{ Jaccard coefficient} = N_c / (N_1 + N_2 - N_c) \times 100$$

$$(b) \text{ Proportional overlap} = N_c / N_s \times 100$$

where: N_c is the number of common sites in a pair of reserve networks, N_1 and N_2 are the number of sites in the pair of reserve networks and N_s is the number of sites in the smallest reserve network containing data for both groups. Thus the Jaccard coefficient measures spatial congruence as a proportion of the total number of sites selected in both reserve networks,⁴⁴ while the measure of proportional overlap measures spatial overlap as a proportion of the maximum overlap possible.^{21-23,25,43,45}

Because flexibility is an inherent characteristic of many reserve selection techniques,^{6,9,20} the use of spatial overlap is perhaps not an acceptable means of assessing similarities between different indicator-based reserve networks. In recognition of this a technique measuring the Pearson's product moment correlation of the order in which sites are selected by reserve selection procedures based on different indicator taxa has been proposed.^{23,46} This selection order of sites for a reserve network indicates the sites' importance in terms of their diversity or conservation values. The sites selected first have a high diversity value because they contain more species, more rare species or more complementary species, depending on the specific reserve selection criteria. This second method of assessment of indicator taxon validity compares the selection order of sites within reserve networks, i.e. the diversity value of those sites, across indicator taxa and thus allows for the assessment of site similarities among different indicator taxa.

The third type of assessment applied in the more recent conservation literature measures the species representativeness of each indicator-based reserve network.^{6,21-23,25,27,40,43,47-49} This technique investigates how well each reserve network, identified on the basis of one indicator taxon, captures non-target species or overall biodiversity in the region. This technique can also include evaluation of the representation of rare and endemic species in the indicator-based reserve networks and determines how well these networks represent species essential to effective conservation.^{6,21-23,50,51}

These different types of analyses have been conducted on various indicator taxa in many regions of the world and all provide differing levels of support for the surrogate value of indicator taxa. A lack of general support, because of low levels of spatial congruence, has been demonstrated in several studies.^{21-23,40,43-45} Conversely, high levels of support for indicator taxa as biodiversity surrogates have been demonstrated using measures of species representativeness.^{21-23,25} Many reasons have been advanced for the differing levels of support found in the various studies, including the fact that studies

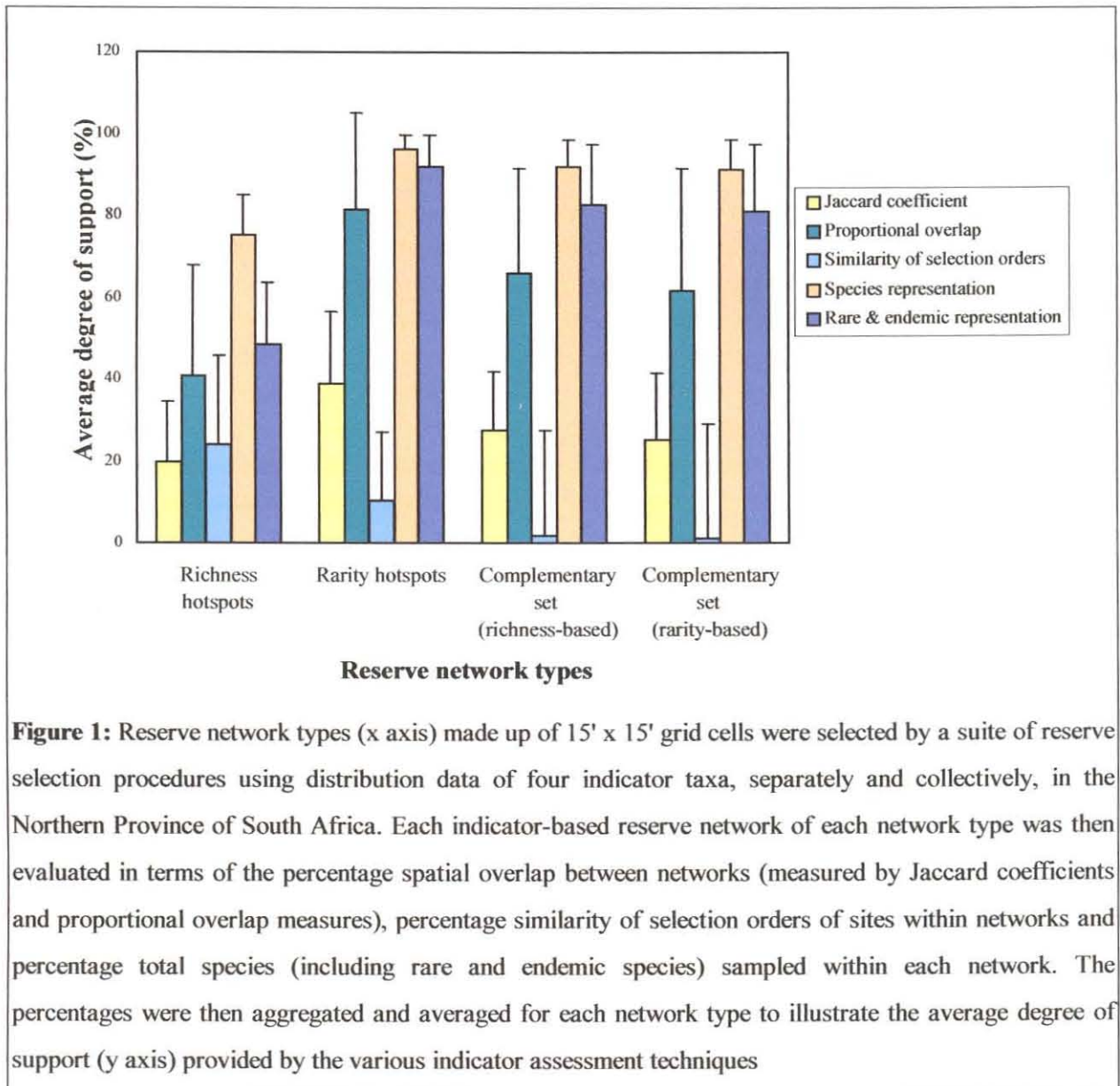
conducted in different regions or using different indicator taxa will not agree with one another.^{25,47} However we consider that the range of assessment techniques employed to evaluate the validity of surrogate indicator taxa has a large impact on the outcomes of the studies conducted. Thus in the present study we applied all the assessment techniques discussed above to a suite of indicator-based reserve networks, keeping the study region and taxa involved constant, and evaluated the degree of support provided by each technique to indicator taxa as biodiversity surrogates.

Using 59063 unique distribution records of 1588 bird, butterfly, mammal and vascular plant species in 15' x 15' grid cells (*ca.* 700 km²) in the Northern Province of South Africa we identified a variety of indicator-based reserve networks. These networks were identified by selection procedures using distribution data on indicator taxa of birds, butterflies, mammals and vascular plants. The procedures used these indicator taxa, separately and collectively, to identify different types of reserve networks including richness hotspots, rarity hotspots, and complementary sets of grid cells selected by rarity and richness-based complementary reserve selection algorithms. The degree of similarity within each network type based on different indicator taxa was then assessed, e.g. richness hotspots for birds, butterflies, mammals, plants and all taxa combined were assessed for spatial overlap, selection order correlation and species (including rare and endemic species) representation.

Figure 1 illustrates the widely varying levels of support for the indicator-based surrogate approach assessed using different indicator assessment techniques. Similar to findings by van Jaarsveld *et al.*,⁴⁴ Jaccard coefficients of overlap are low ($\bar{x} = 28\%$), and although measures of proportional overlap are higher ($\bar{x} = 63\%$), these results indicate the relatively low levels of spatial overlap between reserve networks based on different indicator taxa and are in agreement with the low values of spatial congruence found in previous studies.^{21-23,25,44}

Thus the low levels of spatial congruence appear to question the value and perhaps reject the notion of indicator taxa as biodiversity surrogates. The low degree of similarity ($\bar{x} = 9\%$) of selection orders within each reserve network type based on different indicator taxa is similar to that found by Reyers *et al.*²³ (Chapter 2) and Gaston *et al.*,⁴⁶ suggesting very different conservation or diversity values for different taxa within each site, providing limited support for indicator taxa as surrogates.

The high levels of species representativeness ($\bar{x} = 89\%$) within the indicator-based reserve networks suggest that a network based on one particular taxon captures high levels of non-target species within the region. This appears to support the use of indicator taxa as surrogates and is in agreement with the high levels found by Prendergast *et al.*²¹ and Howard *et al.*²⁵ Although moderately high numbers of rare and endemic species are represented within the reserve networks ($\bar{x} = 76\%$), of the species excluded by the reserve networks an average of 84% are rare and endemic, which casts doubt on the validity of these networks in the effective conservation of all regional biodiversity.^{6,23,50,51}



It thus appears that the biodiversity indicator assessment technique used influences the strength of support for indicator taxa as biodiversity surrogates. This is an obvious outcome, as each assessment technique is, in fact, testing a different facet of the indicator-based reserve network. Jaccard coefficients and measures of proportional overlap evaluate spatial aspects of indicator-based networks; selection order correlations assess the taxon specific diversity or conservation value of sites; and species representation (including rare and endemic species representation) is an indication of how completely the regional species pool is sampled. All methods have their strong and weak points and although measures of congruence have important implications for conservation, key measures are those that look at species capture (all species but especially rare and endemic species).

The lack of spatial congruence between reserve networks based on complementarity, richness, rarity and endemism, illustrates that indicator taxa cannot be relied on to illustrate similar trends in other, unsurveyed groups. The reason for this could be that reserve networks selected for a particular taxon at a regional and local scale often contain species with narrow habitat requirements (e.g. rare and endemic species), and thus these networks are not likely to correspond across different taxa.⁴⁸ This would also explain the different diversity values of each site within reserve networks for a specific taxon demonstrated by the highly dissimilar selection orders of sites for different indicator-based reserve networks. However, if one considers the amount of non-target species recorded within the indicator-based reserve networks, the picture is far less bleak, perhaps because representing a high level of diversity within one taxon, samples a large number of varied habitats and therefore also represents diversity in other unsurveyed taxa.^{25,47,48} The high numbers of rare and endemic species excluded support the notion that species from one taxon with narrow habitat requirements do not coincide across taxa and suggest the need for caution before implementation of these principles in conservation planning.

In conclusion it appears that the biodiversity indicator assessment technique used does influence the degree of support for the use of indicator taxa as biodiversity surrogates. This, together with the lack of unqualified support for the indicator taxon strategy, raises important questions about the validity of the indicator approach. Finally, we believe there is a need for the standardisation of assessment techniques employed, otherwise levels of support will continue to fluctuate and consensus on the adequacy of indicator taxa as biodiversity surrogates will remain elusive.

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