Reduced survey intensity and its consequences for marine reserve selection[1]

WILLIAM GLADSTONE* and JENNIFER DAVIS

Centre for Sustainable Use of Coasts and Catchments, University of Newcastle, PO Box 127, Ourimbah NSW 2258, Australia; *Author for correspondence (Tel: + 61 2 4348 4123; fax: + 61 2 4348 4145; e-mail: wgladsto@mail.newcastle.edu.au)

Abstract. There has been much interest in the potential of short-cuts in biodiversity surveys (e.g. physical surrogates, indicator groups, and lower taxonomic resolution) in systematic processes to select networks of representative marine reserves. This study tested the consequences for reserve selection of reducing survey intensity in intertidal rocky shores in south-east Australia. Using a reference data set of species' distributions based on surveys of two replicate sites in each of 15 locations, a reduction in survey intensity was simulated by randomly eliminating the data from one of the replicate sites in each location. A complementarity-based reserve selection algorithm was used to determine the number of locations required to represent all species once in a reserve network and the irreplaceability value of locations. A reduction in survey intensity led to increases in: the size of reserve networks (of between 8 and 17%); the irreplaceability value of locations; and the number of

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irreplaceable locations. These changes were caused by a reduction in the observed

range sizes of species in the data sets simulating a reduced survey intensity.

Key words: biodiversity; coastal zone management; intertidal rocky shore; marine

protected area; surveys

Introduction

Global recognition of the potential value of marine reserves for biodiversity

conservation has prompted systematic programmes of reserve selection in several

countries (Kelleher et al. 1995; Walls 1995; Yurick 1995; Thackway 1996; ANZECC

1999; Gladstone et al. 1999). Experience from terrestrial systems has shown that

reserve networks selected on the basis of complementarity and irreplaceability are

more efficient at representing biodiversity, compared with the *ad hoc* acquisition of

land for reserves (Margules and Pressey 2000). However, these procedures rely on

detailed biodiversity data across all locations being considered. The paucity of

detailed data on biodiversity in many countries and the costs involved in gathering the

necessary data are potential obstacles to the systematic selection of reserves using

these procedures. As a consequence of these limitations, there has been great interest

in the value for reserve selection of rapid methods of biodiversity assessment. These

short-cuts include physical and habitat surrogates (Wessels et al. 1999; O'Hara 2001);

lower taxonomic resolution (Balmford et al. 1996; van Jaarsveld et al. 1998;

Vanderklift et al. 1998; Balmford et al. 2000); and indicator groups (Ryti 1992; Csuti

et al. 1997; Howard et al. 1998; Ward et al. 1999; Pharo et al. 2000; Reyers et al.

2000; Gladstone 2002). All have shown some promise for reserve selection, although very few of these studies have been conducted in marine systems.

In this paper we evaluate the consequences for reserve selection of using an alternative short-cut approach to biodiversity surveys: a reduction in survey intensity. In this case, survey intensity refers to the number of replicate sites surveyed within replicate locations of the same habitat type (intertidal rocky shores) and follows the use of 'intensity' adopted in Freitag and Van Jaarsveld (1998). In the present study we evaluate whether data collected from only one site in a location can be used for reserve selection in place of data from more extensive biodiversity inventories based on surveys of replicate sites within each location. The data used in this study were derived from surveys of two replicate sites within each of 15 locations representing intertidal rocky shores in south-east Australia. The reduction in survey intensity was simulated by randomly deleting the data from one site in each of the 15 locations. The consequences of using data from only one site were evaluated in two ways:(1) by comparing the size of reserve networks chosen by reserve selection algorithms using data from both sites in each location and data from only one site in each location; and (2) by comparing the irreplaceability value of each location based on data from both sites in each location and data from only one site in each location. For (1) we test the hypothesis that a reduced survey intensity will lead to a smaller reserve network being selected. This hypothesis is based on the following: (1) a reduction in survey intensity should lead to a reduction in the total number of species recorded in each location because of small-scale spatial variability in species composition; and (2) a number of other studies have shown relationships between total number of species

and the size of reserve networks chosen by complementarity-based reserve selection algorithms (Pressey et al. 1999; Rodrigues and Gaston 2001).

Materials and methods

Field surveys

The study was undertaken in the Hawkesbury Shelf bioregion, south-east Australia. This bioregion extends approximately 210 km between Stockton ($32^0$54.9'S, $151^0$47.0'E) and Kiama ($34^0$39.9'S, $150^0$51.1'E) on the coast of New South Wales (IMCRA Technical Group 1997). Fifteen locations representing the same habitat type (intertidal rock platform) were surveyed in December 1999 - February 2000 (Figure 1) around low tides on days of calm seas. The range of intertidal rocky shore habitats in south-east Australia includes rock platforms, boulder fields, and cliffs plunging directly into the sea. This study was confined to the organisms inhabiting rocky shores with intertidal rock platforms. All locations surveyed were on exposed sections of coastline. The aspect of the seaward edge of the rocky shores ranged from northeast (Dudley, Norah Head, Crackneck, Long Reef, Bass Point), east (Bar, Frazer, Terrigal, Maitland Bay, Killcare, Bronte, Clovelly, Jibbon, Garie) and southeast (Birdie). These differences in aspect are not likely to be significant in producing differences in species composition amongst these locations because variations in the prevailing weather conditions meant that all locations are effectively exposed. The physical structure of the locations surveyed consisted of a flat to sloping intertidal platform, with an abruptly dropping seaward edge, and a margin of boulders at the

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landward edge. The width of the rocky shores from the seaward edge at low tide to the limit of distribution of the intertidal animals varied from 23 to 143 m. The majority of rocky shores surveyed were composed of fine-coarse grained sandstones. Differences included Frazer and Birdie (both conglomerate) and Bass Point (volcanic rock). There is insufficient information to indicate that differences in geology between rocky shores produce consistent differences in species composition between shores (Caffey 1982; McGuinness 1988; Keough et al. 1997; Underwood and Chapman 1998a).

Two replicate sites were randomly chosen in each location. Each site was 30 m in width and extended shoreward to the limit of intertidal organisms. Replicate sites were separated by at least 30 m. A site width of 30 m was selected to address the spatial variation in species composition that was likely to be present within each location. The organisms surveyed in this study were restricted to macroscopic species (generally larger than 5 mm in size) that could be easily observed and identified in the field. The meiofauna that occur within sediments in these habitats, and other smaller and cryptic organisms that occur within algal beds were not surveyed. Each site was searched for a total of 3 person hours at low tide, based on 3 persons each searching for 1 hour. This search effort was chosen from species accumulation curves developed during a pilot study. Sites included a range of microhabitats: flat platform, boulders on the rock platform, rock pools, cracks in the flat platform, the vertical faces and overhangs of large boulders, and beds of algae on the low-mid shore. Each microhabitat present in a site was searched during the 3 hr period and the presence of species noted. The suite of species observed in each site was combined to give a total species richness for each location.

The species composition of the two sites in each location were compared by Jackard coefficient. The Jackard coefficient is calculated as $CC_j = c/S$, where c is the number of species common to both sites and S is the total number of species in both sites (Magurran 1988). Values of the Jackard coefficient can potentially range between 0 (indicating no species common to the northern and southern sites in a location) and 1 (indicating the same suite of species occur in both the northern and southern sites).

The effects of surveying a reduced number of sites within locations on the outcomes of reserve selection

A simulated reduction in survey intensity was achieved by randomly removing the species recorded in one site from each of the 15 locations and undertaking reserve selection on this reduced data set. Reserve selection was done using a rarity-based algorithm in WORLDMAP (British Museum of Natural History) for the representation target of each species being represented at least once in a reserve (Margules et al. 1988; Csuti et al. 1997; Williams 1999). This algorithm begins by first selecting locations containing species that do not occur anywhere else. It then searches for the rarest species that is not represented in the locations already selected, and selects from amongst the locations where it occurs the location that contributes the greatest number of unrepresented species. Where there are ties between locations in the latter step, the algorithm selects the location with the groups of species occurring in fewer locations. These steps are repeated until all species are represented. The final set of locations is re-ordered by complementary richness (Margules et al. 1988; Williams 1999). The outcome of the rarity-based algorithm is

a 'near minimum set' of locations, as progressive rarity algorithms are the most effective of a range of reserve selection algorithms in selecting the minimum number of locations required to represent all species (Kershaw et al. 1994; Csuti et al. 1997). The simulation of a reduced survey intensity followed by reserve selection was repeated 15 times.

There are potentially many combinations of locations of the same number that will achieve the stated representation target, depending on the pattern of distribution of species between locations (Pressey et al. 1994; Hopkinson et al. 2001). This characteristic of reserve selection is termed 'flexibility' (Pressey et al. 1994). The number of all such possible combinations in which a location occurs is a measure of its relative contribution towards the achievement of the representation goal, or its 'irreplaceability' (Pressey et al. 1994). Locations that occur in all possible combinations of locations are irreplaceable for achieving the representation target. Irreplaceability is difficult to measure for large data sets consisting of many locations and may species, because of the large number of possible combinations of locations (but see Ferrier *et al* (2000) for recent developments in predicting irreplaceability for large numbers of locations). Irreplaceability value of locations has therefore been estimated from the effective maximum rarity (EMR) among the species in each location (Pressey et al. 1994). The EMR value of locations is calculated in the following way: (1) identify locations with the rarest species (i.e. those occurring in the fewest locations in the data set) and allocated EMR values according to the formula 1/frequency (where frequency = number of locations in which a species occurs); (2) identify locations with the next rarest species not represented in locations from the previous step and allocate EMR values by the same formula; (3) repeat the previous

step until all species in the data set are represented; (4) identify locations with no unrepresented species and allocate to these locations minimum EMR values of 1/number of locations in the data set (Pressey et al. 1994). The EMR value of all locations was determined using WORLDMAP based on data from both sites, and for the 15 sets of 15 locations from which the species in one site had been randomly removed.

Results and Discussion

A total of 225 species were observed, representing chlorophyta (8 species), phaeophyta (39 species), rhodophyta (40 species), magnoliophyta (2 species), porifera (9 species), cnidaria (5 species), platyhelminthes (1 species), annelida (6 species), sipuncula (1 species), arthropoda (20 species), mollusca (80 species), bryozoa (1 species), echinodermata (9 species), chordata (4 species). The species richness of locations ranged from 70 (Birdie) to 123 species (Bass Point). Sites randomly chosen for survey within locations were separated by distances of 30-210 m. The difference in species richness between sites in each location varied from 1 to 25 species (Table 1). Because of the survey method used in the present study (a timed search to the limit of intertidal organisms), sites varied in area from 705 m^2 to 4290 m^2. The regression between site area and species richness, however, was non-significant ($r^2 = 0.002$, $F_{1,28} = 0.05$, $P = 0.82$). The greatest difference in richness between sites within a location occurred at Bass Point and was not associated with any obvious physical difference between the two sites. Values of the Jackard coefficient (Table 1) ranged from 0.52 (Bass Point) to 0.67 (Killcare). The location with the least similarity

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between sites (Bass Point) also showed the greatest difference between sites in species richness (Table 1). These results agree with those from other studies that have reported variations in the composition of intertidal rocky shore assemblages at a variety of spatial scales (Jernakoff 1985; Foster et al. 1988; Astles 1993; Archambault and Bourget 1996; Underwood and Chapman 1998a,b).

Reserve selection on the complete data set (i.e. using both sites in all locations) resulted in a near minimum set of 12 locations, which was the minimum number of locations required to represent all species at least once. This near minimum set consisted of 11 irreplaceable locations and one partially flexible location. The partially flexible location (Bar Beach) contributed four goal-essential species, and could be replaced by both Dudley and Killcare because each contributed two of the goal-essential species. Randomly eliminating one site from each location led to an increase in the size of the near minimum set of locations required to achieve the representation goal: a majority of trials (12 of 15) required 14 locations to achieve the representation target; three trials required 13 locations. In 14 trials all locations were irreplaceable for achieving the representation goal. Species were accumulated at a slower rate at each step of the reserve selection algorithm when using the data set from which one site in each location had been randomly deleted, compared with the complete data set (Figure 2). The first location selected by the algorithm for the complete data set contributed 54.7% of species in that data set whereas the first location selected by the algorithm for the reduced data set contributed $49.5 \pm 0.75\%$ (mean $\pm$ standard error) of species in that data set. There was no difference between the two data sets after eight locations had been selected.

The irreplaceability values of locations calculated using data from both sites in all locations varied from 0.07 to 1.0, with 11 locations being irreplaceable (EMR = 1.0) for achieving the representation goal (Table 2). Eliminating data from one site in each location increased the number of irreplaceable locations from 11 to 13 (Table 2). This increase occurred because of an increase in the irreplaceability value of the Bar Beach and Killcare locations from 0.5 in the complete data set to 1.0 in all trials of the reduced data set. In addition, a further location (Dudley) was irreplaceable in 11 trials. The location with the lowest irreplaceability value in the complete data set (Birdie) retained this value in all trials of the reduced data set. All locations that were irreplaceable with the complete reference set of data were still irreplaceable after data from one site had been randomly removed. In summary, a simulated reduction in survey intensity led to an increase in the number of locations that were irreplaceable for achieving the representation goal of each species being represented at least once in a reserve.

Near minimum sets of areas are chosen by complementarity-based reserve selection algorithms, which have the aim of selecting the smallest number of locations required to represent all features (e.g. species, assemblages, ecosystems) a given number of times. The size of near minimum sets (expressed as the number of locations selected or the total area of locations selected) and the number of alternative near minimum sets will depend on the size of dataset of features; levels of local endemism; the representation goal; and the numbers of areas available for conservation (Pressey et al. 1994; Pressey 1999; Rodrigues and Gaston 2001). Several studies of the effects of variations in these features on the outcomes of reserve selection are worth exploring because of their relevance to the results of the present

study. Willis et al. (1996) found, for the limestone flora of the Cape Floristic Region in South Africa, that 77% of sites were irreplaceable because of high levels of local endemism. Similarly, Lombard et al. (1999) found, for the Succulent Karoo of South Africa, that a large % of total area was required to conserve at least one representative of each species because of high levels of local endemism and high species turnover between sites. Of the species studied by Lombard et al. (1999), 46% were recorded from only one location. Pressey et al. (1999) altered a data matrix of 248 types of land systems in the Western Division of New South Wales to simulate three increasing levels of rarity and found significant increases in the number and area of reserves required to represent all features as rarity increased. Similarly, Rodrigues and Gaston (2001) systematically altered a data set of bird species from southern Africa and found that the size of near minimum sets increased as the size of the data set increased and as the levels of endemism increased.

The observed changes in both the size of the near minimum set and the irreplaceability value of locations following a simulated reduction in survey intensity appear to be due to changes in species' distribution patterns in the randomly reduced data set. The 15 data sets simulating a reduction in survey intensity contained between 186 and 201 species, representing 82.7% - 89.3% (mean $\pm$ SE = 84.7 $\pm$ 0.45%) of the reference data set. Species contributing to the increased irreplaceability value of Bar, Dudley and Killcare with the reduced data sets (Table 2) represented phaeophyta (4 species), rhodophyta (5 species), porifera (1 species), annelida (1 species), arthropoda (1 species) and mollusca (1 species). Of these, a subset of phaeophyta (1 species), rhodophyta (3 species) and porifera (1 species) contributed to increases in irreplaceability value in a majority (i.e. 8 – 10) of trials. These species

occurred in 2-3 locations and were usually observed in only one site in each location. Despite predictions from the literature that decreases in the size of a data set will lead to decreases in the size of near minimum sets, the simulated reduction in survey intensity in the present study led to an increase in the size of the near minimum set from 12 to 14 locations, and an increase in the number of irreplaceable locations from 11 to 13. These increases appear to have occurred because of a decrease in the range size of species in the data set resulting from the reduced survey intensity (Figure 3). Although there was no significant difference in the distribution of numbers of species among the classes of range sizes (Pearson Chi square = 4.28, $df = 4$, $P = 0.37$), there was an increase in the % of species occurring in only 1-3 locations and a decrease in the % of species occurring in 13-15 locations in the data set resulting from the reduced survey intensity (Figure 3). A consequence of this increase in number of unique occurrences was that locations not selected in the near minimum set based on the reference data set were included in the near minimum sets of some or all of the 15 data sets resulting from the simulated reduction in survey intensity because they now contained species that occurred in no other locations (so called 'goal-essential species'). For example, two locations (Dudley, and Killcare) not selected for the near minimum set from the reference data because they contained no-goal essential species contained between 1-3 (Dudley) and 1-8 (Killcare) goal-essential species in the reduced data sets.

Despite the potential significance of variations in sampling effort for the outcomes of reserve selection, it is surprising that there have been very few attempts to quantify these effects. Freitag and Van Jaarsveld (1998) evaluated the consequences for reserve selection of randomly reducing the number of grid cells

containing records of the mammalian fauna in the north-east region of South Africa. They found that increasing the % of excluded grid cells resulted in smaller sets of grid cells required to achieve the representation target, but only by a small amount. Exclusion of 60% of grid cells led to an average drop of 2 grid cells (from 23 to 21) in the size of reserve networks. Freitag and Van Jaarsveld (1998) found that the reserve selection outcomes were most sensitive to reductions in either survey intensity (i.e. the number of data records) or the number of species surveyed. They concluded that it was not possible to specify one element of survey design over another, and recommended a strategy that addressed taxonomic diversity, survey intensity and survey intensity. There is considerable scope for exploring this important question further in other terrestrial and marine systems with different biodiversity.

The results of the present study suggest that adopting short-cuts in survey methodology will have consequences for the outcomes of reserve selection. Simulated reductions in survey intensity increased both the number of locations selected for a complementarity-based reserve network and the number of irreplaceable locations. This study was undertaken at only one point in time and involved a limited number of locations and a relatively small data set of species, with a distribution pattern of many species occurring in only a limited number of locations. Addressing the balance between appropriate survey design and practical constraints are important, especially in the context of the current interest in the declaration of marine reserves and the need for large-scale surveys of biodiversity. To more fully understand the effects on reserve selection of variations in survey methodology further investigations of the sort undertaken in this study are required in different habitats with different

patterns of species' distributions, and they need to be repeated through time to confirm the temporal stability of results.

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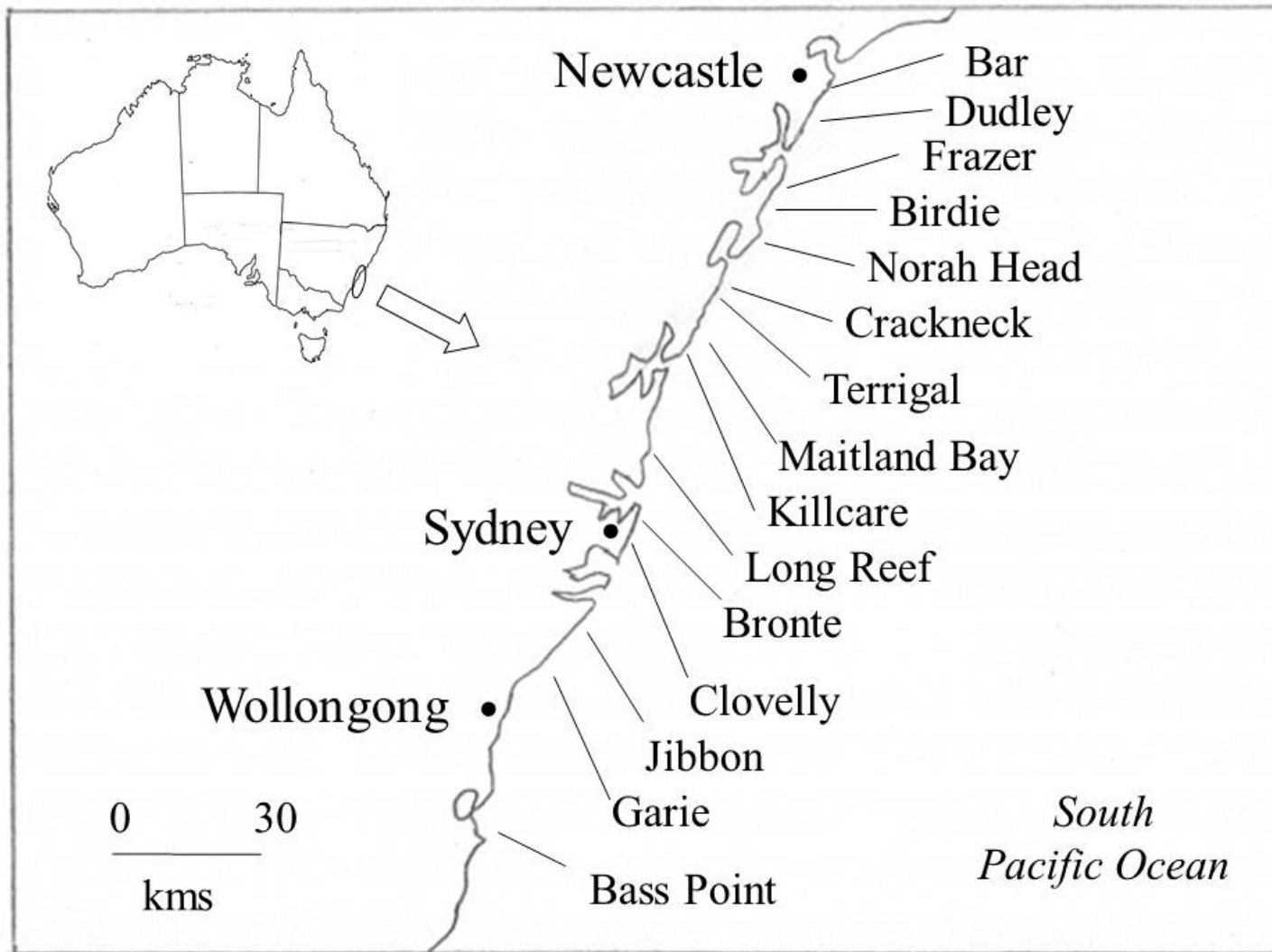Privately distributed, London

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Reserve systems for limestone endemic flora of the Cape Lowland Fynbos: iterative
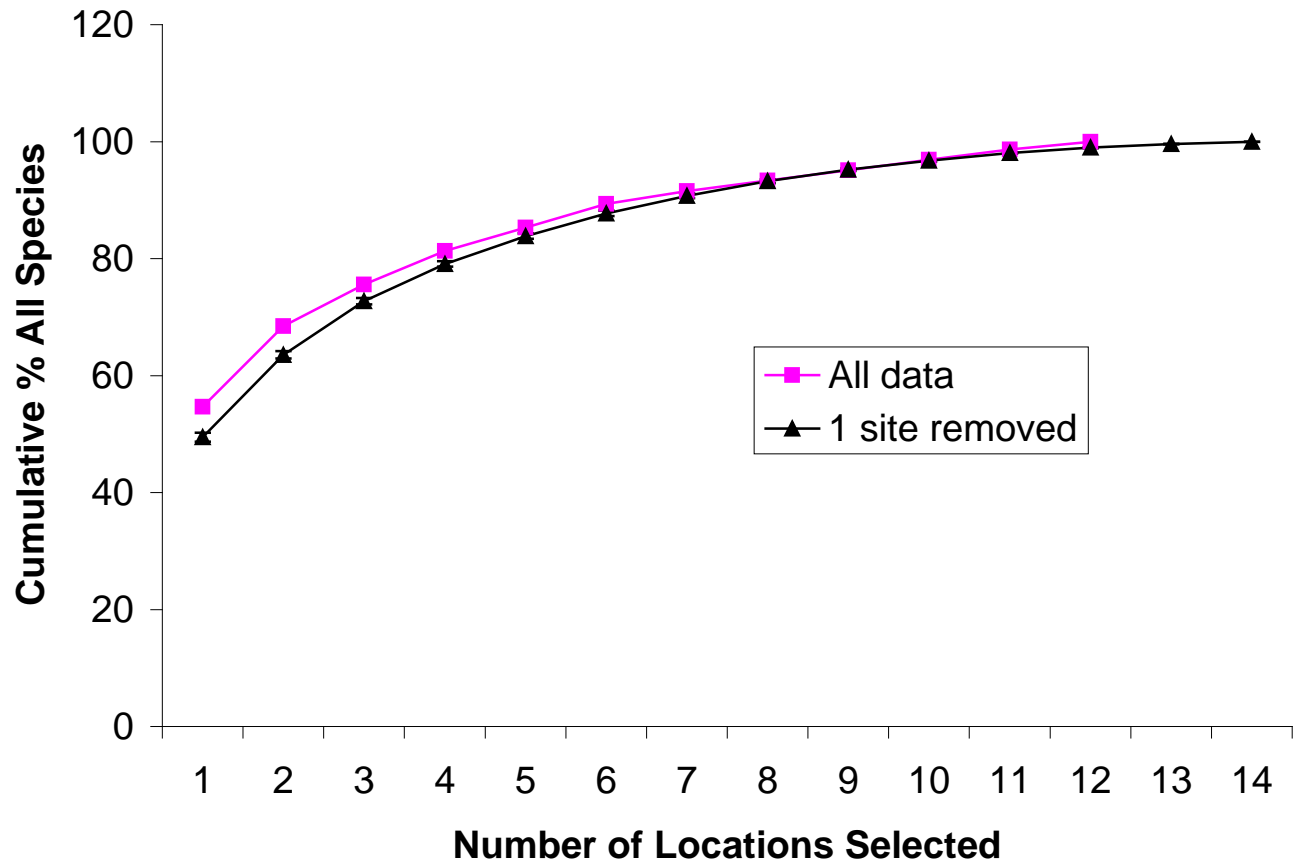versus linear programming. Biological Conservation 77: 53-62

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Figure 1. Survey locations used in the present study.

Figure 2. Comparison of rate of species accumulation at progressive steps of the reserve selection algorithm using data from the complete survey protocol and data simulating a reduction in survey intensity. Values shown for the reduced survey intensity are mean ± SE from 15 trials.

Figure 3. Frequency distribution of range sizes (number of locations in which a species was observed) for all species recorded using the complete survey protocol and species from the data set simulating a reduction in survey intensity. Range sizes from the data set simulating a reduction in survey intensity are the mean ± SE from 15 trials.

Newcastle •

Bar
Dudley
Frazer
Birdie
Norah Head
Crackneck
Terrigal
Maitland Bay
Killcare
Long Reef
Bronte

Sydney •

Wollongong •

Clovelly
Jibbon
Garie

Bass Point
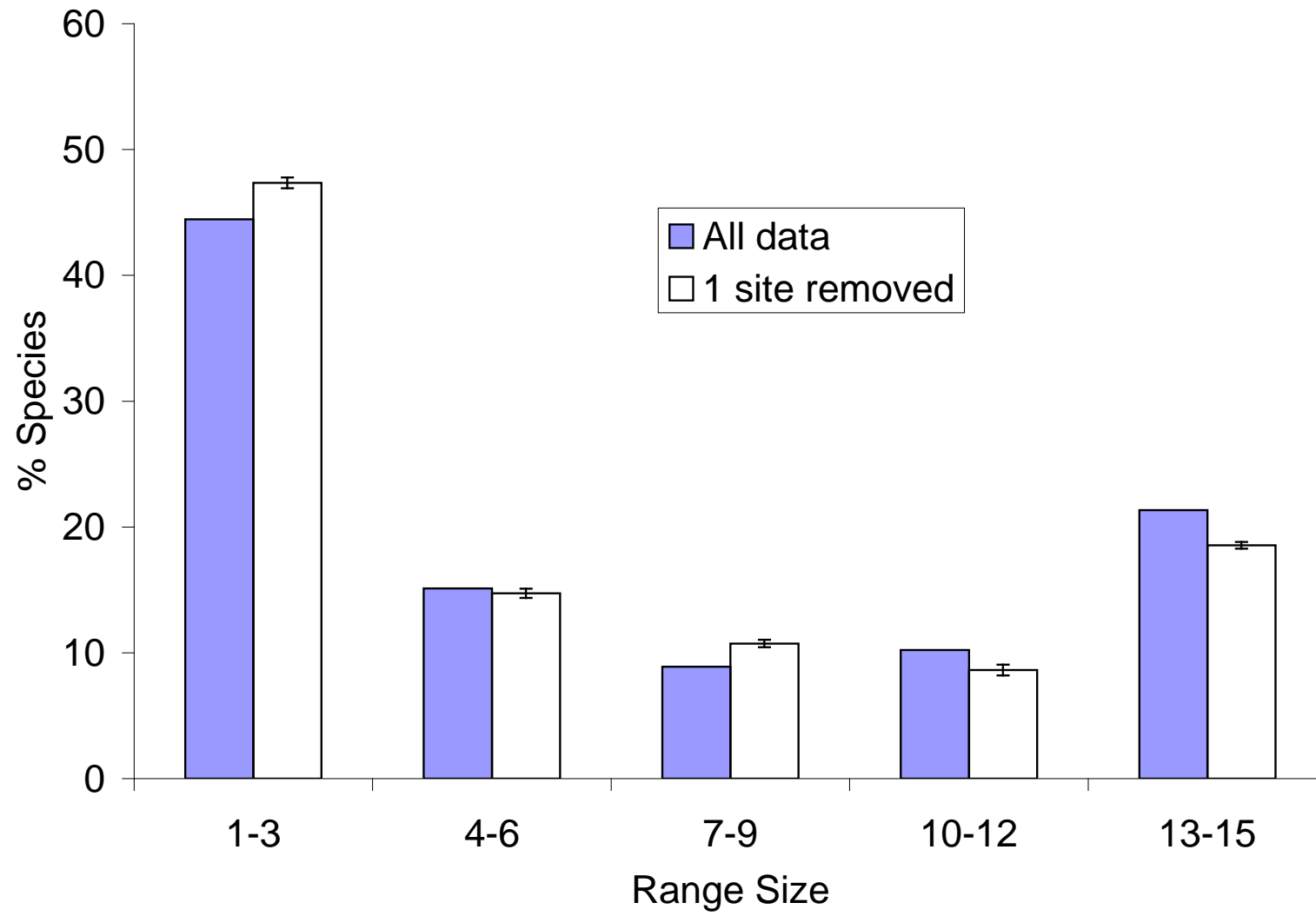
South Pacific Ocean

0   30

kms

Table 1. Species richness in the each replicate site surveyed within each location. Also shown is the area surveyed within each location, representing the combined areas of the replicate sites. CC_j = value of Jackard coefficient comparing the identity of species between sites within each location.

Location	Location Area (m^2)	Location Richness	Site 1 Richness	Site 1 Area (m^2)	Site 2 Richness	Site 2 Area (m^2)	CC_j
1. Bar	4,740	82	70	2,580	60	2,160	0.59
2. Dudley	4,020	89	74	2,370	64	1,650	0.55
3. Frazer	1,818	80	66	705	61	1,113	0.59
4. Birdie	2,850	70	58	1,740	56	1,110	0.63
5. Norah Head	7,380	100	82	3,720	72	3,660	0.52
6. Crackneck	8,010	88	67	4,290	70	3,720	0.56
7. Terrigal	5,142	119	89	2,592	99	2,550	0.55
8. Maitland Bay	4,800	102	81	1,950	82	2,850	0.60
9. Killcare	1,920	95	71	1,080	88	840	0.67
10. Long Reef	5,340	91	65	3,030	80	2,310	0.59
11. Bronte	1,740	110	90	840	85	900	0.55
12. Clovelly	3,150	99	74	1,380	89	1,770	0.65
13. Jibbon	2,610	88	71	1,410	75	1,200	0.64
14. Garie	2,700	94	80	930	74	1,770	0.64
15. Bass Point	3,120	123	82	1,380	107	1,740	0.52

Table 2. The effects of removing one site from each location on the irreplaceability value of each location. The results shown are the irreplaceability values of all locations based on the reference data set, and the irreplaceability values of all locations following the removal of one site from each location.

Location	Irreplaceability value (based on reference data set)	Distribution of irreplaceability values of locations after removal of data from one site (expressed as % of 15 trials)		
		0.07	0.5	1.0
Bar	0.5	0	0	100%
Dudley	0.5	20%	6.7%	73.3%
Frazer	1.0	0	0	100%
Birdie	0.07	100%	0	0
Norah Head	1.0	0	0	100%
Crackneck	1.0	0	0	100%
Terrigal	1.0	0	0	100%
Maitland Bay	1.0	0	0	100%
Killcare	0.5	0	0	100%
Long Reef	1.0	0	0	100%
Bronte	1.0	0	0	100%
Clovelly	1.0	0	0	100%
Jibbon	1.0	0	0	100%
Garie	1.0	0	0	100%
Bass Point	1.0	0	0	100%