



Defining conservation targets for fish and molluscs in the Port Stephens estuary, Australia using species-area relationships



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ABSTRACT

Effective planning for marine protected areas should be based on conservation targets that are representative of underlying habitats and species distributions. Here, we present the results of an investigation into using species-area relationships (SARs) to define habitat conservation targets for two dominant taxonomic groups (fish and molluscs) using data from the Port Stephens estuary in New South Wales, Australia. Results demonstrated that planning conducted using variable habitat targets, based on SARs, provided significant improvements in representation of habitats and species, compared to planning using uniform (fixed percentage) habitat targets. Planning based on SARs was also found to provide significant improvements in species protection for fish and molluscs when compared with planning implemented without the benefit of detailed biodiversity information. However, SAR targets were found to be sensitive to the function type chosen to represent species distributions (i.e. power-law and exponential), and to the method used for estimation of species richness. Therefore, where SARs are used to set targets in conservation planning, it is important to ensure that they are representative of underlying species distributions. Overall, the improved performance of conservation planning based on SARs indicates the potential for broader application of this technique in planning marine protected areas.

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1. Introduction

Effective conservation planning in marine protected areas (MPAs) involves systematic scientific investigations and consultation with stakeholders (Airamé et al., 2003; Fernandes et al., 2005). Given important MPA features are not readily apparent from the surface, planning for MPAs therefore needs to be based on accurate information, and robust methodology (Fernandes et al., 2005; Stewart et al., 2003). Despite this, MPA planning decisions are often made on an *ad hoc* basis, or with incomplete information, leading to inefficient, or inadequate design (Pressey, 1994; Stewart et al., 2003).

Marine conservation planning is implemented to accomplish a range of objectives including achieving social and economic goals (Ban et al., 2011; Stewart and Possingham, 2005), protecting rare and threatened species (Leslie, 2005; Powles et al., 2000) and

conservation of biodiversity (Agardy et al., 2003; Leslie, 2005). Within this broader management framework, planning to protect biodiversity is frequently conducted using uniform conservation targets for habitats or regions, with a 10% target specified for marine areas in Convention on Biological Diversity Aichi Target 11, and 20% targets widely applied in marine protected area planning (Fernandes et al., 2005; Green et al., 2009). The use of uniform targets has, however, been criticised because they imply that all regions or habitats are adequately protected by the same criteria, which ignores biological variations across regions and habitats (Agardy et al., 2003; Pressey et al., 2003). Alternatives to uniform targets are therefore needed (Pressey et al., 2007; Svancara et al., 2005) and conservation targets based on species-area relationships (SARs) are increasingly being used for this purpose in marine conservation planning (Ashworth et al., 2010; Foster et al., 2013; Metcalfe et al., 2013).

The species-area relationship is one of the most widely recognised patterns in ecology (Connor and McCoy, 1979), with the number of species in a taxonomic group increasing with total area (Arrhenius, 1921). It therefore follows that the number of species protected will rise as the size of an effective protected area

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increases, and that SARs can therefore be used to calculate targets aimed at protecting a specified proportion of local species richness (Desmet and Cowling, 2004). This conservation approach provides a scientific basis for quantitatively setting non-uniform targets for habitats to protect the species they shelter (Metcalf et al., 2013), and has been identified as being especially useful where protection of a broad range of species is required (Neigel, 2003).

Habitat targets for species protection defined based on SARs (SAR habitat targets) depend on the taxonomic group (Holt et al., 1999), the type of SAR function (Connor and McCoy, 1979), and the methodology used to derive functions from measured species data (Metcalf et al., 2013). Multiple functions are available to represent SARs (Connor and McCoy, 1979), with power-law functions generally having the broadest applicability (Connor and McCoy, 1979; Williamson et al., 2001). However exponential functions are also widely applicable (Tittensor et al., 2007; Williamson et al., 2001) and other types of functions have been derived (Smith, 2010; Tjørve, 2003). Previous studies examining the use of SARs to set conservation targets for MPAs have generally been based on benthic fauna (Foster et al., 2013; Metcalf et al., 2013; Rondinini, 2011), and have often selected power-law functions *a priori* to represent SARs (Metcalf et al., 2013; Rondinini, 2011). However, the influence of taxonomic group and type of SAR function on SAR habitat targets has not been fully examined.

Given the complexity associated with defining SAR habitat targets, it is important to demonstrate that this methodology offers benefits, in terms of species protection, compared with using simpler uniform habitat targets, or conservation planning without detailed biodiversity data. Here, we investigate using SARs to set habitat conservation targets for two taxonomic groups (fish and molluscs) for the Port Stephens estuary, New South Wales, Australia, using data gathered over a 15 month period (Davis et al., 2016a). We further examine the impact on SAR derived conservation targets for habitats (SAR habitat targets) of using different SAR functions (power-law and exponential), and different algorithms for estimating species richness, with the objective of determining the sensitivity of targets to SAR modelling assumptions. We test the hypothesis that SAR habitat targets provide improved protection for fish and mollusc species, compared to uniform habitat targets. Finally given the Port Stephens estuary is within a large multi-use marine park, we examine the potential for implementing SAR habitat targets within the estuary using Marxan conservation planning software (Ball et al., 2009). The study aims to provide marine park management agencies with new approaches to use in conservation planning for protection of sub-tidal estuarine habitats and species.

2. Material and methods

2.1. Study site

The study was conducted using data from the Port Stephens estuary (Fig. 1) which lies within the existing Port Stephens-Great Lakes Marine Park (PSGLMP), managed by the New South Wales (NSW) Marine Estate Management Authority. The PSGLMP is the largest marine park in NSW and was zoned into NSW protection-level categories, including no-take marine sanctuaries, in 2007 (NSWMPA, 2007). The Port Stephens estuary is a tide-dominated drowned river valley (Roy et al., 2001), which contains a diverse range of estuarine and marine habitats (Davis et al., 2016b). The estuary is of importance in NSW as it contains extensive areas of the threatened seagrass *Posidonia australis* (Creese et al., 2009), is the only known location where the soft coral *Dendronephthya australis* occurs in abundance (Poulos et al., 2013) and is important for threatened and protected species (Harasti et al., 2014a;

Wiszniewski et al., 2009).

2.2. Assessment of biological assemblages

Within the Port Stephens estuary, habitats were classified into eight major categories (Table 1) by Davis et al. (2016b) using the Australian CATAMI system for classifying underwater imagery (CATAMI, 2013). Biodiversity data were gathered in each habitat type, every three months from June 2014–August 2015, for fish (Davis et al., 2016a) and molluscs, giving twelve randomly situated replicate underwater visual census (UVC) belt transects (25 × 5 m) in each habitat, with methods adapted from Smith et al. (2008). These taxonomic groups were selected as they have been shown to provide useful surrogates for other phyla in marine assemblages (fish (Ward et al., 1999), and molluscs (Smith, 2005)). As biodiversity measures for habitats should be based on resident species, and exclude accidental or temporary immigrants, non-resident species (e.g. tropical and pelagic species) were excluded from all calculations. Tropical species typically occur in the study area only for brief periods (Booth et al., 2007), and pelagic species are highly variable at small spatial scales (McClanahan et al., 2007).

The ability of power-law functions (Eq. (1)) and exponential functions (Eq. (2)) to represent fish and mollusc SARs was evaluated by fitting both types of functions to species accumulation curves generated for fish and mollusc data (Fig. 2),

$$S = c A^z \quad (1)$$

$$S = d + e \log(A) \quad (2)$$

(S = species, A = area, z = slope in log-log space, e = slope in log-linear space, c , d = constants dependent on function and region).

Species accumulation curves were generated by averaging across 100 random transect sequences, using EstimateS (Colwell, 2013), for the 96 transects conducted (i.e. twelve replicate transects in eight habitats). The accuracy of SAR function fit to measured species accumulation curves was assessed for both power-law and exponential functions using least-squares error estimates. Exponential functions (fish, $R^2 = 0.998$ and molluscs, $R^2 = 0.982$) provided a superior fit to observed distributions, compared with power-law functions (fish, $R^2 = 0.928$ and molluscs $R^2 = 0.963$, Fig. 2), indicating that exponential functions provide more accurate representation of SARs for fish and molluscs within the study area.

2.3. Evaluation of conservation target sensitivity to SAR modelling assumptions

To evaluate sensitivity of SAR habitat targets to SAR modelling assumptions, targets were calculated for two taxonomic groups (fish and molluscs), for two different SAR function types (power-law and exponential), and two different algorithms for estimating species richness (Bootstrap and Jackknife 2). SAR habitat targets were calculated to protect 80% of the selected taxonomic group within each habitat, with the species protection level set at 80% as recommended by the Joint Nature Conservation Committee for conservation of marine species (Ashworth et al., 2010). Comparisons among SAR habitat targets for alternate methods were conducted using two-tailed paired Student's *t*-tests.

Species-area relationships were derived for each habitat, taxonomic group, function type, and species richness estimation technique, using the methodology proposed by Desmet and Cowling (2004), with functions fitted through (S_h , A_h), where S_h = the average species richness per transect in habitat- h , and A_h = habitat transect area (0.015 ha), and (S_{Th} , A_{Th}), where S_{Th} = the estimated

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