Marine Biodiversity Hub

National Environmental Science Programme

Expanding our spatial knowledge of marine biodiversity to support future best practice reviews

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MUSEUMS VICTORIA

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Project Leader's Distribution List

Department of Agriculture Water and the Environment (DAWE) – Parks Australia	
DAWE – Biodiversity Conservation	
DAWE – Heritage, Reef and Marine	
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DAWE – Climate Adaptation and Resilience	

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Executive Summary

Bioregionalisations are spatial frameworks that have been used to identify areas that have particular conservation values, describe ecosystem boundaries, delineate bioregional planning activities, organise environmental inventories, contextualise environmental assessments, and map the marine domain. The Integrated Marine and Coastal Regionalisation of Australia (IMCRA) products have informed the creation of a National Representative System of Marine Protected Areas (NRSMPA) and provided a spatial framework for marine bioregional planning. It is assumed that up to date and improved versions of IMCRA will be required to inform future reviews, e.g. statutory decadal reviews of Commonwealth Marine Reserve Network Management Plans, noting the South-East Network Management Plan extends from 2013-2023, and reviews of marine bioregional plans.

However, this report argues that a new marine biodiversity spatial management system would be more cost effective and useful than a dedicated updated IMCRA bioregionalisation process.

Firstly this is because, with the implementation of the NRSMPA, management priorities now include site (km scale) based management, i.e. to identify sites with high biodiversity values within parks (zoning) or outside of parks (natural heritage), to manage expected or unexpected human activities, and to predict the outcomes of climate change.

Secondly, a robust statistical analysis of biological data from a randomised sampling design across the Australian marine domain would be unlikely to generate a meso-scale bioregionalisation comparable to IMCRA. The meso-scale IMCRA regions do not represent centres of endemicity, large habitat patches (e.g. geomorphic features), enviro-regional classifications (based on oceanographic data) or (in most cases) community ecology classifications. Instead they were a useful geographical proxy for the design of the National Representative System of Marine Protected Areas, based loosely on biophysical patterns, from an era when there were few national biological datasets. Most actual biological differentiation is at either at small scales (habitat, including depth layers) or at continental scales (biogeographic province) and is relatively minor at geographic scales of 100-1000 km. Moreover, the biogeographic and environmental change around Australia is characterised by transitions and gradients rather than sharp discontinuities. Bioregional boundaries are artefacts of the bioregionalisation methodology. Moreover, the boundaries of the meso-scale bioregions are biased by a focus on coastal morphological features.

A new analysis could improve or validate the current provincial scale IMCRA bioregionalisation by using more biodiversity datasets and updated analyses. However, such maps are of limited management utility, unless further large-scale spatial planning is envisioned.

We propose that a more informative approach going forward is to develop a fine-scale (km) system of species distributional data which could be used to both address current management priorities AND produce a new provincial-scale bioregionalisation, when and if required.

This system would require three main elements

1. A species distribution database that contains raw collection data as taxonomic identification, geolocation, depth, collection date, collection gear, sample size, abundance/ biomass.

Essentially, this is similar to that currently held by the Atlas of Living Australia (ALA) with a few modifications. Expert verification of existing data is critical.

2. A software pipeline that interpolates the distribution of priority species across the Australian marine domain from the ALA biodiversity data and environmental data layers. Existing species distribution modelling tools could be plugged into a new pipeline or modifications made to existing ones.
3. Decision support system(s) that analyse the biodiversity maps produced in (2) to assist with spatial management decisions. A spatial prioritisation tool such as 'Zonation' already has the capacity to identify sites of high or low conservation value and quantify how much of each species range is protected under different spatial management options, including marine parks, or would be vulnerable to new site-based activities such as the expansion of existing fishing grounds or development of new offshore industries. Further refinement of existing tools or development of new tools should be based on extended dialogue between researcher and research users aimed at defining particular management questions that are tractable given the current status of biodiversity data and environmental data layers.

Background

Bioregionalisation versus biogeography and habitat

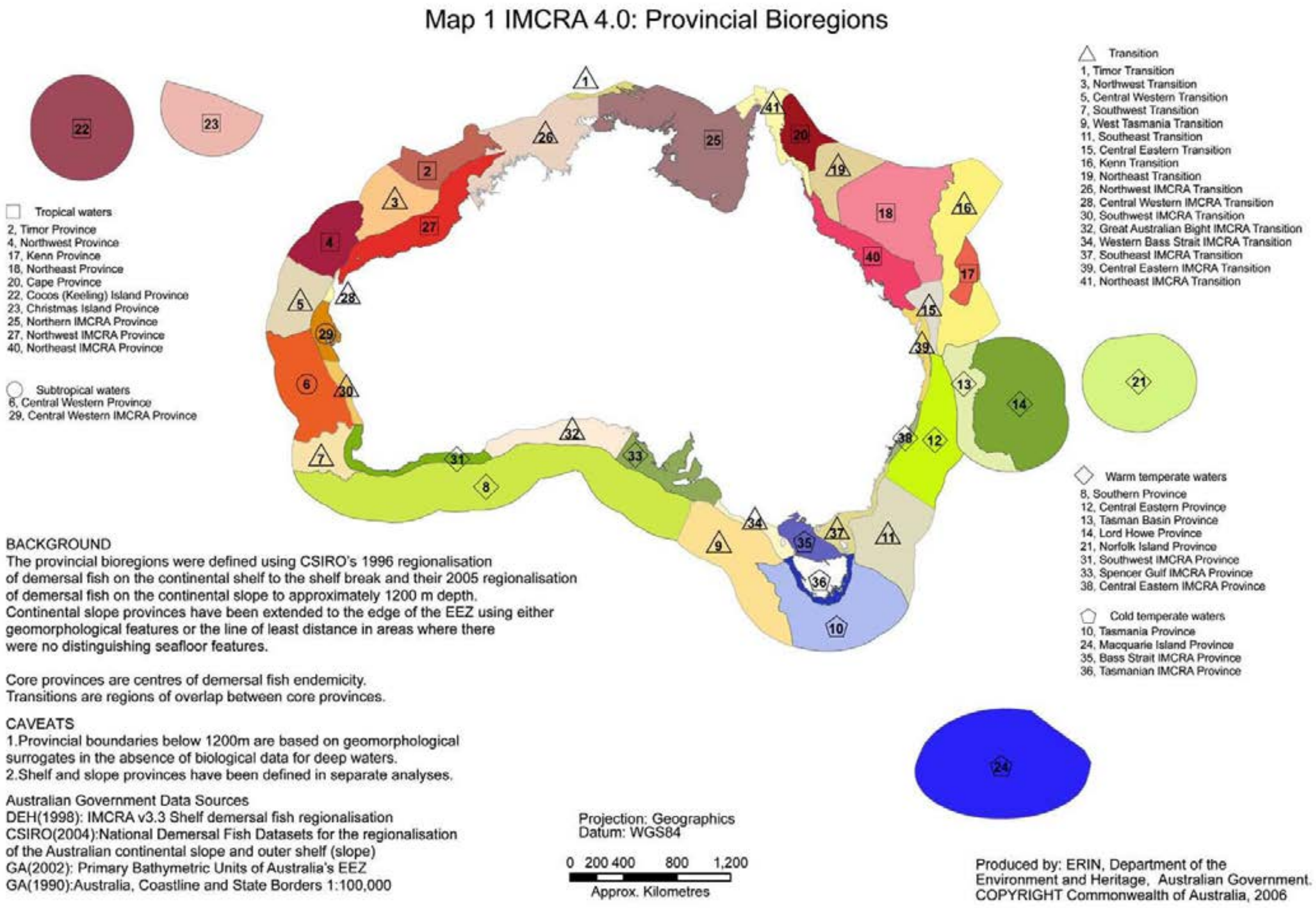
IMCRA bioregionalisations

The primary goals of the IMCRA bioregionalisation were 1) as a biodiversity surrogate to assist in the establishment of a National Representative System of Marine Protected Areas (NRSMPA), and 2) to delineate geographical units for bioregional or ecosystem management [1,2].

The IMCRA bioregionalisation v4.0 incorporated two separate layers of biological information [1]. 1) A provincial-scale bioregionalisation based on quantitative analyses of distributional ranges of Australian fish on the continental shelf [3] and continental slope [4]. 2) A meso-scale bioregionalisation amalgamated from various State-based analyses based on both biological and physical datasets. A third regionalisation, based on mapping geomorphological features, is not considered here.

The provincial-bioregionalisation (Fig. 1) was closest to traditional biogeographies (see Box 1). The analysis produced nine provinces and seven transitions around Australia. The slope classification was new (Fig. 2) [4], representing the first time that a national distributional dataset (as fish species ranges around the continental margin) had been accumulated for animals below 40 m. Various depth layers (bathomes) from 40-1500+ m were combined into a single 'slope' dataset to define a set of bioregions [4]. The final bioregionalisation included additional qualitative-defined deep-water regions in the Tasman Sea and around Australia's offshore islands [1].

The meso-scale bioregionalisation (Fig. 3) was also the first time the Australian coast and continental shelf had been classified into regions at this scale (100s-1000s km). Due to lack of consistent national biological datasets, this process used both State-based quantitative analyses of biological/physical variables (e.g. [5]) and qualitative expert opinion.


Map 1 IMCRA 4.0: Provincial Bioregions

BACKGROUND

The provincial bioregions were defined using CSIRO's 1996 regionalisation of demersal fish on the continental shelf to the shelf break and their 2005 regionalisation of demersal fish on the continental slope to approximately 1200 m depth. Continental slope provinces have been extended to the edge of the EEZ using either geomorphological features or the line of least distance in areas where there were no distinguishing seafloor features.

Core provinces are centres of demersal fish endemicity. Transitions are regions of overlap between core provinces.

CAVEATS

1.Provincial boundaries below 1200m are based on geomorphological surrogates in the absence of biological data for deep waters.
2.Shelf and slope provinces have been defined in separate analyses.

Australian Government Data Sources
DEH(1998): IMCRA v3.3 Shelf demersal fish regionalisation
CSIRO(2004):National Demersal Fish Datasets for the regionalisation of the Australian continental slope and outer shelf (slope)
GA(2002): Primary Bathymetric Units of Australia's EEZ
GA(1990):Australia, Coastline and State Borders 1:100,000

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Figure 1. Australian IMCRA 4.0 provincial bioregions based on a quantitative analysis of demersal fish distributions (40-1200 m), reprinted from Commonwealth of Australia [1].

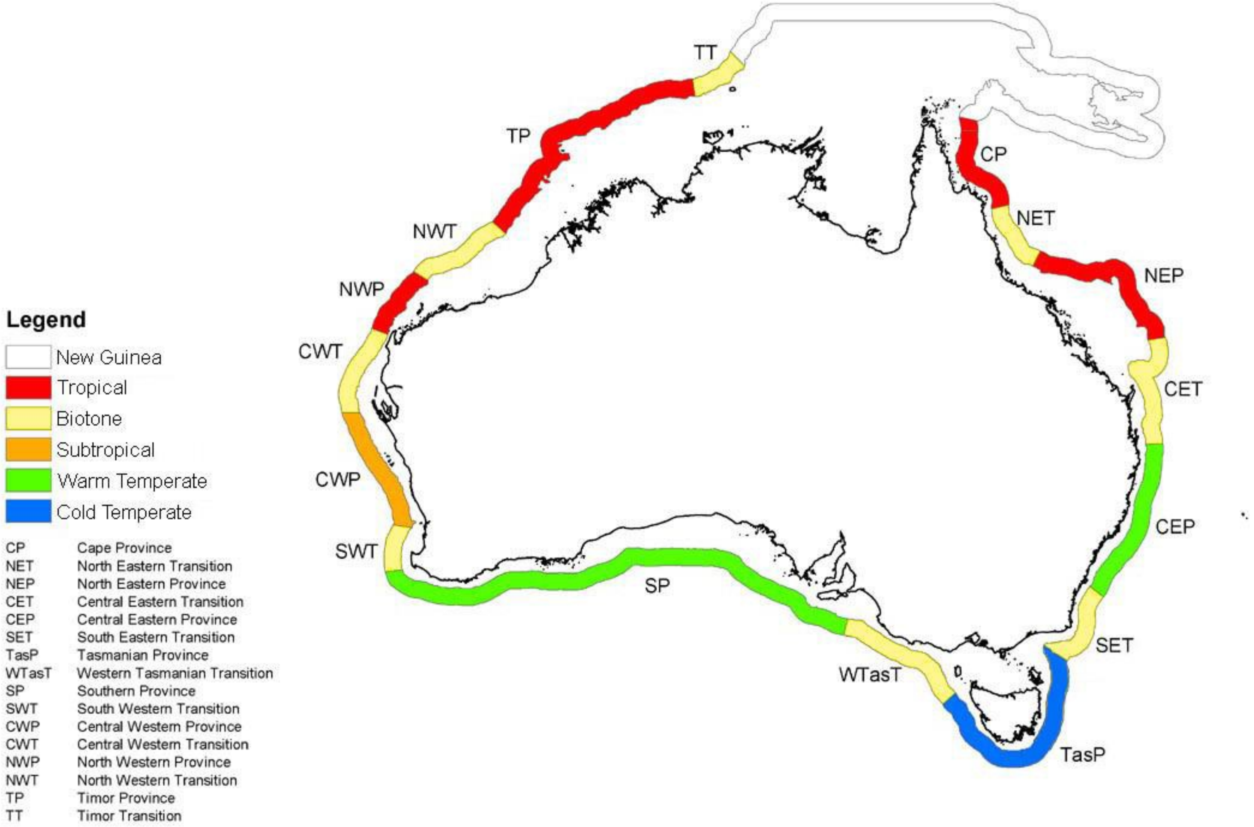
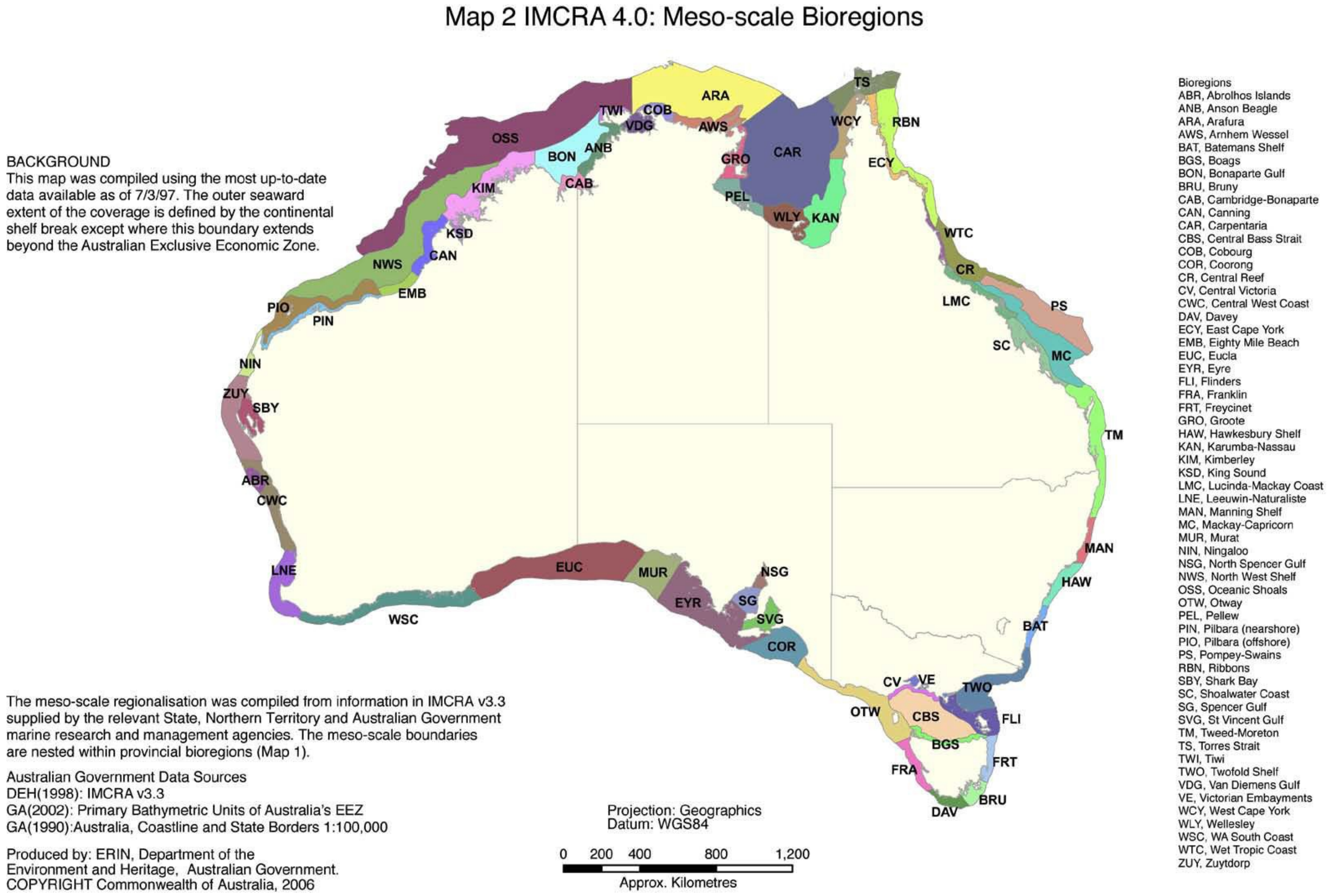


Figure 2 Australian offshore marine bioregionalisation of demersal fishes (>40 m), reprinted from Last et al. [4].



Map 2 IMCRA 4.0: Meso-scale Bioregions

BACKGROUND
This map was compiled using the most up-to-date data available as of 7/3/97. The outer seaward extent of the coverage is defined by the continental shelf break except where this boundary extends beyond the Australian Exclusive Economic Zone.

The meso-scale regionalisation was compiled from information in IMCRA v3.3 supplied by the relevant State, Northern Territory and Australian Government marine research and management agencies. The meso-scale boundaries are nested within provincial bioregions (Map 1).

Australian Government Data Sources
DEH(1998): IMCRA v3.3
GA(2002): Primary Bathymetric Units of Australia's EEZ
GA(1990):Australia, Coastline and State Borders 1:100,000

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Projection: Geographics
Datum: WGS84

Bioregions
ABR, Abrolhos Islands
ANB, Anson Beagle
ARA, Arafura
AWS, Arnhem Wessel
BAT, Batemans Shelf
BGS, Boags
BON, Bonaparte Gulf
BRU, Bruny
CAB, Cambridge-Bonaparte
CAN, Canning
CAR, Carpentaria
CBS, Central Bass Strait
COB, Cobourg
COR, Coorong
CR, Central Reef
CV, Central Victoria
CWC, Central West Coast
DAV, Davey
ECY, East Cape York
EMB, Eighty Mile Beach
EUC, Eucla
EYR, Eyre
FLI, Flinders
FRA, Franklin
FRT, Freycinet
GRO, Groote
HAW, Hawkesbury Shelf
KAN, Karumba-Nassau
KIM, Kimberley
KSD, King Sound
LMC, Lucinda-Mackay Coast
LNE, Leeuwin-Naturaliste
MAN, Manning Shelf
MC, Mackay-Capricorn
MUR, Murat
NIN, Ningaloo
NSG, North Spencer Gulf
NWS, North West Shelf
OSS, Oceanic Shoals
OTW, Otway
PEL, Pellew
PIN, Pilbara (nearshore)
PIO, Pilbara (offshore)
PS, Pompey-Swains
RBN, Ribbons
SBY, Shark Bay
SC, Shoalwater Coast
SG, Spencer Gulf
SVG, St Vincent Gulf
TM, Tweed-Moreton
TS, Torres Strait
TWI, Tiwi
TWO, Twofold Shelf
VDG, Van Diemens Gulf
VE, Victorian Embayments
WCY, West Cape York
WLY, Wellesley
WSC, WA South Coast
WTC, Wet Tropic Coast
ZUY, Zuytdorp

Figure 3. Australian IMCRA 4.0 meso-scale bioregions based on a quantitative and qualitative analysis of State-based biological and physical datasets, reprinted from Commonwealth of Australia [1]*.*

Evaluation of the IMCRA Provincial bioregionalisation

The shelf and slope bioregionalisations were not integrated and the bioregions do not align. These two depth layers may well have different bioregional patterns, but it will require an integrated analysis to determine that [2]. The offshore provinces in the Coral/Tasman Seas (e.g. Kenn, Tasman Basin) and around remote islands (Macquarie, Cocos Keeling, Christmas, Lord Howe, Norfolk) were also added on the basis of expert opinion not analyses.

The analyses of fish distributions prioritised the identification of bioregions over depth zones (bathomes), even though the compositional changes due to depth were greater than those between bioregions [6]. Bathome data were subsequently provided by province.

Although the shelf provincial bioregionalisation is broadly congruent with biogeographical studies (see Box 1), some provinces are potentially over-split. On the inner continental shelf, the traditional ‘Flindersian’ province is divided into three core areas (Central Western, Southwestern and Spencer Gulf provinces) and the ‘Maugean’ province into two (Bass Strait and Tasmanian provinces). On the other hand, the slope bioregionalisation is broadly congruent with subsequent analyses, although the boundaries can differ in position (e.g. [7]).

The precise delineation of the provincial boundaries does not match biological reality. There are few clear biogeographic breaks around Australia. Instead there is prominent overlap of neighbouring biota, which can vary in strength between taxon-specific groups. Although broad overlap zones (with few endemic fish species) are recognised as “biotones” [2] or “transitions” [1] in the IMCRA analyses, they are themselves represented by defined boundaries on the IMCRA bioregionalisation which are equally unlikely to exist. Two biological samples taken either side of these mapped boundaries are likely to be highly similar in composition.

Box 1. Traditional bioregionalisation of Australia’s marine fauna

The current scientific consensus is that the primary division of the Australian benthic marine fauna is depth-based, between the fauna/flora of the coast/continental shelf compared with that of the continental slope/abyssal plain. The coast/shelf experiences sunlight, heat, wave energy and tides. It is also disturbed by rising and falling sea-levels over time scales of 40,000-100,000 years [8]. In contrast, the deep-sea, and in particular the lower bathyal (2,000-3,500 m) and abyss (>3,500 m), depends on organic matter sinking from the surface for its energy needs. The phylogenetic (tree-of-life) differences between the shelf and slope/abyss faunas are profound, with different taxonomic families, orders or even phyla dominating [9]. These differences are ancient, with some specialised lineages extending back to the beginning of the Mesozoic Era (>250 mya) [9,10]. Thus the separate analyses for shelf vs slope fauna are justified.

Within each of these depth biomes, Australia’s continental marine fauna is divided into two main realms or latitudinal biomes [11-14]. The north of Australia is part of the huge tropical Indo-Pacific realm, stretching from Africa to Easter Island. Southern Australia forms a temperate biome, sometimes including New Zealand. In shallow water, this fauna first appears as fossils in the late Eocene (42 mya) [15] mainly originating from tropical lineages adapting to global cooling [9]. There is a broad zone of overlap of these two realms on the western (Rottnest Island to Shark Bay) and eastern (Eden to Moreton Bay) coasts. Interestingly, the slope/abyssal fauna has an almost identical pattern [14]. The southern Australian deep-sea fauna originated from both tropical and Southern Ocean lineages [9].

The shallow water fauna (and flora) of each of these biomes has been typically divided into 2-3 provinces. The southern coast has been divided into Flindersian (SW), Maugean (SE) and Peronian (NSW) provinces [16-19]. These provinces are correlated with environmental conditions (two warm temperate provinces separated by the cool-temperate SE). Although each of these areas have numerous endemic species, their boundaries are more zones of overlap than biogeographical breaks. For example, eastern Victoria (east of Wilsons Promontory) is sometimes classified with the Maugean or Peronian provinces depending on the taxa [18].

The northern coast was traditionally divided into the NW Dampierian and NE Solanderian (Great Barrier Reef) provinces with the boundary occurring at Torres Strait [16,17]. More recent biogeographies have separated the NW into separate NW and Northern provinces, with the boundary at the western end of Joseph Bonaparte Gulf [20,21]. Again these provinces are well marked, with numerous endemics at the species level. Torres Strait has been closed for much of the past 5 million years, only opening during periods of exceptionally high sea-level [20].

Attempts to further divide the fauna appear to be ecological in nature or taxon specific. Numerous authors have commented on the differences between coastal and offshore coral reefs on both the NE [22,23] and NW [20] coasts. However, this was controversial with other authors preferring to consider this an ecological or habitat distinction rather than a biogeographic one [13,20]. The fauna of the offshore reefs tend to be almost exclusively widespread Indo-Pacific species that can disperse over long distances [20] which gives these reefs a distinct character.

Evaluation of the IMCRA meso-scale bioregionalisation

There is no precise definition of what the IMCRA meso-scale bioregions were supposed to represent. This lack of definition partly reflects the divergent state-based origins of the meso-scale analyses [24]; every state (and the Northern Territory) conducted its own analysis using an inconsistent set of physical/biological datasets and expert opinion. The v3.3 IMCRA report [2] states that various State-based datasets were classified using a variety of analyses into “ecologically meaningful regions”. Bioregions that crossed State boundaries were amalgamated on the basis of similar “biophysical attributes and region descriptions” and bioregions were nested within provinces to provide continental context. Subsequent authors have also attempted to construct a hierarchy of marine biodiversity. Last et al. [25] described a level of biodiversity at the meso-scale as “geomorphological features” (e.g. a canyon or bay), which is mid-way between provinces and biotopes (mappable habitats). Wilson [20] provides the clearest distinction between provinces and meso-scale bioregions. Provinces are regions with a recognisable endemic biota that has resulted from restricted gene flow with neighbouring regions and a common geological and climatic history. Meso-scale bioregions on the other hand are characterised by “distinctive environments, assemblages and habitats”, not by the presence of endemic species (although they may be present).

Short range endemics are known to occur around the coastline in various places but they are not numerous (e.g. [18,20]). Clusters of local endemics have been noted in SE Tasmania, the South

Australian Gulf region, SW Western Australia and around remote islands such as Lord Howe Island [5,18,26]. However, in general, rates of marine endemism at meso-scales are low. Within the State of Victoria endemism rates were 1-4% of species depending on the taxonomic group, but these rates are likely to be an overestimate as many of the endemics were taxonomically uncertain and known from only a few specimens [27]. Rates of endemism are unknown for deep-sea habitats. There are numerous species recorded from a single location, but many of these distributions are likely to be due to under-sampling rather than local endemism [28].

The IMCRA meso-scale regions do not represent single geomorphic or mappable habitat features. Even a region such as Ningaloo, with its large distinctive coral reef, will have a variety of habitat patches, including sandy beaches, seagrass beds and inter-reef areas. Moreover, the bathymetric habitat range of the IMCRA bioregions is also inconsistent. While many bioregions extend from territorial waters to the limits of the continental shelf (200 m), separate offshore bioregions were defined along the Great Barrier Reef, Gulf of Carpentaria, NW Shelf, and Bass Strait etc.

The IMCRA meso-scale bioregions also do not represent a multivariate cluster analysis of oceanographic data into “enviro-regions” (*sensu* [29]). Most oceanographic variables (e.g. temperature, salinity, nutrients, oxygen, wave energy and tidal range) are strongly correlated with bathymetry then latitude [3,30,31] (e.g. Fig. 4). A meso-scale classification of this data leads to more depth and latitude bands than IMCRA-style bioregions spaced along the coastline (O’Hara unpublished data). Moreover, species range limits tend to be clustered around environmental thresholds (e.g. the tropical-temperate transition or other biogeographical boundaries) rather than being spaced evenly along an environmental gradient [29].

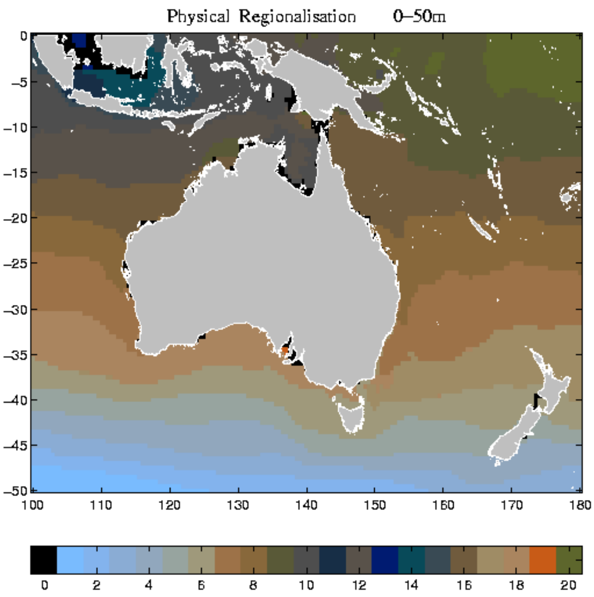


Figure 4. Multivariate analysis of oceanographic data for surface waters (0-50 m deep) by L. Belbin, CSIRO [3]

Finally, few of the IMCRA meso-regions represent unique assemblages of species or habitats, i.e. regions characterised by variation in species abundance rather than turnover of species themselves.

This could be useful from a conservation perspective if the core populations of different species were in different regions. However, it appears that only the State of Tasmania collected a suitable biological dataset (visual transects on rocky reefs) that could be used to delineate such assemblages[5]; all other states used expert opinion informed by qualitative/quantitative biological/physical datasets [24]. However, the analysis was restricted to data from one habitat (shallow rocky reefs) that maximises spatial rather than bathymetric differentiation.

Similar to the provincial bioregionalisation, there is no justification for hard boundaries around the meso-scale regions. The composition of biological samples on either side of most boundaries would likely be very similar. Few boundaries have biological reality, particularly away from the coast. Instead many are artefacts of the classification process imposed on continuous environmental gradients.

So in summary, the meso-scale IMCRA regions do not represent centres of endemicity, large habitat patches (e.g. geomorphic features), enviro-regional classifications (based on oceanographic data) or (in most cases) community ecology classifications. Instead they were a useful geographical proxy for the design of the National Representative System of Marine Protected Areas, based loosely on biophysical patterns, from an era when there were few national biological datasets. A standard statistical analysis of biological data from a randomised sampling design across the Australian marine domain would be unlikely to generate a meso-scale bioregionalisation similar to IMCRA. Most actual biological differentiation is at the scale of habitat (including bathomes) and biogeographic province and is relatively minor at scales of 100-1000 km. The regional boundaries are artefacts of the bioregionalisation methodology and are biased by a focus on coastal morphological features.

Requirements of spatial management of biodiversity

The IMCRA bioregionalisation was a tool that assisted in the design of the NRSMPA. Provincial bioregional boundaries supported the initial division of the Australian marine environment into management bioregions. The following four goals provided guidance for features to be included in each marine bioregion of the National Representative System of Marine Protected Areas in Commonwealth Waters [32]:

1. The different large-scale ecological systems, i.e. provincial bioregions.
2. All depth ranges, because different biological communities live at different depths.
3. All large-scale biological and ecological features.
4. All types of sea-floor features, for example seamounts, canyons and reefs, because different ecological communities are associated with these features.

Meso-scale IMCRA regions were also considered but not as an essential goal in the design process.

IMCRA is still being used to assist NRSMPA design in State waters. For example, New South Wales has begun assessing spatial management of its marine biodiversity on a bioregion by bioregion basis [33]. Although the NRSMPA has known gaps (for example in the EEZ around Cocos Keeling and Christmas Island Territories [34]), the initial design is largely complete, and other spatial management priorities need to be considered.

An update of the IMCRA bioregionalisations would benefit from all the new data and methodological development that has occurred over the past 20 years [35], particularly for the provincial bioregionalisation (see above). However, it is important to note that the same biological and physical data that can be used to inform an updated bioregionalisation or marine park design can (and should) also be used to inform other management decisions. Examples include the proposed expansion of oil and gas production into new areas and the anticipated development of offshore aquaculture and renewable energy industries.

These additional management priorities could include:

1. Updates to marine park management plans, including the identification and mapping of biological or ecosystem values within parks to inform zoning of permitted uses.
2. Identification of sites with special biological values outside parks that can be used to inform impact assessments.
3. Identification and mapping of Key Ecological Features.
4. Strategic/industry-wide environmental assessments
5. Distinguishing and responding to climate change impacts.

The key to these priorities, as well as bioregionalisation and MPA design, is knowing where species live and how they respond to changes in human use and climate. In other words we need to understand their niche (the parameters that determine where species live). This captures both small scale (habitat) and large scale (biogeographic) patterns. Species range limits (biogeography) are also set by niche requirements, where the dispersal capacity of a species is insufficient to expand its range across zones of unsuitable habitat [36], for example a long stretch of sandy beaches can limit the distribution of rocky shore animals [37] or a large body of warm water (e.g. the tropics) can limit the distribution of temperate species [9,14].

Except for a few high profile species, our knowledge of species' niches is derived from records of where they have been found. Since we will never have the resources to sample all locations, we need to model (interpolate) their distribution from known distribution records and a set of environmental parameters. These models can then be used to create maps of potential species distributions. The resolution of the maps will be determined by the resolution of the environmental layers.

In a few high-profile species, a species distribution map may be upgraded to reflect actual, rather than potential distributions (i.e. if not all suitable habitat is occupied), and the importance of some sites to the ongoing conservation needs of the species (e.g. breeding sites), along the lines proposed for threatened and migratory marine species [38]. However, this information will be lacking for most marine species.

Species niche models or maps, in combination with maps of human use, can be used in a variety of decision support tools. They can be stacked or analysed to produce a quantitative bioregionalisation. They can identify priority areas that lie outside an MPA system designed from CAR (comprehensive, adequate and representative) guidelines. They can be used to identify sites of biological significance both within and between existing MPAs. They can be used to assess the scale of existing or proposed human impact. For example, the scale of a new dredging program could be quantified as a percentage of the known range of impacted species. Cumulative impacts can be assessed. Future development could occur with the minimum biological impact by looking for areas with the fewest biological values (reverse prioritisation). Zonation is one software tool that can be used for these assessments (Box 2). Future biological distribution patterns can be modelled from predicted climate change scenarios.

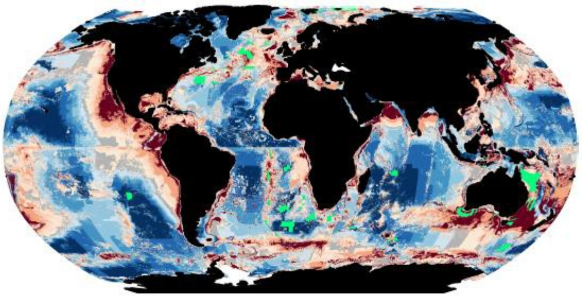
Box 2: Zonation

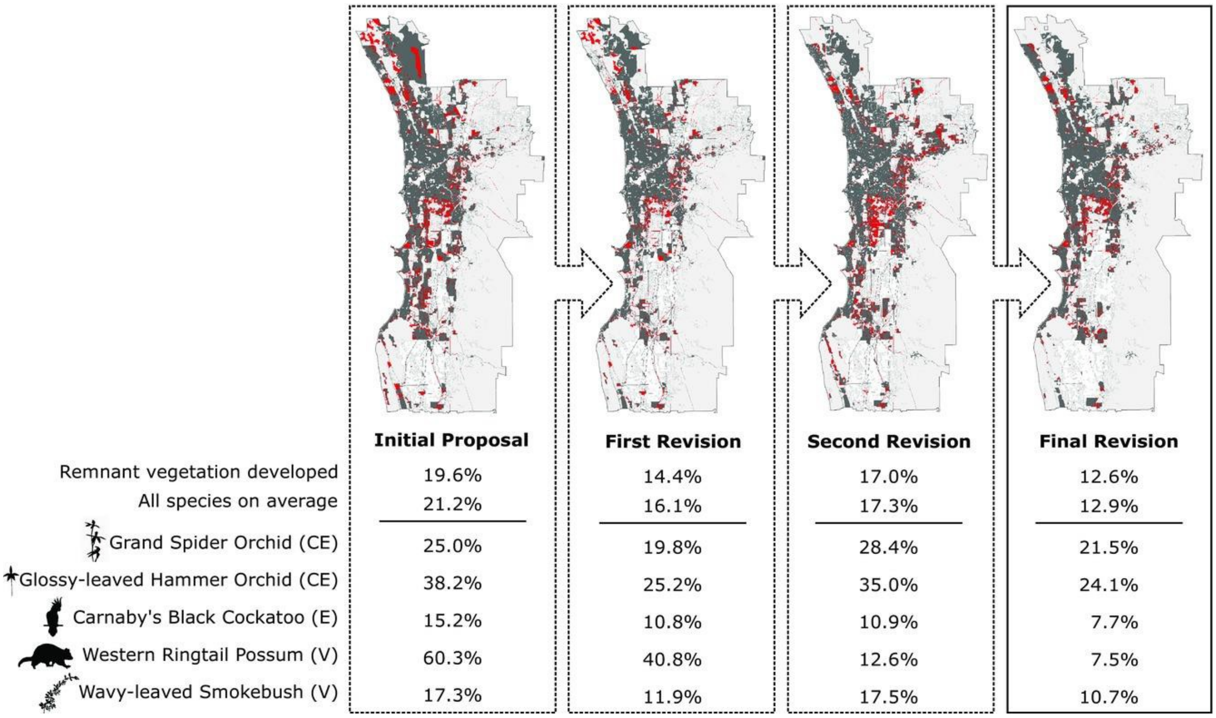
Zonation [39] is one of a number of software tools that can be used for spatial conservation planning. It is used here to show examples of what can be achieved with a combination of species distribution and human usage maps.

Zonation has a number of features that make it suitable for spatial management analyses [39].

- The import of either individual species distribution maps or other biological features, e.g. species archetypes (faunas), habitats or communities.
- Species trait weights, e.g. evolutionary distinctness, IUCN categories, uncertainties.
- Sites trait weights across a landscape, e.g. breeding colonies, dispersal source/sinks.
- Ecological interactions
- Regional administrative units that allow the prioritisation to be run separately in different regions. This can be useful to allow for regional specific variations in biological features. For example, without this feature, the shallow water tropical sites would be ranked higher than temperate or abyssal sites as species richness is higher.
- Threat layers, either as a persistent condition layer or negative feature, or as a manageable condition via a marginal cost. These enable reverse prioritisation analyses (see below).
- Various reserve network aggregation algorithms.

Figure 5. Global prioritisation model for protection of deep sea diversity, expanding existing protected areas based to the Aichi reserve target of 10% of marine habitats 37. This prioritisation is based on the distribution of 870 brittle star and squat lobster species modelled from global oceanographic parameters. (Woolley et al., in prep)





	Initial Proposal	First Revision	Second Revision	Final Revision
Remnant vegetation developed	19.6%	14.4%	17.0%	12.6%
All species on average	21.2%	16.1%	17.3%	12.9%
Grand Spider Orchid (CE)	25.0%	19.8%	28.4%	21.5%
Glossy-leaved Hammer Orchid (CE)	38.2%	25.2%	35.0%	24.1%
Carnaby's Black Cockatoo (E)	15.2%	10.8%	10.9%	7.7%
Western Ringtail Possum (V)	60.3%	40.8%	12.6%	7.5%
Wavy-leaved Smokebush (V)	17.3%	11.9%	17.5%	10.7%

Figure 6. Identification of priority conservation areas. There is a reduction in predicted biodiversity loss (red areas) with iterative development plans. Values describe the proportion of each biological feature's distribution within the region that will be lost to development. Reproduced from Whitehead et al. (2017) Conserv. Letters [40]

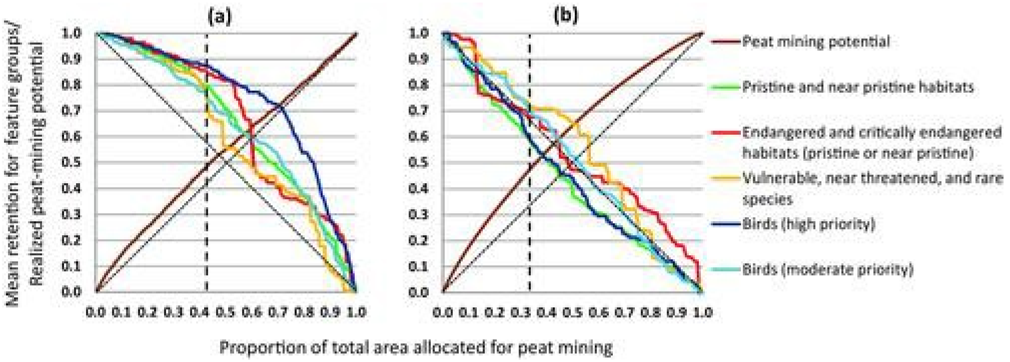


Figure 7. Performance curves for inverse prioritizations of peatlands, identifying 7,000 ha of peatlands (dashed vertical line) with the lowest biological value, (a) is a baseline scenario and (b) allocates areas to mining. Inverse spatial conservation prioritization can be used to identify areas suitable for economic development while simultaneously limiting total ecological effects. Reproduced from Kareksela et al. (2013) Conserv. Biology [41].

The proposal

This proposal is to create a marine biodiversity data flow that can be used to inform spatial management decisions at scales of 1.0 km, including new bioregional maps, data gap analyses, site conservation values (within and outside of parks), environmental pre-impact assessment, environmental post-impact response, and environmental offsets. Essentially all these decisions are underpinned by similar biodiversity data requirements: the ability to map biodiversity data from local (km) to biogeographic (continental) scales.

Australia's marine domain is the third largest in the world (after USA and France) and a comprehensive biodiversity survey of the entire domain is not practical, achievable or even necessary. Instead, if we understand the niche of each species, we can interpolate (or predict) the distribution of biodiversity across the seascape from survey and environmental data.

Thus conceptually, a biodiversity spatial management tool has three elements.

1. A species distribution database that contains raw collection data as taxonomic identification, geolocation, depth, collection date, collection gear, sample size, abundance/ biomass. Essentially, this is similar to that currently held by the Atlas of Living Australia (ALA) with a few modifications. One important modification is the need to add a table of survey/sample metadata, so that collection effort can be estimated and absence of species can be inferred. Biodiversity data gaps can be identified by mapping collection effort over the marine domain. Secondly, large databases such as ALA that aggregate data from many sources are known to be degraded by inaccurate data. It is important that taxonomic experts and survey leaders validate the datasets to flag inaccurate, uncertain or erroneous data.
2. A system that interpolates the distribution of species or other biodiversity units across a seascape from the biodiversity data in (1) and environmental data layers. In the marine environmental this would include oceanographic data (e.g. temperature, salinity, nutrients, oxygen, and wave energy) and geomorphological data (e.g. fine scale bathymetry, topology and substratum from AusSeabed or SeaMap Australia). Many systems (including ALA, Aquamaps) use species distribution models to interpolate from 'presence-only' biodiversity data (where species have been found) as this is the most common data available from museum collections, or they create ranges from expert opinion (e.g. fishmap in ALA). However, predictions are greatly improved if collection effort, abundance/biomass and absence data are included in the models. A second issue is that of rare species. Species models frequently require numerous sample points to train the model. This is a problem for species known from only a few samples, but which may be valuable from a conservation perspective. Thus alternative systems (e.g. using expert opinion, or modelling aggregated biodiversity units [42]) will be required for rare species. However, these approaches can be conducted in a statistical framework that enables estimates of precision, subsequent verification and updating as new data become available. Outputs of this process can include new bioregional maps, created by clustering species ranges into separate bioregions, or climate change predictions, created using predicted rather than actual oceanographic data.

3. Decision support system(s) that analyse the biodiversity maps produced in (2) to assist with spatial management decisions. A software tool such as Zonation (see Box 1.2) can identify sites of high or low conservation value and quantify how much of each species range is protected in parks or will be impacted by new developments. Additional data requirements for these systems are maps of impact or human use, site weights (e.g., important breeding sites, connectivity sink/source sites, or survey effort) and species weights (e.g. IUCN classification, evolutionary distinctness, or ecosystem function).

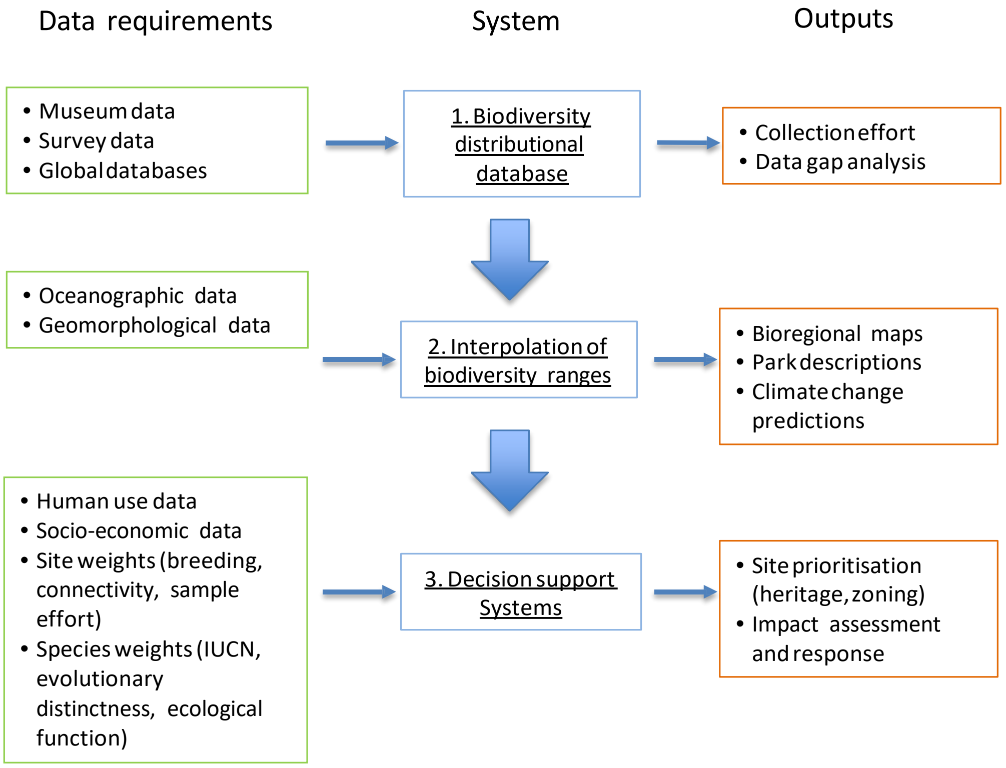


Figure 8. Schema of the proposed marine spatial management system.

Data considerations

Biological datasets

Taxonomic groups should be added to the database on the basis of their diversity (lots of species), abundance (found frequently in surveys), distribution (across habitats), extent that distributional data has been collected and digitised, taxonomic certainty (tools or literature to identify species or OTUs), availability of taxonomic expertise (to verify unusual records) and conservation value. Seafloor biota should be given priority as benthic habitats exhibit more fine-scale environmental variability (see below), and existing biological datasets have more depth resolution and extent (most planktonic studies are in shallow water and deeper pelagic samples generally have poor depth precision). A qualitative assessment (Table 1) indicates that macro-algae, hard corals, gastropods, ophiuroids, barnacles, decapods and fish would make good candidates. Within each taxonomic group, priority could be given to families that have been reported as having relatively small distributional ranges, e.g. the Volutidae within the gastropods [20].

Datasets include museum collections and taxonomic literature, commercial catches, surveys and citizen science (e.g. Reef Life Survey) initiatives. Some of these projects are going beyond presence-absence data to provide trend data for use in environmental management. Increasingly meta-genomic data is also becoming available, particularly for unicellular organisms. Eventually, genetic data will great improve our ability to identify species units, as cryptic species complexes are very common in marine systems [43]. Moreover, metagenomics projects offer great potential to build up temporal datasets. However, to date, most meta-genomic surveys have utilised conserved DNA sequences (e.g. 18S, 16S) that cannot provide species-level resolution. Moreover, reference libraries of DNA sequences (linking sequences to species) are very limited for most taxonomic groups, so many recorded sequences remain unidentified.

A necessary step in the creation of accurate maps is to have an expert verify species distributions, preferably by re-examining museum/herbarium specimens, or by flagging records as dubious or uncertain. A concentrated effort can validate voucher specimens and examine outlier specimens in a cost effective and timely manner, as already been done for ophiuroids [14], squat lobsters [44], corals [21] and fish [6] (Table 1 below).

Table 1. Qualitative assessment of the usefulness of various taxonomic groups to a spatial system. In the totals column, red cells indicate taxa or primary priority, blue cells taxa of secondary priority.

Taxonomic group	S^b	N^b	B^b	C^b	T^b	E^b	V^b	Total	Notes
Macro algae (brown, green and red seaweeds)	3	3	2	2	3	3	2	18	Shallow water only. Mostly southern.
Sponges	3	3	3	1	1	2	2	15	Many undescribed species, many gaps, VMEs
Scleractinians (stony corals)	2	2	2	3	3	3	3	18	Mostly tropical coral reefs. VMEs.
Octocorals/antipatharians (soft corals, sea fans, black corals)	2	2	2	2	2	2	2	14	Many undescribed OTUs. VMEs.
Hydroids	1	3	3	1	2	1	1	12	
Anemones/zooanthids	1	2	3	1	2	2	1	12	
Platyhelminthes (flat worms)	2	1	3	1	1	1	1	10	
Bryozoans	3	3	3	1	2	1	1	14	
Brachiopods	1	1	2	1	3	2	1	11	
Annelids (marine worms)	3	3	3	1	2	3	1	16	
Nemerteans	1	1	2	1	1	1	1	8	
Bivalves (scallops, pipis)	2	3	2	2	3	3	1	16	Mostly infaunal
Gastropods (snails and nudibranchs)	3	3	3	2	2	3	2	18	
Cephalopods (octopus, cuttlefish and squid)	1	1	3	3	3	3	3	17	
Pycnogonids (sea spiders)	1	1	3	2	2	2	1	12	
Barnacles	1	2	3	2	3	3	3	17	
Decapods (crabs, lobsters and prawns)	3	3	2	3	3	3	2	19	Mostly shallow water
Smaller crustaceans (e.g. amphipods, isopods, tanaids)	3	3	3	1	2	2	1	15	
Crinoids (feather stars)	1	2	2	2	3	1	1	12	Mostly tropical, hard substrata
Asteroids (seastars)	2	2	3	2	3	1	1	14	
Ophiuroids (brittle stars)	2	3	3	3	3	3	1	18	
Echinoids (sea urchins)	1	2	3	2	3	2	1	14	

Holothurians (sea cucumbers)	2	2	3	2	3	2	2	16	
Tunicates (sea squirts)	2	1	2	1	2	2	1	11	
Fish	3	3	3	3	3	3	3	21	
Mammals, birds and turtles	1	1	2	3	3	3	3	16	Restricted to shallow waters, mostly pelagic, well curated databases exist

[a] 1=low, 2=medium, 3=high value for biogeographical analysis

[b] S=Species diversity, N= Abundance and frequency of collection, B=Biogeographic extent across the Australian domain (latitude/depth), C=Extent of collection and digitisation, T=Taxonomic tractability, E=Expertise available in Australia, V=Conservation value.

Environmental datasets

Environmental factors that are known to most affect marine species distributions include temperature, oxygen, carbon flux (food), water movement and substrata (e.g. rock/sand/mud). Surface waters are also affected by salinity (e.g. fresh water outflows), wave energy, storms and tides. Plants (including phytoplankton) are also affected by light and nutrient availability (e.g. phosphate, nitrate, iron). Specialised faunal/microbial communities have evolved to exploit chemical discharges from cold seeps and hydrothermal vents.

The usefulness of these variables depends on the resolution of the data. The scale of the predictor should match the scale of the effect. Many existing oceanographic datasets are at a coarse resolution but that may not matter, as variables such as temperature, salinity and nitrate change relatively slowly across space. For example, the CARS oceanographic models (no longer actively supported but used to create the 2005 biogeography) of water temperature, salinity, oxygen, phosphate, nitrate, and silicate are at 0.5 degree resolution for 80 depth layers, i.e. all areas across a 0.5 x 0.5 degree cell (55km x 28-55 km, depending on latitude) are assumed to have the same temperature within each depth layer. This assumption is more dubious with variables that interact with topology, such as wave energy, water movement, carbon availability, and substrata. Seafloor photos indicate that these can vary at metre scales. Such variables need to have an effect at the scale of measurement to be useful as species predictors. Carbon flux [45] and wave energy [5] have been found to be useful predictors at coarse scales in some environments.

The key to fine-scale species distribution maps for benthic animals is 1) fine-scale bathymetry [46] and 2) satellite estimates of net primary productivity (NPP) for deeper habitats. The depth of the seafloor can be used to 3D interpolate oceanographic data to fine scales [14] (as such variables vary far more by depth than geography, especially in shallow water) and topology can be used to model water flow, wave energy and substratum composition. NPP is currently available at a scales of 1.0 km from the MODIS satellites (at least in areas without heavy cloud) and can be useful for modelling species distributions in the deep-sea, as oceanographic variables do not vary much by latitude or bathymetry at great depths [45].

There is a lack of direct data about what determines marine species geographic range limits. In shallow water, it is presumed to be primarily water temperature (although this has rarely been shown experimentally). However, as stated above, water temperature and other oceanographic variables do not vary as much at bathyal or abyssal depths and it is unclear what factors limit species ranges [14]. Consequently, it is often necessary to include latitude, longitude and depth into species distribution models as a surrogate for unknown limiting factors[14]. This may be a problem for climate change predictions for deep-sea animals as the unknown factors may in future vary independently from geographic coordinates.

Connectivity

The limits to species ranges are frequently determined by their inability to disperse across a patch of unfavourable habitat (in the broad sense, including environmental and biotic factors such as competition, predation and disease) [36]. This is difficult to capture in a species distribution model as distributional ranges (and barriers) are the result of long-term multi-generational processes. A species range may have been formed from past environmental and water flow regimes that no longer exist today. Populations within the range may have been connected by larval dispersal in the past but not so today. Connectivity at a pelagic larval stage may depend on the oceanography of a different depth zone than that in which the adults are sampled. Consequently, “connectivity” maps that have been created from modern water flow models are not necessarily an accurate predictor of species ranges. Nonetheless, connectivity data is useful from the point of view of site restoration. An area that receives high levels of larvae from similar habitats elsewhere is likely to recover more quickly. An area that provides larvae to many other areas may have greater importance for long-term population sustainability.

The view taken for this proposal is that modern “connectivity” biophysical dispersal data is of relevance to conservation management, but not necessarily a useful predictor of species distributions. Consequently, it is proposed to include measures of particle inflow, outflow and self-recruitment [47] as site weights in the Decision Support module with the caveat that their effect needs to be monitored and adjusted if necessary.

Socio economic cost/impact datasets

Many impacts (including cumulative impacts), socio-economic values, and human values for the Australian marine domain have been prepared as part of NESP Marine Biodiversity Hub Project C1 [48], and are being extended into shallower (State/NT) waters as part of Projects A12 and SS2. It is important that the resolution of these maps is similar to that of the biological data.

Site weights

In a conservation assessment, sites can be up- or down-weighted by many factors other than the presence of biodiversity. Three types of weights are suggested for benthic habitats.

1. Critical habitat of highly valued species (e.g. a breeding or nursery ground). This data is only available for a few highly-valued vertebrate species, such as marine mammals, birds, turtles or some fish species.
2. The identification of dispersal source/sink sites from biophysical dispersal models [49,50]. Krueck [47] suggested three site-based ‘connectivity’ measures could be input into MPA design software: a measure of inflow, outflow and site retention.
3. Uncertainty or collecting effort. Site prioritisation software can been criticised for not incorporating uncertainty estimates from species distribution models. However, variation in sample effort can be included in these analyses through the down-weighting of sites with low collection effort, i.e. sites with mostly interpolated rather than actual biodiversity data.

A process that balances the importance of these weights needs to be undertaken with conservation managers. It will be important that this system is at least partly interactive, so that alternative options can be identified as management needs or scientific information changes. However, it is also important that a ‘best option’ be identified on a periodic basis so that there is some certainty for regulators and proponents during development of EIAs and management plans.

Species weights

Similarly, species can be weighted in a prioritisation analysis according to their conservation significance. These weights could include:

1. A conservation classification, e.g. the IUCN Red List of Threatened Species or The Environment Protection and Biodiversity Conservation Act 1999 (EPBC Act) listing of rare, endangered or vulnerable species. However, it should be noted that most marine animals and plants are data deficient. Mostly charismatic shallow-water organisms are listed.
2. Evolutionary Distinctiveness [51,52]. This is an index that measures the phylogenetic uniqueness of each species, which is high for species with few known relatives (e.g the Coelacanth) or low for a very diverse lineage. This measure could only be applied quantitatively to a limited subset of taxonomic groups for which there is comprehensive phylogenetic (DNA) data, such as fish and ophiuroids.
3. Functional or conservation importance. A species could be weighted if it is known to have an important or keystone role in the ecosystem (crown-of-thorns seastar) or is held in high public value (e.g. whales). However, no comprehensive quantitative data exists for most species.

Again a process with conservation managers is needed to balance these species-based weights.

Analysis considerations

Modelling of species ranges

Modelling of species distributions, and the ability to monitor any trends over time, is much improved if absence, abundance/biomass and expert opinion data can be jointly modelled alongside museum presence-only data.

A second issue is that a distinct process is required to map rare species with too few distribution records to model successfully. Many marine species are represented by five or fewer records. Instead, ranges can be constructed from expert opinion, by creating a kernel around the few distribution points in environmental space, or not interpolating the range at all (i.e. using site data only). Another alternative is to use joint-prediction or species archetype models, which use common species to assist with the mapping of rare species with similar niches. These issues need to be resolved through collaboration with biostatisticians.

Thirdly it is important that uncertainty is adequately carried through the analyses and represented in outputs. Consolidated maps of model uncertainty also can be input as site-specific weights in the prioritisation module.

The overall aim is to be develop an agreed and robust software pipeline that can 1) periodically extract verified data from the Atlas of Living Australia and 2) output maps of species or biological features across the Australian marine domain at scales of 1.0 km.

Spatial management system

Existing prioritisation software can deliver all of the perceived requirements of a spatial management system. The species maps can be input as biological features, human impact as a persistent condition layer or negative feature, and socio-economic data as a marginal cost (see Box 2). Site weights can include uncertainty, connectivity and critical habitat and species weights can include phylogenetic uniqueness, threatened species classification, ecosystem importance and public value (see section above). Outputs can include site prioritisation inside (for zoning) and outside (for national heritage protection) of parks, assessment of environmental impact from human activities, and reverse prioritisation to design development zones (e.g. for offshore wind farms).

What is required is a set of subprojects that combine the site and species weights into a conservation framework specified by the spatial managers, and the correct incorporation of impact and cost data.

Required subprojects

1. Upgrades to Atlas of Living Australia to include ability to a) screen uncertain or inaccurate records, b) utilise known but undescribed species, c) store sample metadata, and d) download verified datasets for periodic upload into interpolation (species map) pipeline.
2. Validation of ALA outlier records for selected taxonomic groups, addition of new data from museums, literature or surveys (including DNA metagenomic/barcode sources).
3. Downscaling of oceanographic data to a fine-scale resolution (if required).
4. Development of analytical techniques and software pipeline to automatically generate marine species distribution maps from selected environmental datasets, ALA data (presence only, absence, abundance) and expert opinion for both common and rare species.
5. Development of a new provincial bioregionalisation for Australia under current and future climate scenarios.
6. Development of site and species weighting schemes to reflect DAWE management priorities.
7. Mapping priority biodiversity sites for the Australian marine environment, including within the existing marine park system, under existing and climate change scenarios. Mapping of uncertainty and data gaps.
8. Documentation of methodologies to assess the impact of proposed or unanticipated (e.g oil spill) developments on species ranges.

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