National Environmental
Research Program

MARINE BIODIVERSITY hub

# Towards an IMCRA 5

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## Project 3.2 –
## National maps of connectivity and biodiversity - National Ecosystems Knowledge theme

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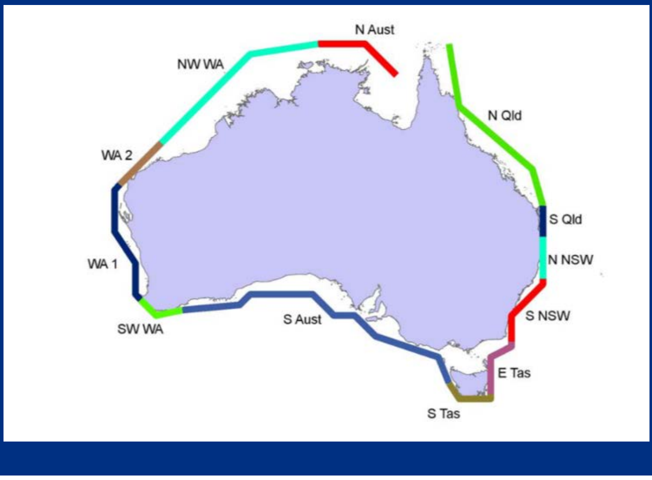

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## Important Disclaimer

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# EXECUTIVE SUMMARY

Australia is a world leader in spatial conservation planning. The IBRA (terrestrial) and IMCRA (marine) bioregionalisation programs were significant conservation management achievements. However, such initiatives require periodic review and updating in order to incorporate new data and tools. While IBRA is in its seventh version, the IMCRA marine bioregionalisation is in its second substantial version. It was last updated in 2006 (IMCRA v4.0) with the recommendation that it not be updated before 2010. Triggers identified for updating IMCRA v4.0 were: 1) substantial new biodiversity or process data; 2) jurisdictional need, and 3) international obligations. Areas that could be addressed to improve the utility of IMCRA were: conceptual classification models; improved data coverage, and improved ecosystem understanding, including the role of surrogates. New biodiversity data collated since 2006 have identified numerous inconsistencies in the formation of existing marine bioregions, particularly for inshore areas and island territories. There has been a considerable accumulation of national biological and environmental datasets and the development of new analytical tools. Our understanding of processes that structure biodiversity at large scales has also changed, with an increased emphasis on the importance of depth, carbon flux and connectivity. Some of this new knowledge, including identification of Key Ecological Features, was used in designing the Commonwealth Marine Reserve (CMR) network, but the data were never added to IMCRA. New observations have refined our understanding of when surrogates are useful. New genetic datasets have provided a novel conceptual model that distinguishes long term evolutionary change and shorter term ecological processes. These scientific advances justify revising IMCRA. It would be useful to have a revised IMCRA available to inform reviews of marine reserves and reserve networks and marine bioregional plans, for example the South-east CMR Network Management Plan is expected to be reviewed in 2023 when it expires. Up to date and improved versions of IMCRA also have the potential to inform ongoing environmental impact assessments of new or planned activities.

In working towards a best-practice bioregionalisation, a number of challenges remain. This includes filling large remaining biological data gaps, finalising national datasets of important environmental variables, and extending analytical techniques so that they can rigorously incorporate biological data from mixed sampling regimes (e.g. most museum data), historical (genetic) information and connectivity (dispersal) data.

# 1. PURPOSE AND USE OF A BIOREGIONALISATION

Natural resource management requires frameworks and products that reduce the complexity of biological ecosystems data to knowledge at a level that can inform planning and decision making processes. 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 [1]. They are also an important tool for scientific investigations and education.

For terrestrial environments, the Interim Biogeographic Regionalisation for Australia (IBRA) is the planning framework for the systematic development of a representative National Reserve System. IBRA is acknowledged by all levels of government as a key tool for identifying conservation areas under Australia's Strategy for the National Reserve System 2009-2030. As such, IBRA is regularly updated to ensure that managers and planners have access to the latest scientific data. The latest updates of IBRA were in 2000 (v5.1), 2004 (v6.1) and 2012 (v7).

For marine environments, 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 [1]. The 1998 ‘interim’ version (v3.3) was replaced by the first ‘integrated’ version (v4.0) in 2006 (see next section). Although, there have been some updates in available data [2], there have been no subsequent updates to IMCRA.

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. There is also potential for future versions IMCRA to meaningfully inform ongoing environmental impact assessments of new or planned activities.

# 2. THE INTERIM/INTEGRATED MARINE AND COASTAL REGIONALISATION FOR AUSTRALIA

## 2.1 IMCRA versions 2.0 and 3.3

The Interim Marine and Coastal Regionalisation for Australia (IMCRA) was developed as a regional framework for planning resource development and biodiversity conservation [3]. The Commonwealth funded a project in March 1995 to produce an integrated Australia-wide marine regionalisation from datasets and spatial analyses previously developed by State, Territory and Commonwealth agencies. IMCRA v2.0 primarily focused on coastal waters [4]. The process was informed by a collection of quantitative and qualitative datasets as well as expert-opinion often focussed on a specific taxonomic group or abiotic dataset. For example, the Victorian coastal bioregionalisation was largely derived from a quantitative analysis of physical (geological and oceanographic) datasets, whereas in New South Wales, it was guided by expert opinion about the coastal distribution of red algae. Finally, workshops synthesised the bioregions across jurisdictions. IMCRA v3.3 also contained bioregionalisation of offshore waters based on demersal and pelagic fish distributions (to 200 m) and an analysis of oceanographic data of the Exclusive Economic Zone [3].

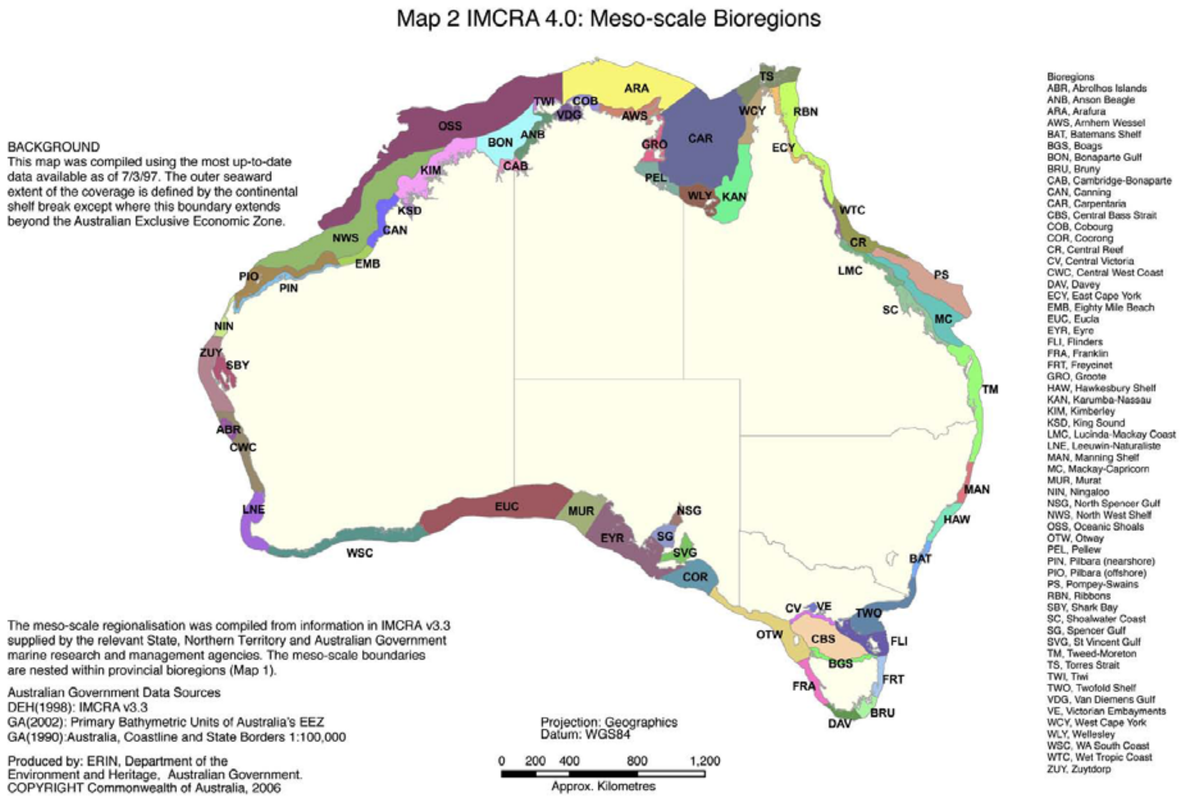


*Figure 1. Australian IMCRA v4.0 meso-scale bioregions based on a qualitative synthesis of various State, Territory and Commonwealth analyses, reprinted from Commonwealth of Australia [1].*

The 2005 National Marine Bioregionalisation project contributed assessed waters beyond the continental shelf within the Australian EEZ to complement IMCRA v3.3. The project undertook a quantitative analysis of national biophysical datasets [5] and a quantitative analysis of demersal and pelagic fish distributions around Australia from the outer continental shelf and upper slope (>40 m) of Australia's Exclusive Economic Zone (EEZ) [6, 7] (Figure 2). At the time of preparation, fishes were the only national-scale biological group that could provide spatial, ecological and evolutionary breadth, combined with required levels of taxonomic understanding to undertake these analyses. However, an additional dataset was compiled for sponges of Australian tropical waters to examine the distribution of endemic species within provincial boundaries.

## 2.2 IMCRA version 4.0

The latest version of IMCRA (v4.0, 2006) incorporated the earlier (IMCRA v2.0) coastal analysis as its meso-scale bioregionalisation (Figure 1), combined the demersal fish analyses from continental shelf (IMCRA v3.3) and slope (National Marine Bioregionalisation) to produce a hierarchical map of provincial bioregions (Figure 3), and included a map of geomorphic units.

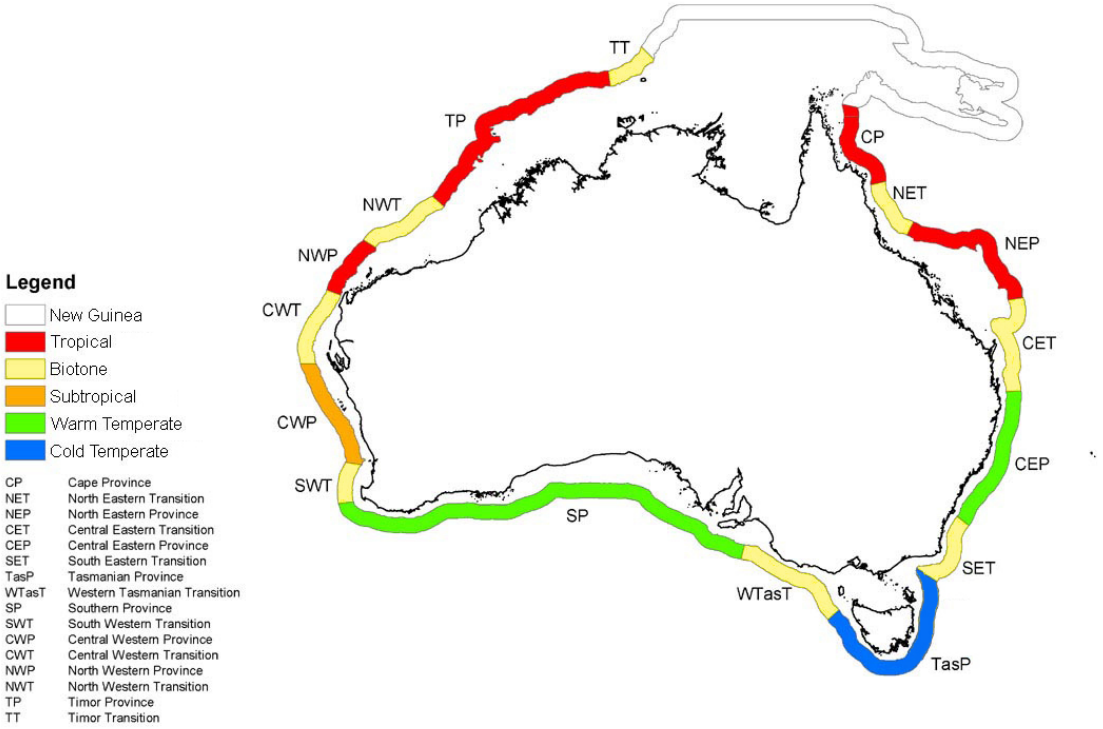
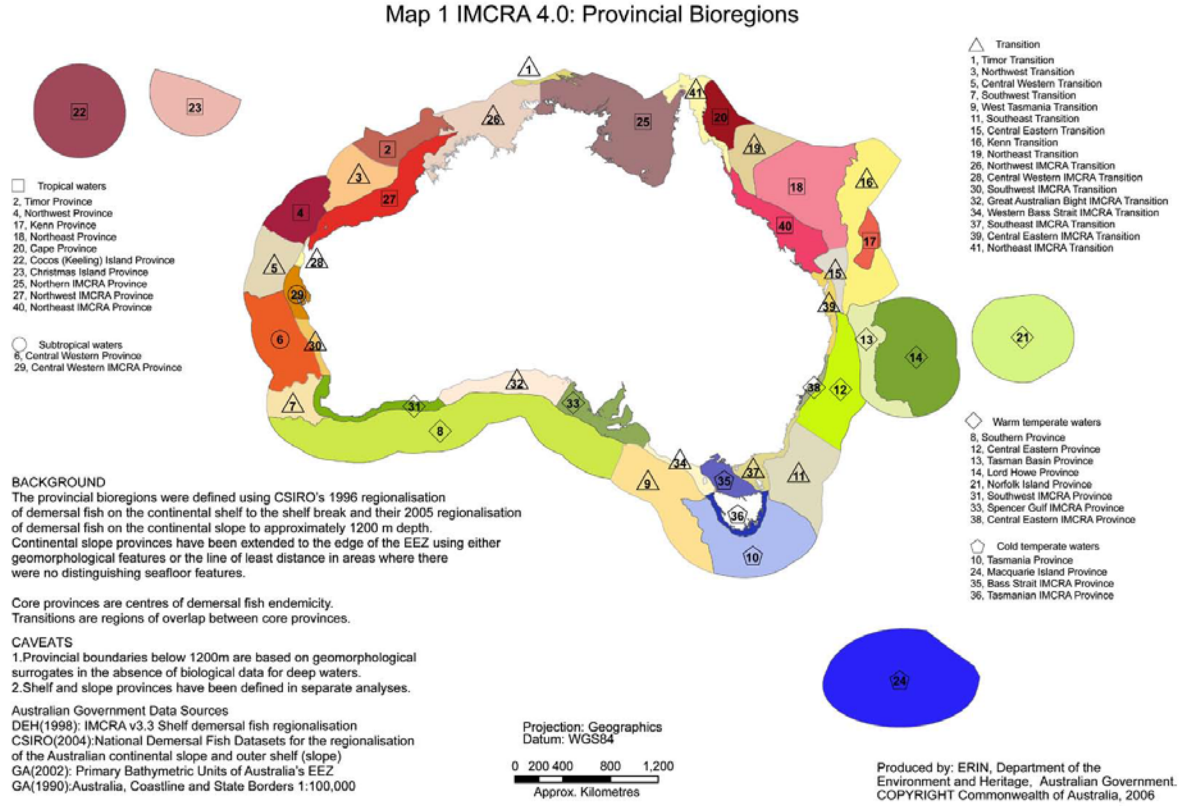


*Figure 2. Australian offshore marine bioregionalisation of demersal slope fishes (>40 m), reprinted from Last et al. [6].*

In developing IMCRA v4.0, the following areas were identified that if addressed could improve the utility of IMCRA:

- Conceptual classification models;
- Data coverage; and
- Ecosystem understanding and ecosystem surrogates.


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

# 3. REASONS FOR UPDATING IMCRA

The current IMCRA 4.0 (2006) bioregionalisation was based on a synthesis of a) divergent state-based analyses of coastal waters, combined with b) an offshore analysis of oceanographic/geomorphological surrogates and a single (but extensive) biological dataset (demersal fishes). While each iteration of IMCRA was compiled from the best-available data at the time, the qualitative and political compilation of the coastal bioregions led to numerous inconsistencies. For example, across Bass Strait, the Otway (OTW) and Twofold (TWO) regions extend from the shore to the continental shelf margin (200 m), whereas the Central Victorian (CV) and Boags (BGS, northern Tasmania) bioregions are restricted to the coastline, being separated by an artificial Central Bass Strait (CBS) bioregion. There is no biological justification for this [6, 8]. The Victorian Embayments (VE) are an anomalous and artificial group of quite divergent ecosystems [9]. It is unclear why the Abrolhos Islands (ABR) of SW Australia are considered a separate bioregion, but the Solitary Islands off New South Wales are not.

While the offshore bioregionalisations were compiled from the best-available data available at the time of development, there were a number of recognised limitations. At the time of preparation, fishes were the only national-scale biological group that could provide spatial, ecological and evolutionary breadth, combined with required levels of taxonomic understanding to undertake these analyses. IMCRA analyses have also suffered from limited computing power and the limited availability of statistical methods to handle large-scale point-based analyses. The museum point data suffered from sampling biases, the impact of differing collection methods, poor sampling coverage, and false absences. Consequently, a novel, three-dimensional 'string' approach was employed to analyse the data. However, this method obscured discontinuities in species distributions and the sampling biases of the underlying data.

National scale biological datasets are now available for other taxonomic groups, notably sponges and ophiuroids, and may provide a different representation of biological transitions due to their dissimilar life histories and dispersal potential compared to fish.

Finally, the environmental surrogates used were those available from satellite, buoy or ship-based mapping instruments, and are not necessarily those that structure biological communities at biogeographic scales (e.g. carbon flux to the seafloor). For example, there is little evidence that the geomorphological structures that underlie the seabed (i.e. those covered by sediment) influence biological composition [10, 11].

## 3.1 A decade of new data

The IMCRA bioregionalisation process identified key data gaps, a number of which have been addressed by subsequent projects funded by the Australian Government, primarily through its CERF and NERP Marine Biodiversity Hubs.

The NORFANZ voyage on RV Tangaroa in 2003 was jointly funded by then National Ocean's Office and the New Zealand Ministry for Fisheries with a specific intention to address knowledge gaps in the deep waters of the Tasman Sea identified by Last et al (2005). There were targeted expeditions to survey the shallow water fishes of south-western Australia [12] and the benthos of the outer shelf and upper slope of south-western (SS07/2005 and SS10/2005) and north-western Australia (SS05/2007) in order to fill major gaps in biological data and inform planning for the south-west and north-west marine bioregions. These surveys resulted in numerous new species descriptions, spatial assessments of biodiversity and new methods for analysing biodiversity patterns [13-18]. In addition, the Commonwealth Environmental Research Facility (CERF) Marine Biodiversity Hub (2007-2010) funded the sorting and identification of quantitative samples of infauna from these expeditions. This resulted in the first large scale spatial or biodiversity analyses of macrofaunal sized animals from deep-water off Australia [19-21].

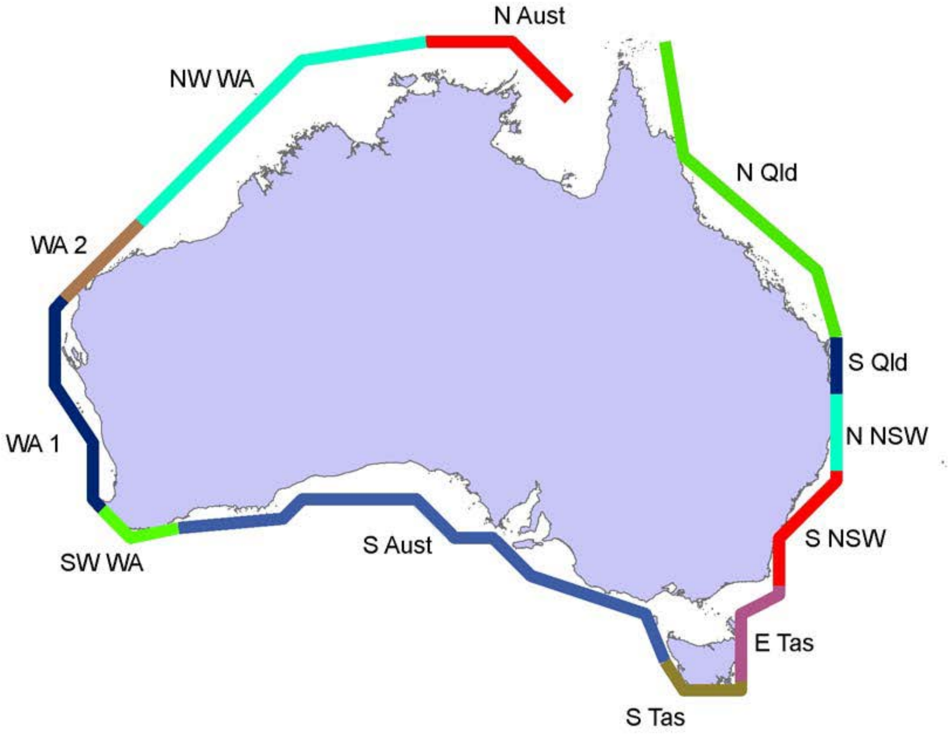

*Figure 4. An example of a regionalisation based on recently compiled data: An offshore bioregionalisation (50-1500 m) derived from modelled distributions of ophiuroids [22]. The province 'N Aust' is restricted to outer shelf habitats only.*

Through the CERF Marine Biodiversity Hub, 1500 fish species distributions were used to improve marine bioregionalisation in Australia, especially through improved characterisation of depth related structure (bathomes) [23], and these results were used in the planning of the Commonwealth Marine Reserve network.

Both the CERF Hub and National Environmental Research Program (NERP) Marine Biodiversity Hub (2010-2014) also funded regionally-focussed surveys to collect biological and physical data within and near various CMRs and KEFs (e.g the Gascoyne CMR, Oceanic Shoals CMR, Flinders CMR). Biological data from these surveys have been analysed in relation to a range of environmental variables [24-27], results of which further contribute to an understanding of national patterns. In 2015 there were two industry-funded programs to investigate biodiversity and ecology of the Great Australian Bight.

The National Maps of Biodiversity and Connectivity project of the NERP Hub funded the collection of all available data for two invertebrate groups, ophiuroids and galatheids (squat lobsters). This new dataset included material from Australian, New Zealand, European, Russian, Japanese and American museums from the coast to abyssal depths. This new dataset facilitated the mapping of biogeographic assemblages [28] (Figure 5 and Figure 6), species richness and beta diversity [29]. In addition, genetic data was sequenced from representatives of both groups in order to map phylogenetic endemism [30].

## 3.2 New bioregionalisation tool box

Methodologies and datasets have improved considerably since IMCRA v4 was published in 2006. We can now compare national patterns of biodiversity between several animal groups. There have been efforts to collect comprehensive phylogenetic data so that we can better understand how history influences current distributions and weigh the conservation value of species by their evolutionary distinctiveness (phylodiversity)[30]. There are also initiatives to standardise operational taxonomic units and unnamed species across taxonomists, and regions (e.g. www.spongemaps.org), thereby allowing direct comparisons among survey collections for national assessments. Global oceanographic models have grown in sophistication and accuracy, for example for Australia we now have the BlueLink forecasting system [31], four-dimensional connectivity models [32], and global biogeochemical models [33]. In the first two years of operation, ARGO robotic floats collected more sub-surface oceanographic data than had been collected since scientific measurements began. Methods of modelling species and assemblage distributions have advanced rapidly [e.g. 11, 17, 34, 35].

## 3.3 Current knowledge for marine planners and managers

Studies produced to date indicate there is a need for refining IMCRA bioregions to reflect the new distributional and environmental data. This is likely to happen in several ways. Firstly, there has been increasing recognition that marine biodiversity is fundamentally structured by depth [28, 36]. There is more biological change in marine systems over 1000m of depth than 1000 km of geographic distance [37]. The continental shelf and slope have a substantially different fauna, characterised by different taxonomic groups that evolved hundreds of millions of years ago [38]. On the other hand, many marine genera are very widespread, and sister species at similar depths can be separated by ocean basins [e.g. 39, 40]. While for some marine groups, the peak of ecological and evolutionary biodiversity occurs in shallow tropical waters (eg coral reefs), for others the peak is on the upper continental slope in tropical regions (O'Hara unpublished), a habitat not usually emphasised in conservation assessments.

An up-to-date bioregionalisation would represent the fundamental part of the evidence base to improve biodiversity conservation responses at national and regional scales using the best available data. This would include ongoing management and future review of reserve networks. The bioregionalisation should also provide consistency in biological patterns across jurisdictions, not a mix of divergent jurisdictional management priorities.

A future best-practice review of Australia's bioregionalisation or reviews of marine spatial planning and management (e.g. decadal reviews of CMR network management plans, starting with the South-East CMR network management plan 2013-2023) will have to incorporate substantial amounts of new biological and environmental data, comprehensive oceanographic models, and newer innovative analyses and conceptual models. While these are scheduled a few years in the future, creating the consistently identified and comprehensive taxonomic datasets that will contribute to these reviews is an ongoing process, currently supported by the NESP Marine Biodiversity Hub and Australian museums.

The National Marine Science Plan [41] calls for further exploration and mapping of the marine estate to fill in knowledge gaps in order to be able to conserve marine biodiversity and keep ecosystems healthy. In particular, the Plan calls for a focus on building the knowledge base to support our new National Marine Reserve System.

A number of challenges remain, such as filling remaining data gaps, obtaining better coverage of important habitat variables (e.g. seafloor hardness), extending some analytical techniques so that they can utilise biological data from biased or mixed sampling or variable detection regimes (e.g. most museum data), and the need to evaluate the biogeographical significance of newly created environmental datasets such as current models.

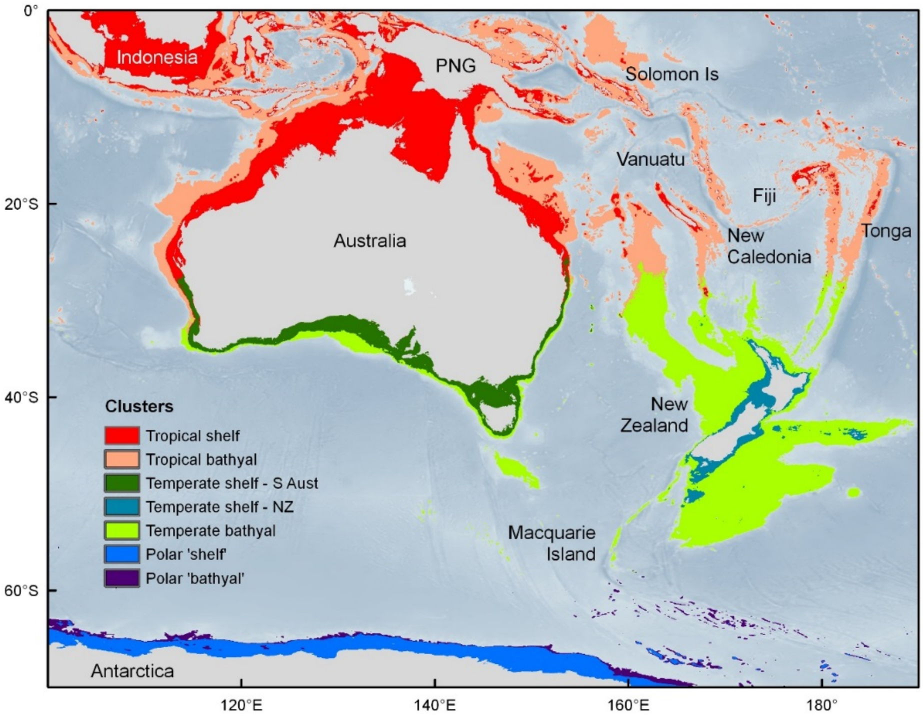

*Figure 5. Mapped 7-cluster classification of seafloor assemblages from multivariate synthesis of predictions from maximum entropy (MaxEnt) modelling of 267 ophiuroid species [28].*

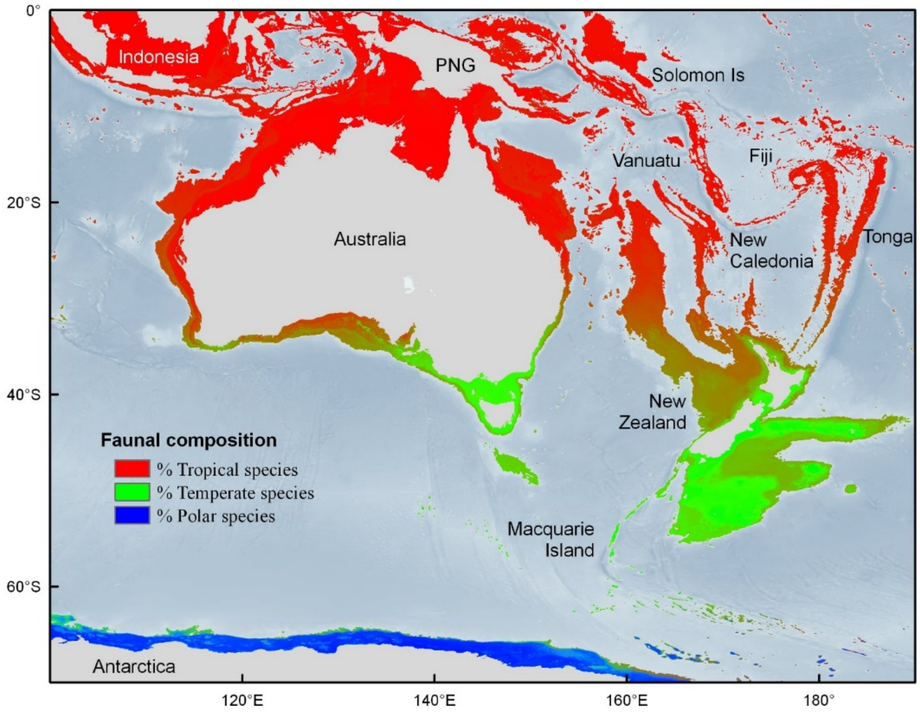

*Figure 6. A visualization of spatial turnover of ophiuroid species, formed by assigning colours to the proportion of tropical (red), temperate (green), and polar (blue) species from Max-Ent modelling at each pixel [28].*

# 4. OPPORTUNITIES TO STEP TOWARD IMCRA 5

We now have new data and bioregional tools to significantly improve the certainty and resolution of Australia's marine bioregionalisation and make it more useful to planners and managers (as outlined below). To progress towards a best practice bioregionalisation, the following are required:

1. Biological datasets of multiple taxonomic groups across the entire marine domain, including vertical distribution (pelagic, demersal, benthic, infaunal), filling in major gaps in knowledge

2. The utilisation of advanced environmental data layers, particularly fine scale bathymetry, oceanographic and modelled connectivity data

3. Phylogenetic data to separate the effects of ecological from historical processes

4. A model-based analytical framework that explicitly acknowledges uncertainty in the data.

The year 2016 represents the tenth year for the current version of IMCRA (v4). An important question for policy makers and scientists is at what point does the current version of IMCRA need to be updated to reflect current understanding. Such an update would be highly desirable to be timed to inform reviews of the Marine Bioregional Plans (MBPs) established under the EBPC Act 1999 or reviews of Commonwealth Marine Reserve Network management plans. The first of the network plans expires in 2023. An opportunity exists to undertake much of the above work in preparation for IMCRA v5.

## 4.1 Biological datasets

While there is already scientific information to justify an update of IMCRA v4.0, important gaps in our knowledge remain. Filling some of these gaps will make the next IMCRA version more robust to additional scientific discovery providing for a greater longevity.

### 4.1.1 Data gaps

From a biogeographic perspective the major gaps in knowledge about seafloor biological communities are: 1) the deep seafloor below 2000 m anywhere across Australia's marine domain, 2) the Indian Ocean Territories around Cocos Keeling and Christmas Island, 3) much of the Coral Sea below diving depths (Figure 7).

#### *4.1.1.1. The lower bathyal and abyss (2500-5500 m)*

The seafloor is at abyssal depths for over 47% of the global oceans and thus this environment plays a critical role in the biodiversity of the planet [42]. However, knowledge of the fauna of Australia's abyssal (deeper than 3500 m) environment is almost non-existent, despite it forming 32% of the EEZ. Only a handful of biological samples have been collected from Australia's abyss. Three by Russian and New Zealand vessels in 1976 and 1982, and several more as part of the Great Australian Bight exploration program in 2015. The number of samples that have been collected on the lower continental slope and rise between 2500-3500 m is also very limited. We have no biological data for the abyssal seafloor of Australia's network of Commonwealth marine reserves and limited samples and imagery [e.g. 43] at continental slope depths.

Far from being a constant environment, research in the North Atlantic indicates that the abyssal seafloor can be subjected to benthic 'storms', pulses of food ('marine snow') arriving from the surface, and large recruitment events [44]. Despite its remoteness, humans are increasingly impacting this environment: mining leases have been allocated in the abyssal Pacific Ocean, discarded waste is commonly present, and pesticide residues detected in the fauna. Life in the abyss is critically dependent on deep-water circulation patterns and export of food from the surface layers, both of which are predicted to change in response to the climate [45]. Australia has little baseline biological data against which changes to the abyssal environment can be detected, including for the CMR network.

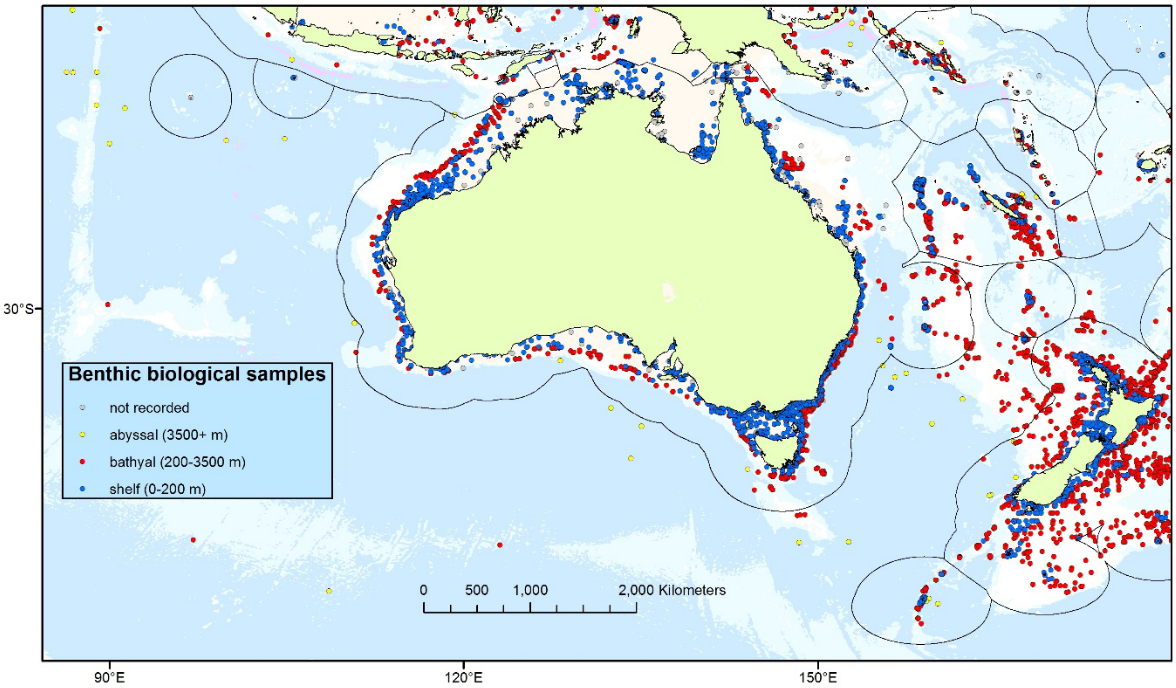

*Figure 7. The location of known benthic biological samples from museum and literature records. From a biogeographical perspective, the major data gaps are (a) the abyssal environment (>3500 m depth) across the Australian EEZ, (b) the Indian Ocean Territories (Cocos Keeling and Christmas Island Territories), and (c) bathyal (200-3500 m) depths in the Coral Sea.*

A first step to understanding this environment is to describe large scale macro-ecological patterns. The most prominent marine biodiversity changes in the shallower water (0-2000 m) are those associated with latitudinal and bathymetric gradients [28]. A sharp tropical-temperate transition occurs between 30-40°S; even at depths of 1200-2000 m only 6% of species of ophiuroids are common to both tropical and temperate latitudinal bands [28]. A similar pattern is observed for fish [36]. Sparse sampling by Russian vessels suggest that a Southern Ocean abyssal fauna may be distinguished from those in the Indian or South-western Pacific Oceans [46], but this has never been adequately examined, particularly in the Australian context. Benthic diversity of some faunal groups peaks at 2000-3000 m in the North Pacific and Atlantic Oceans, thereafter declining into the abyss [47]. Deep-sea ecologists have theorised that the abyss is a diversity-sink and reliant on planktonic dispersal from the populations on the lower continental slope to maintain populations [48], although this hypothesis has rarely been tested. The implications for managing these environments are profound, with the abyssal diversity being potentially dependent on slope populations.

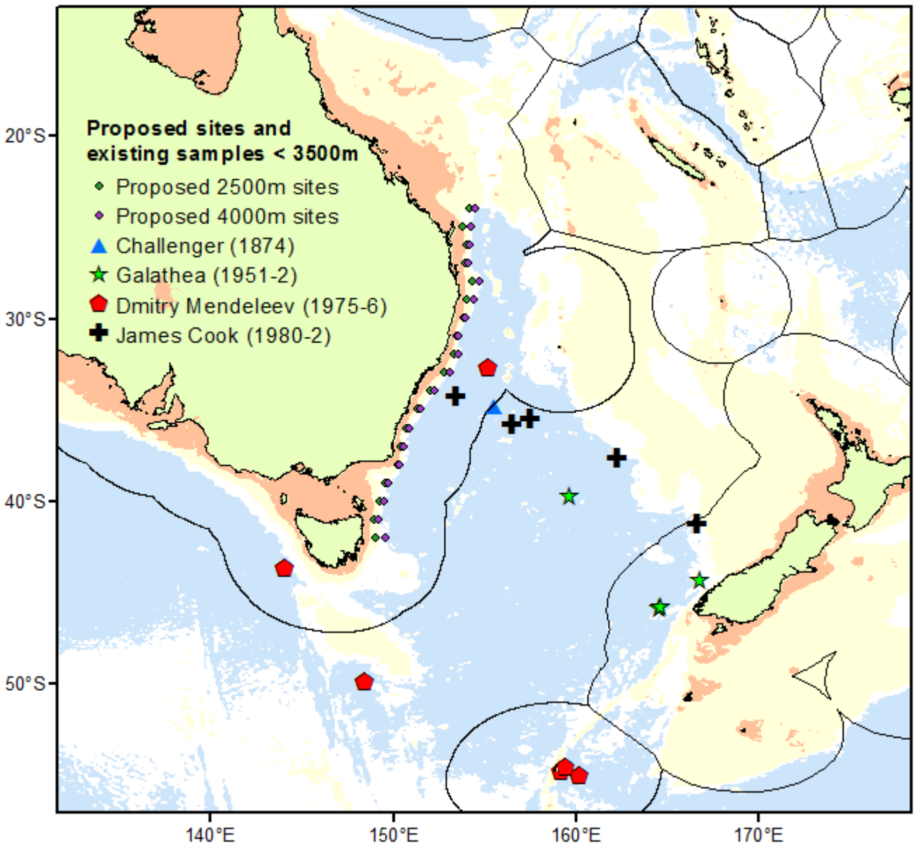

*Figure 8. Scheduled survey (mid 2017) of the deep-seafloor (2500-4000 m) along Australia's eastern coastline. The few existing abyssal samples are also shown.*

An international consortia of Museum and other deep-sea researchers were successful in obtaining 35 days to survey deep (2500 and 4000 m) biological seabed communities on Australia's MNF Investigator in May 2017 (Figure 9). The scientific focus of the survey is to describe latitudinal diversity and connectivity patterns along Australia's east coast at these depths and investigate the source of food for the abyssal communities using isotope analyses. However, the survey also represents a low cost opportunity to discover and highlight the conservation values of abyssal areas of Australia's East CMR network through the use of deep-towed video and sled-mounted cameras, and ship-board aquaria to obtain high definition imagery of selected animals.

#### *4.1.1.2. Cocos Keeling and Christmas Island Territories*

The biological communities of the Cocos-Keeling and Christmas Island Territories are almost completely unknown. Only the shallow water seafloor communities, 0-10 m, directly around the islands have been explored, albeit qualitatively. The territories are the major spatial gap in national marine biodiversity datasets. Australia lags far behind other nations (e.g. France, UK, USA, Japan, Chile and Brazil) in its commitment to understanding the marine environment around claimed offshore/island territories. There has been only one substantive benthic expedition to the area - that of the German ship Sonne in 2009 (SO199 CHRISP). This was principally a geology cruise that sampled mainly at abyssal depths (mean depth of the rock-dredge samples was 3900m) generating few biological specimens [49].

These territories are likely to harbour distinct biological communities within the Australian region because of their location in the eastern Indian Ocean [1]. The lack of benthic sampling is unfortunate as these territories are positioned in a biogeographical transition zone between Australia, SE Asia and the central Indian Ocean. Shallow water examples suggest the biological communities will be composed of a complex mix of endemic, Indonesian, Australian and West-Indian Ocean elements [50, 51]. For example, the Crown-Of-Thorns Sea star (*Acanthaster* 'planci'), a keystone species that preys on coral reefs, is actually composed of four separate species, three of which intersect in the region of Australia's Indian Ocean Territories (Figure 9) [51, 52].

The seamounts in the Territories are mostly of late Cretaceous age (65-80 my) [53] and such ancient seamounts may harbour palaeo-endemic communities [54]. The only bioregionalisation of the Territories to date [53] had to rely exclusively on geological and oceanographic surrogates. Seamount communities worldwide are highly vulnerable to disturbance by fish trawling, longlining or mining for cobalt-rich ferromanganese crusts, particularly if they harbour coral communities [55].

The most cost-effective solution to overcoming this data-gap is to adopt the abyssal survey model and apply for ship-time on the MNF Investigator with an international team of taxonomic and ecological principal investigators. This expedition would investigate benthic and pelagic assemblages, surveying 1) the seafloor of the banks, ridges and seamounts within these areas, and 2) pelagic aggregations of sharks, mammals and predatory fin-fish. A multi-institutional proposal for ship time to survey

12 seamounts in the territories (Figure 10) will be resubmitted for the next round of MNF 'Investigator' expeditions from July 2018 to June 2019.

Figure 9. The distribution of the four species of Crown-of-Thorns Seastars derived from an analysis of mitochondrial DNA [51], three of which have range limits in or near Australia's Indian Ocean Territories.

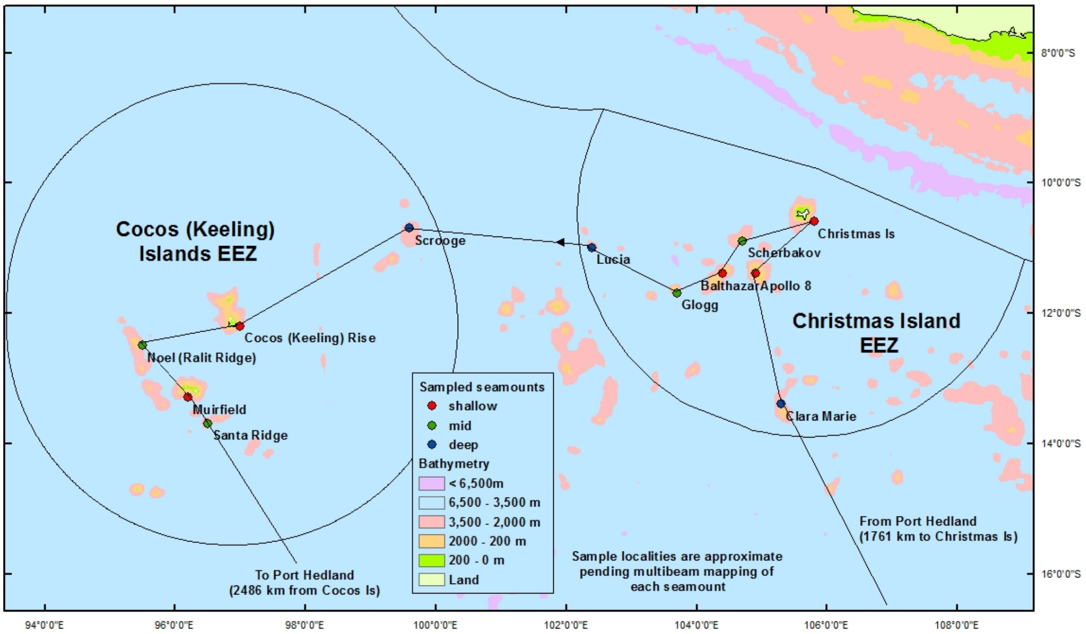

Figure 10. Proposed survey of 12 seamounts in Australia's Indian Ocean Territories around Christmas and Cocos (Keeling) Islands.

#### 4.1.1.3. Coral Sea

The bathyal seafloor communities in the Coral Sea are under-sampled, particularly in the eastern section near the Exclusive Economic Zone of New Caledonia and Papua New Guinea. This is an important zone of transition between the fauna of Australia's continental margin and the south-western Pacific. Coral Sea waters beyond depths reached by divers is also one of the largest and most important data gaps for the demersal fishes [56], as was recognised during preparation of biological dataset that was used to create Australia's 2006 Marine Bioregionalisation [6].

A scheduled survey of some seamounts in the south-west of the Coral Sea as part of a joint Australia/US MNF Investigator Expedition in August 2016, was cancelled due to lack of funds. Another possible way to address the data gap is form a collaboration with French researchers at INFREMER and the Museum National d'Histoire Naturelle in Paris who have extensively surveyed the EEZ of New Caledonia, Vanuatu, Solomon Islands and recently the North of Papua New Guinea (Figure 7). This follows the very successful Australian-New Zealand NORFANZ collaboration in 2003, which surveyed remote sections of the Lord Howe Rise and Norfolk Island Ridge, and the joint Australian-New Zealand MacRidge expedition to the Macquarie Ridge in 2008.

### 4.1.2 Multiple biological datasets

IMCRA v4.0 was developed from patterns of offshore demersal fish and environmental surrogates [1]. The NERP Marine Biodiversity Hub has developed national datasets for three additional groups of seafloor animals that are abundant in offshore environments (brittle-stars, squat lobsters, sponges). However, it is unclear whether other unrelated taxonomic groups will fit these general patterns. Moreover, it is unclear whether other environments such as estuaries or coastal zones have the same biogeographic patterns as the IMCRA 4 offshore fish data. These environments are under pressure from urbanisation, recreation, marine infrastructure development, changes to hydrology and climate change.

The generality of the biogeographic patterns could be tested in the first instance by focusing on a small group of benthic invertebrates that are abundant in bays and estuaries, thus including both an additional group of animals and an additional habitat in the bioregionalisation project. For example, the polychaete (worm) family Nereididae would be particularly suited to this task as there are relatively few species (180 Australian species), they are known to be distributed in bays and estuaries around Australia, and have large existing datasets including distributional and genetic data. Another possibility is a family of molluscs, many of which are more speciose and have more regional to local endemics than most marine taxa. A second test of the generality of the biogeographic patterns could focus on a small group of gastropods (e.g. cone shells) that are relatively well known, have a pattern of local endemism and for which there exists some existing genetic data.

## 4.2 Environmental data

### 4.2.1 Oceanographic and geological drivers of species distributions

The national datasets developed under NERP allows for the prediction of the species pool potentially present at scales of 100s km across the Australian EEZ, a resolution limited by the coarse oceanographic datasets available. However, conservation management often requires an understanding of biodiversity present at smaller spatial scales, e.g. for siting of marine infrastructure, assessment of sites of conservation significance, etc. The development and synthesis of fine scale habitat mapping of the continental shelf across Australia, including bathymetry, geomorphology, bottom hardness, and current flow, will potentially allow for the fine scale prediction of species presence on smaller habitat features of conservation concern.

A project investigating the potential for bioregionalisation maps to be downscaled to under 10 km resolution is possible for sections of the Australian continental shelf that have been mapped extensively. This project could build on NESP-funded projects such as 'Evaluating and monitoring the status of marine biodiversity assets on the continental shelf' which aims to compile continental scale maps of seafloor features for the shelf.

### 4.2.2 Connectivity

Dispersal is a fundamental biogeographical process that structures biological communities over short (ecological) to long (evolutionary) timeframes. For example, dispersal is hypothesised to be important for natural restoration of damaged ecosystems and in facilitating migration due to climate change and in the long term conservation of the biota in a reserve network. A focus during the CERF program was to identify the population structure of 3 invertebrate groups (corals, brittle-stars & squat lobsters) on seamounts south of Tasmania, many of which are now contained in the South-East CMR network, and further afield. Recent years have seen the emergence of sophisticated oceanographic particle models that potentially offer insights into dispersal processes. The NERP program generated large scale predictive maps of connectivity for parts of the Australian EEZ [32]. However, these models have not been tested for their potential to explain the assembly and limits of marine communities.

A pilot project is required to test the importance of connectivity for bioregionalisation, in particular its role in determining species range limits. The focus should be on areas of high biogeographical turnover, particularly at bathyal depths (200-3500 m) where temperature and other water mass characteristics appear unable to explain species distributions. The mid-west and mid-eastern Australian continental margins are the ideal location for such a study which could be generated from previously collected material. High resolution multi-locus genetic data will be required to assess intra-specific population dynamics. To test these would require compilation of trait data (e.g. breeding ecology, larval duration) for species of interest, ideally in combination with development of community-level genetic data to ground truth model predictions.

## 4.3 Phylodiversity

Representing the evolutionary history of organisms in area-based assessments of biodiversity has become a key focus for terrestrial conservation efforts [30]. Phylodiversity approaches attribute additional conservation value to organisms with relatively divergent genetic composition. Global biogeographic maps have had to be altered to reflect phylodiversity [57, 58].

As a result of NERP Marine Biodiversity Hub research, we now have the biogeographical and phylogenetic datasets to test the utility of these approaches for the first time in shallow to bathyal marine environments (0-2000 m) from the equator to Antarctica. This project investigating the importance of phylodiversity to Australia's marine bioregionalisation has been funded in the National Environmental Science Program (NESP). The scope of the analysis will include shallow-water and bathyal marine ecosystems (0-2000 m) from the northern Australia to Antarctica. The methodology will include 1) using a tapestry approach to maximise phylogenetic coverage by combining next-generation sequencing data with legacy single-gene data from public databases [59], 2) filling data gaps by a limited amount of additional sequencing, 3) interpolating marine species ranges using species distribution models [28], and 4) analysing the resulting data using existing methodologies including PD (phylogenetic diversity) and PE (phylogenetic endemism) [30, 60, 61].

## 4.4 Mapping methodologies

Understanding the distribution of Australian biodiversity assets at continental scales is critical to ensuring a coherent national response to detrimental pressures on the natural environment. The biological conservation assets of Australia's massive EEZ have been incrementally explored over 200 years. Information on these assets has been collected using a disparate range of collecting gear and sampling designs often at significant cost. Without systematically sampling all habitats, the most cost effective solution is to extend analytical approaches to utilise these available mixed-resolution data and produce best-evidence bioregional maps.

Most quantitative biogeographical studies to date have relied on dissimilarity coefficients (e.g. Bray-Curtis, Jaccard) as the basis for analysis and visualization of complex species distribution data [28, 62, 63]. However, such approaches cannot indicate how uncertain the results are [64, 65] and rely on a degree of interpretation that is difficult to standardize. Recent statistical advances have resulted in modelling approaches that are appropriate for multivariate ecological datasets and account for collection biases and other problems with the data [65]. Multivariate modelling approaches are now available that facilitate biogeographical mapping and analysis [66-68]. These approaches include two developed under CERF/NERP programs, the species archetype (SAM) and regions of common profile (RCP) models, which can generate bioregional maps from clusters of similar species distributions or sites.

Utilisation of these new methods and data from multiple biological groups can provide a robust and repeatable marine biogeography that can be standardized and updated incrementally as necessary, without requiring the conceptual and process changes required to update IMCRA v4.0. Incremental updates to IMCRA v5 will be able to happen on a timetable to suit marine users rather than as dictated by scientific advances.

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