

Final Report 2007-2010

Marine Biodiversity Hub – Commonwealth Environment Research Facilities



March 2011



MARINE BIODIVERSITY RESEARCH

Prediction and Management of Australia's Marine Biodiversity



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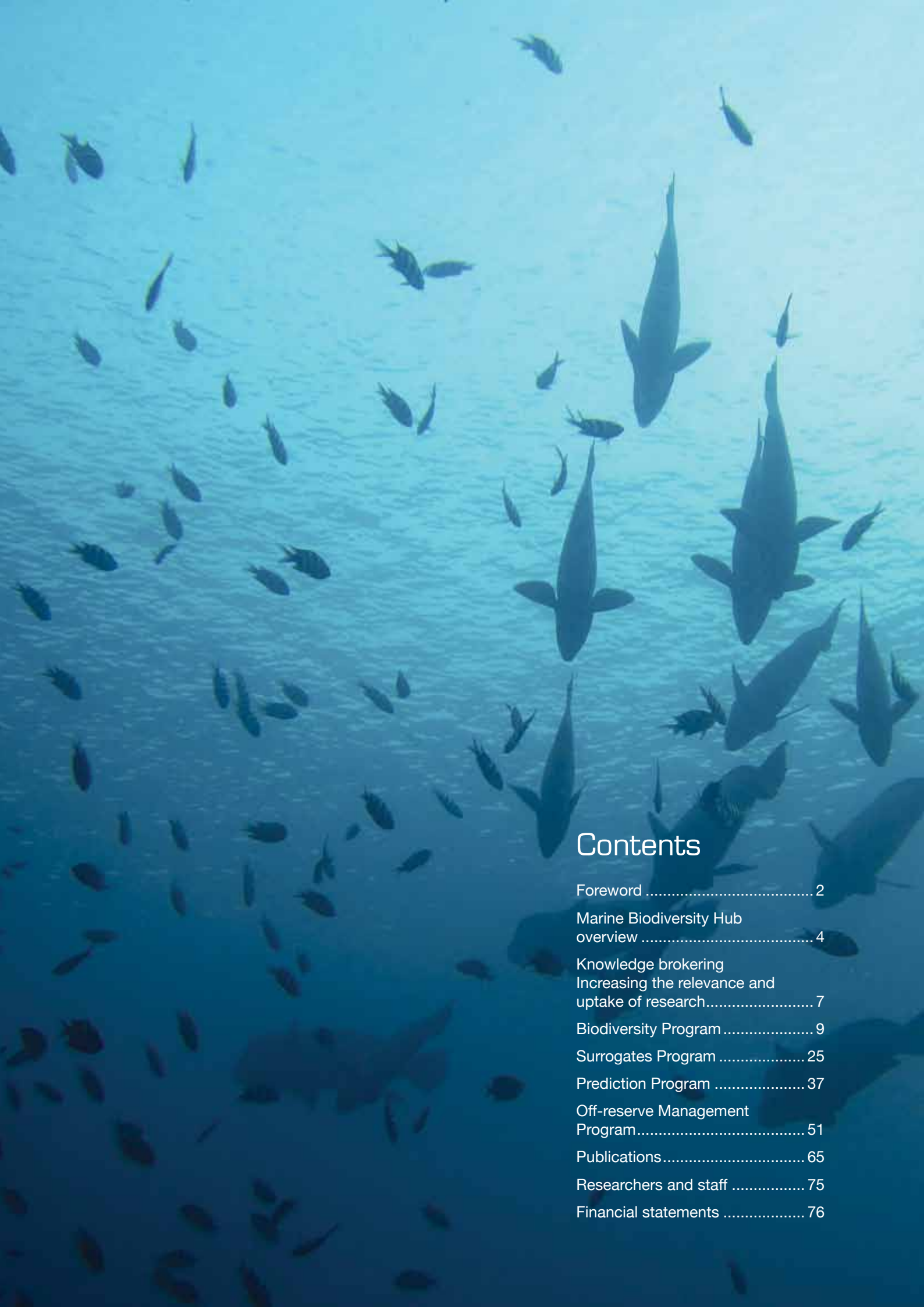
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The ocean hosts the greatest diversity of genes, species and ecosystems on the planet, from deep-sea vents and coral reefs to seagrass beds by the shore. The CERF Marine Biodiversity Hub has contributed a deeper knowledge of Australia's marine biodiversity, as well as tools for its effective management. This report on the achievements of the Hub ends a three-year collaboration between the University of Tasmania, CSIRO, Geoscience Australia, the Australian Institute of Marine Science and Museum Victoria. It summarises extensive research on physical and biological aspects of Australia's marine environment, as well as the functioning of marine systems. Studies of the interactions between biodiversity and marine activities have identified opportunities for improvements in management.

Steering Committee

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Ian Cresswell (CSIRO)

Partners

- Australian Institute of Marine Science
- CSIRO
- Geoscience Australia
- Museum Victoria
- University of Tasmania

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David Johnson, Michael Tudman,
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 (AFMA); John Gunn (CSIRO)

For more than 20 years, significant concerns have surrounded the sustainable use of the world's oceans. The 1992 World Commission on Environment and Development developed a strategy for sustainable development and conservation and established the Convention on Biological Diversity (CBD). Marine and coastal biodiversity have been on the agenda of the CBD since 1994. In that year, Australia ratified the 1982 United Nations Convention on the Law of the Sea, a universal legal framework for the rational management and conservation of marine resources. When the treaty came into force later in 1994, Australia became obligated to protect and preserve its Exclusive Economic Zone, which extends up to 200 nautical miles offshore.

In the past 16 years, numerous UN decisions through CBD and the United Nations General Assembly have encouraged governments to ensure the conservation of biological diversity and the sustainable management and use of oceans. This has included the implementation of ecosystem approaches to management and the establishment and management of marine protected areas. In noting the importance of protecting ecosystems, the need for further study has also been recognised. Australia's Biodiversity Conservation Strategy 2010–2030 identifies the need for new approaches to maintaining and restoring the resilience of terrestrial, aquatic and marine ecosystems.

In establishing the Commonwealth Environment Research Facilities (CERF) program, the Australian Government has shown national leadership in public-good environmental research. The Marine Biodiversity Hub team is to be congratulated for undertaking this research, and for providing new insights into Australia's marine biodiversity. Their work has provided a strong foundation on which to build adaptive management practices for the future, and should serve as model for marine environmental science globally.

While the Marine Biodiversity Hub has delivered new knowledge and understanding, it has also confirmed that Australia's marine biodiversity needs to be better understood. New ways and means must be developed to manage, use and share this diversity in ways that benefit people and maintain the ecosystems on which they rely.



Ian Cresswell
 Chair, Marine Biodiversity Hub
 Steering Committee



Marine Biodiversity Hub Overview

Supporting the management of Australia's marine biodiversity

Origins of the Marine Biodiversity Hub

All governments with responsibilities for Australia's marine jurisdiction have been working to limit the loss of marine biodiversity. Despite extensive efforts aimed at conservation and the ecological sustainability of marine industry sectors, some marine species are experiencing significant declines, raising concerns about the status of Australia's marine biodiversity and ecosystems^{A1}. The effects of several threatening processes are leading to declines in habitats, changes in ecosystems, and threatened and endangered species.

Management Team

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The Australian Government is implementing marine bioregional planning (MBP), including the identification of a network of marine reserves, under the *Environment Protection and Biodiversity Conservation Act 1999* (EPBC Act) to address this continuing decline in biodiversity. Focusing on Commonwealth waters, MBP is an ecosystem based management (EBM) approach designed to improve the way decisions are made under the EPBC Act, particularly as they relate to marine biodiversity protection and sustainable resource use. EBM is evidence-based, supported by monitoring and adaptive management. Scientific research has a key role in supporting evidence-based decision making and EBM, which is a formidable challenge in our oceans.

The majority of Australia's territory is marine (60% excluding Antarctica) – it spans the tropics to temperate latitudes, from shallow waters to the abyss – and we know little about it. Starting with James Cook in 1770, we have still mapped only 12.5% of our ocean territory with biological samples from a far smaller area. Half the species collected in deeper waters typically are new to science^{A2}. We estimate that Australian taxonomists have identified and recorded 33 000 marine species, another 17 000 are known to occur in the Australian EEZ, and there may be as many as 250 000 (excluding microbes)^{B9}.

While much remains to be discovered in Australia's marine territories, and new technologies are increasing the pace of discovery, our existing knowledge can better support the management of this vast estate. The Marine Biodiversity Hub partners agreed that through collaboration, pooling expertise and resources, we could support ongoing marine bioregional planning and improve the scientific knowledge available to support the implementation of marine bioregional plans.

The Marine Biodiversity Hub was developed to address two fundamental questions:

1. How can we predict the distribution of marine biodiversity; and
2. How can we use this improved capability to conserve and manage marine biodiversity in a multiple-use environment?



Achievements

Understanding biodiversity

Marine bioregions are a key component of marine bioregional planning, but are based primarily on the provincial distribution of endemic fish. Hub scientists showed that similar patterns occurred nationally for the broader fish fauna and off western Australia for five sampled invertebrate groups, increasing our confidence that marine bioregions provide a consistent and comprehensive view of marine biodiversity. At the same time we confirmed existing depth related patterns in biodiversity (bathomes), and provided new bathomes for the continental shelf that were immediately used in bioregional planning.

New genetic technologies were used to show that Australia's marine biodiversity is underestimated due to cryptic speciation in many taxa. Combining this new genetic knowledge with the palaeoecological record, we were able to identify underlying causes for our continually evolving marine biodiversity. This improved understanding of the processes shaping modern marine biodiversity and their likely response to future change, and identified new biodiversity attributes for future management.

Genetic technologies also showed a wide variety of population structures within deepwater species on seamounts and larger ridge systems. This variety may be partly explained by the combination of large scale oceanography and differing life history strategies, with implications for marine reserve design management. In particular, the wide variety of population structure indicates that no single reserve design is likely to be adequate for all species, and emphasises the need for combining on- and off-reserve management.

Predicting biodiversity using biological and physical surrogates

Hub partners developed a comprehensive national dataset containing 37 environmental data layers including new disturbance estimates which was provided to the Department of Sustainability, Environment, Water, Population and Communities (DSEWPaC) to assist marine bioregional planning and the mapping of listed species. Biological survey datasets from the partners (many resurrected from previously inaccessible sources) were then used with new statistical methods to predict marine biodiversity nationally at a scale of 1 km² from the physical data. These new maps were

used by DSEWPaC to improve marine reserve design, and subsequently were provided to the states to improve their marine planning. The maps and underlying data will form part of the *Atlas of Living Australia* (www.ala.org.au).

Maps at a scale of 1 km² are appropriate for designing marine reserves, but monitoring and managing reserves requires knowledge at finer resolution. Hub scientists shared expertise and new technologies (including through the Integrated Marine Observing System) to map previously unknown areas of the seabed in four areas around Australia. The mapping was provided to local marine managers who used it immediately to fine tune reserve design. Collaboration between the partners led to a consistent national approach that integrates swath bathymetry, autonomous underwater vehicles, towed video, physical sampling and statistical modelling to improve biodiversity mapping. A consistent national approach enhances prospects for monitoring the developing marine reserve estate and the broader marine environment.

Collaboration between Hub partners was important in developing national comprehensive datasets, testing and integrating a variety of survey tools, and developing and testing new probabilistic models to predict different attributes of biodiversity with uncertainty. Testing new statistical techniques with the partners' diverse and nationally representative data holdings was a powerful approach. It showed that the relative importance of physical surrogates varies for different biota, regions and spatial scales, and that the biological surrogates that appear valid at the larger provincial scale may not be valid within provinces.

New options for managing marine biodiversity

Clear and agreed objectives are a cornerstone of successful management that can be difficult to develop in information-poor environments. Hub scientists demonstrated the potential of expert elicitation in quickly assessing risks to biodiversity (in this case through an international Internet survey), and applied new approaches to work with environmental and resource managers, environmental non-government organisations and fishers that demonstrated common ground on commercial, economic and social objectives for sustainable fisheries management.

At the same time, detailed analysis highlighted variability in the environmental performance of individual operators, which suggested the potential for market-based approaches to improve environmental outcomes. We subsequently showed that spatial incentives could reduce environmental impacts of fisheries more cost-effectively than closures, but that results are area and time specific. These results were then adapted to support DSEWPaC in marine reserve design through more realistic predictions of changes in fishers' behaviour following management intervention.

Offsets were another market-based instrument shown to have potential as a tool for marine conservation, either as an end goal or an interim measure to support technological innovation. This finding led to a joint project with DSEWPaC to assess additional management options for implementing the Commonwealth marine reserve network. Market-based instruments matched with a more outcome-based approach were shown to have the potential to improve biodiversity management on and off reserves by explicitly including management costs as a part of doing business.

The future

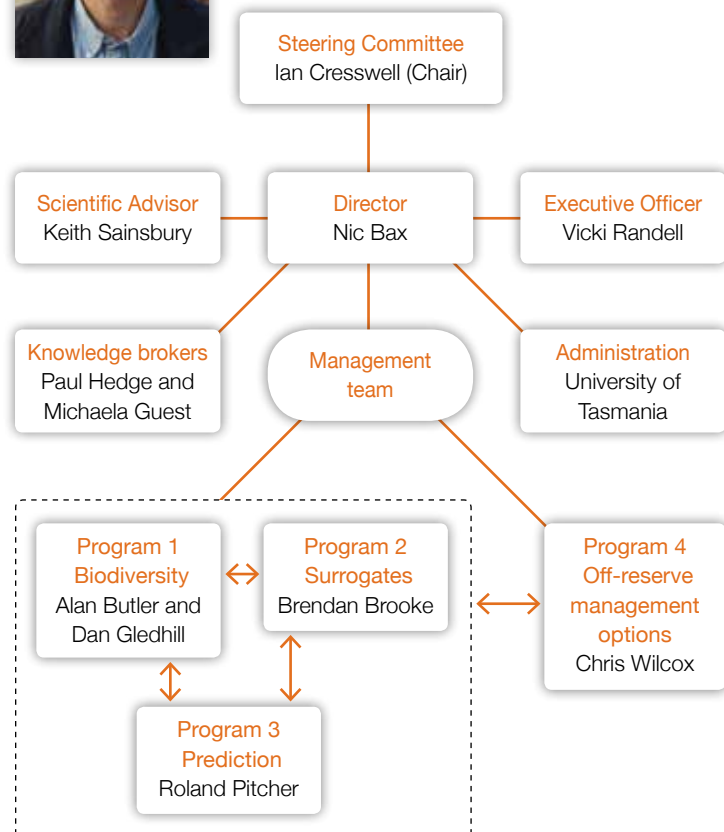
Australia is progressing from marine bioregional planning to its implementation through EBM. The Marine Biodiversity Hub has contributed to the scientific basis for this to develop.

Our scientific understanding has come a long way in three years, with an improved understanding of what our marine biodiversity is, where it came from, and how to predict its distribution in Australian waters. In so doing we have directly supported Australia's marine bioregional planning and set the scene for its management implementation. We are now working internationally to support management of biodiversity on the high seas beyond national jurisdiction.

The Minister for Sustainability, Environment, Water, Population and Communities, the Hon Tony Burke MP, has supported a second Marine Biodiversity Hub. We look forward to further work on developing and testing national ecosystem monitoring, providing cross-jurisdictional, cross-sectoral integrated management, and improving our understanding of marine biodiversity and ecosystem processes relevant to marine bioregional plans. The next four years promises to be as exciting and productive as the previous four.



Nic Bax
Director, CERF Marine Biodiversity Hub



Knowledge brokering

Increasing the relevance and uptake of research

Governance arrangements of the Marine Biodiversity Hub were designed to ensure that the end-users were fully involved in the program. A steering committee was established to oversee the strategic direction, project progress and adoption strategies of the Hub. Steering committee membership includes the major research participants (CSIRO, AIMS, UTAS and GA) and representatives from major stakeholders such as: the Department of Environment and Heritage (DEH now DSEWPaC), the Australian Fisheries Management Authority (AFMA), Department of Agriculture, Fisheries and Forestry (DAFF), the Australian Petroleum Production and Exploration Association (APPEA), WWF-Australia, the Commonwealth Fisheries Association, and the Sustainable Tourism CRC. The steering committee assisted in developing the Hub's research plan and provided strategic direction and oversight.

The Hub implemented and maintained a range of initiatives and activities to ensure its research outputs were well communicated. These included research papers and reports, newsletters, media releases, and sponsored sessions at national and international conferences.

The Hub's knowledge brokering was targeted to meet the needs of its key stakeholders. The Hub director acted as knowledge broker until the specific stakeholder needs were determined. From May 2009, the Hub appointed specialist knowledge brokers (KBs) to ensure research outputs were understood, and where appropriate, used by marine policymakers, planners and managers.



Paul Hedge
Knowledge Broker

Michaela Guest
Knowledge Broker
(not pictured)

Knowledge brokering model

DSEWPaC was identified as the key stakeholder for the Hub because of its focus and momentum on developing marine bioregional plans and identifying marine protected areas for Australia's Exclusive Economic Zone. For this reason, KBs were seconded (two days per week) from the Marine Division of DSEWPaC. Objectives and governance arrangements for the KBs were established to clarify the scope, roles and responsibilities of the position. The objectives of the role were to:

- > identify opportunities for the Hub to strategically contribute to the challenges to better manage Australia's marine biological diversity;
- > engage with Hub program leaders and scientists to understand the contribution of their research outputs and deliverables to managing marine biodiversity;
- > engage with key stakeholders of the Hub to understand their specific needs and expectations regarding research outputs and deliverables;
- > provide advice on how the Hub's research outputs and deliverables can be tailored to meet the specific needs of key stakeholders;
- > identify and manage engagement opportunities between Hub scientists and key stakeholders to increase relevance and uptake of project outputs; and
- > contribute to the development of key messages to stakeholders.

Activities of knowledge brokering

In collaboration with the Hub director and DSEWPaC, the KBs identified essential activities and established a focused work program. The following activities were prioritised and completed:

- > communicate with Hub scientists to understand the purpose and outputs of their research;
- > complete an inventory of agreed key science outputs and products and compile these in a product delivery schedule;
- > communicate to stakeholders the purpose and outputs of the Hub's research to ensure they understand the research being undertaken, how it builds on existing research and why it is relevant to marine policymakers, planners and managers;
- > identify key stakeholder research needs, interests and timelines and priorities;
- > identify opportunities for the Hub to take on new work (not planned for in original CERF funding agreement) to increase relevance of the Hub and meet some of DSEWPaC's priority needs;
- > facilitate the sequencing and delivery of priority research products from scientists to stakeholders in a form that is 'fit-for-purpose' and timely;
- > facilitate the production of a data management strategy to ensure the Hub's products are available to the public; and
- > convene targeted workshops with DSEWPaC, involving additional government agencies and technical experts, and focusing on significant ongoing management challenges to demonstrate how the Hub's research can be used now and in the future.

Significant contributions of knowledge brokering

The KBs worked with a diverse range of researchers, policymakers and managers significantly contributing to the following outcomes:

- > usefulness and relevance of the Hub's research and outputs for stakeholders was understood;
- > national-scale marine bioregional planning and marine protected area programs of DSEWPaC were informed by the Hub's world leading research on biodiversity discovery, understanding and prediction;
- > NGO engagement with DSEWPaC on identification of marine protected areas were informed by the Hub's research;
- > the level of trust and understanding at the science-policy interface was significantly increased to strengthen partnership approaches, particularly between the Hub and DSEWPaC;
- > understanding about the effectiveness of and alternative models for knowledge brokering was significantly increased in both the Hub and DSEWPaC;
- > effective stakeholder access to Hub's research outputs via web-based information management system; and
- > knowledge Brokering was extended to bring in scientific and policy experts from outside the Hub as necessary to meet DSEWPaC's needs.

Lessons learnt

The approach to knowledge brokering adopted by the Hub enhanced the scoping and delivery of marine research outputs to DSEWPaC. Its effectiveness was formally recognised in January 2010 with the presentation of an Australia Day Achievement Award from the Secretary of DSEWPaC. The strength of the current model is that the KB takes part in Hub and DSEWPaC business planning and decision-making processes. This means the KB is well positioned to interpret and make suggestions to accommodate the drivers, issues and needs of both worlds.

It should be noted that the KB model adopted by the Hub was suitable for its particular circumstances. Successful knowledge brokering needs to be fashioned to suit the particular research provider and stakeholder needs. In this context, the model adopted by the Hub will need to evolve to accommodate the National Environmental Research Program's policy settings, evolving DSEWPaC structures and processes for information acquisition and management. Furthermore, it will be necessary to ensure that future Marine Biodiversity Hub projects support DSEWPaC's direct needs and also their interactions with other stakeholders whose marine interests intersect with their own (such as APPEA, AFMA, state agencies, NGOs, and IMOS).



Biodiversity Program

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Alan Butler

Biodiversity Program

Improving management of biodiversity by understanding its origins, structure and dynamics

Surprisingly little is known about the marine environment, particularly about life in the deep sea. Many of the processes investigated for terrestrial environments in the 19th Century remain obscure for marine habitats, especially for depths below 200 m.

For example, can the deep-sea fauna at temperate latitudes be distinguished from that at tropical latitudes? What limits the distribution of deep-sea species? Are assemblages stable over time? How far can deep-sea species disperse? What factors cause speciation in deep-sea lineages? Can the deep-sea fauna adapt or evolve in response to climatic change? While biodiversity and communities in shallower waters are better understood, many of these questions are still to be resolved for all marine environs.

This lack of basic knowledge about biodiversity impedes the management of marine resources. For example, the process of locating offshore marine reserves has relied more on geological and oceanographic proxies than biological data. The capacity of seafloor communities to recover from human disturbance is unknown. Would the mining of a seamount summit threaten endemic species? How long will it take seamount communities to recover from the removal of cold-water coral thickets by trawling for fish? Does it matter if hydrocarbons spill and cover the seafloor on an offshore bank? The deep sea is not immune from terrestrial pollution and other human impacts; pesticides and chlorinated hydrocarbons have been detected in deep-sea animals elsewhere on the planet.

For the majority of species, the available baseline data are insufficient to detect changes in biodiversity. For example, seafloor communities became impoverished from a new pollutant, or from sluggish water circulation as a result of climate change. Only a miniscule number of biological samples have been collected from the seafloor deeper than 3000 m in Australian waters, despite the massive amount of abyssal plain under Australian jurisdiction. Even in shallow water, knowledge of natural variation over time and space is rarely sufficient to reliably detect changes induced by human impact. An understanding of how the biota has responded to change in the past may enable improved interpretation of modern data. Climatic fluctuation has occurred regularly over the Cenozoic Era (the last 65 million years) and the resulting biotic changes have been preserved in the distribution and genetic makeup of the modern day fauna.

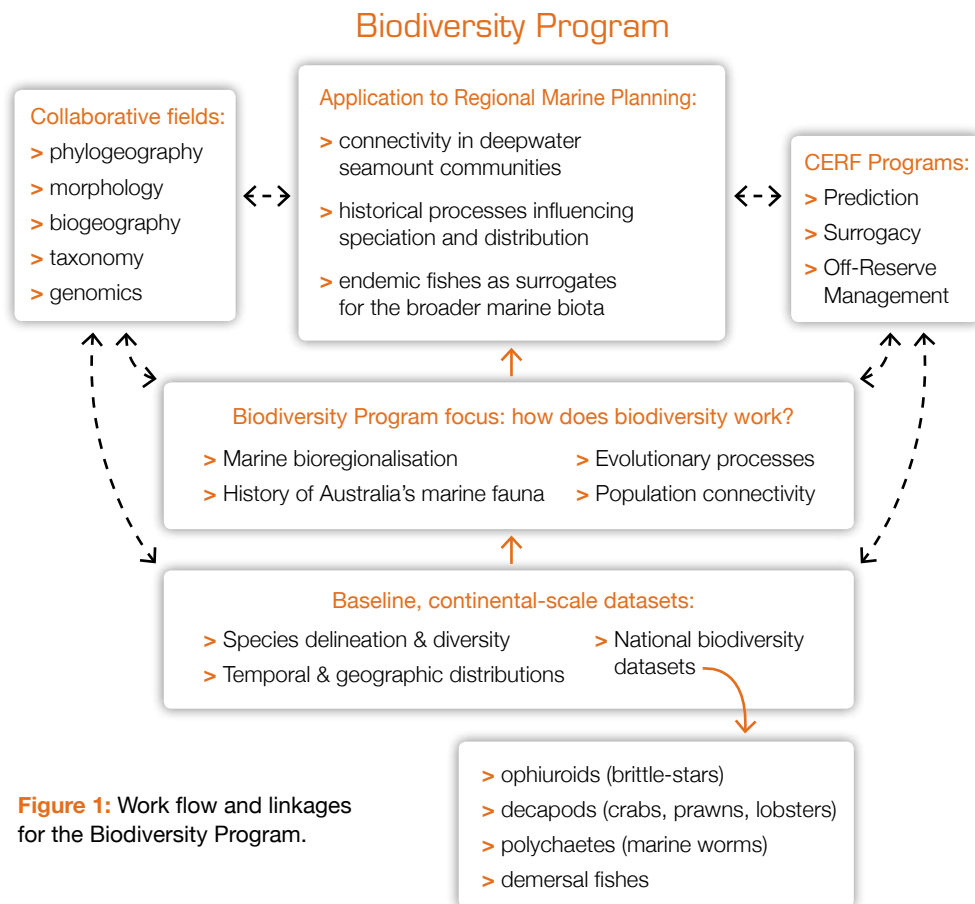


Figure 1: Work flow and linkages for the Biodiversity Program.

Finally, a lack of knowledge about basic marine biodiversity patterns restricts the proposal of management and policy options. Much of the marine environment is out of sight and locations become indistinguishable from each other in all but their physical characteristics. The management trend of declaring broad swathes of marine habitat based on seabed geomorphology as an 'asset' is a case in point. Like any asset, marine habitats in different locations differ in their ecological and conservation values. Understanding the local and regional spatial scales of biodiversity provides resolution to support decision-making in the marine environment and avoids potentially undervaluing and damaging diverse biological assets.

Objectives

The objective of the Biodiversity Program was to synthesise and interpret data from the many previous surveys around Australia. Many of these data have either recently become available, or have become available in a unified taxonomy that enables large scale biodiversity patterns to be identified.

A secondary objective was to use and combine new genetic and oceanographic technologies to better understand the origins of marine biodiversity and its connectivity in deepwater communities.

Approach

Many samples preserved in collections were selectively re-examined and identified to species using a common taxonomy and new genetic techniques. Three datasets were prioritised for this: ophiuroids (brittle-stars), decapods (crabs, prawns, lobsters), and polychaetes (marine worms). Soundly-based continental-scale species-level datasets have been built for these groups, adding to those previously developed for fish. Secondly, national datasets were bolstered by selective and targeted identification of small-sized animals that were previously under-represented. Thirdly, DNA analysis of selected specimens investigated patterns of biogeography, cryptic speciation and population connectivity across Australian marine environments. The national datasets were analysed to better understand Australian biodiversity, as well as present-day and historic processes that influence speciation.

Outputs

- > Upgraded database of Australian demersal-shelf fishes that increased the number of species for which data were available and included contemporary distribution and depth data.
- > An updated national bioregionalisation based on the analysis of large-scale patterns in fish distributions: provincial and bathomic.
- > Endemic fishes were confirmed as an effective surrogate for broader fish fauna.
- > Depth-related structuring in Australian marine demersal fishes was confirmed. Assemblages in the seven bathomes were shown to be distinct and should be treated as separate units for management purposes.
- > Genetic investigations of squat lobsters indicate that levels and patterns of Australia's marine biodiversity have been largely underestimated. Most importantly, results highlight the strength of combining more than one approach (such as molecular and morphological taxonomy) to understand, quantify and protect Australia's marine biota.
- > Evidence exists for parallel micro- and macro-evolutionary events for fishes over several geological periods. These combined with a long period of relative isolation to create high levels of endemism in southern Australia. Drastic geological episodes and recent climate change continue to shape the morphological and genetic diversity encountered today; loss of genetic diversity within species occurs constantly, and is irreversible.

- > The broad scale patterns of distributions of invertebrates are largely consistent with those of fishes and exhibit both differences reflecting separate evolutionary history at a provincial scale, and ecological signals, of which depth is strongest.
- > Populations of some seamount species examined were found to be highly connected, even over large distances. Populations of deep sea corals, however, are largely self-seeding with evidence that corals on separate seamounts and across different MPA and ridge systems are effectively isolated.
- > Deep sea coral communities failed to show signs of recovery 10 years after the cessation of trawling.
- > Reproductive life history appears to explain differences in population structure at continental scales between species of brittle stars.
- > Targeted baseline biological data collection coupled with sophisticated multidisciplinary techniques as used in this Program provide the potential for increasingly rapid advances in understanding the processes that shape marine communities and their likely response to change.

Outcomes

The Biodiversity Program has characterised large scale patterns in marine biodiversity around Australia, confirming and enhancing advice used in marine bioregional planning, and developing new information of relevance to marine bioregional management. Key outcomes to date are:

- > Confirmation of provincial boundaries in IMCRA 4.0, being used in marine bioregional planning, based on additional (non-endemic) fish species and invertebrate taxa.
- > Improved understanding of the biogeography of fish, derivation of nationally consistent datasets for a further three taxa, and an improved understanding of the processes responsible for our marine biodiversity suggest that IMCRA 4.0 can now be improved to support implementation of marine bioregional plans.
- > First depth structuring of shelf communities used in marine bioregional planning.
- > Increased species biodiversity based on new genetic approaches confirms importance of Australia's hierarchical approach to describing and managing biodiversity.
- > Spatial characteristics of micro- and macro-evolutionary events indicate presence of areas of speciation (neo-endemism) and climate refuge (paleo-endemism) with conservation value under a rapidly changing climate.
- > Population structuring for marine invertebrates varies based on taxa and life history. No marine reserve network of acceptable size can account for these different scales of connectivity, emphasising the value of integrated on- and off-reserve biodiversity management.

Update of Australia's marine bioregionalisation (fishes): providing bathomes for Australia's continental shelf

This study complements existing national biodiversity maps by providing the only evidence-based means available to robustly predict depth related patterns of assemblages of demersal fishes on the Australian continental shelf^{A3}.

Objectives

To upgrade marine bioregionalisation datasets used in IMCRA 4.0 to include bathomic (depth related) structuring of the continental shelf. The bioregionalisation, which is used in Australian marine bioregional planning to establish the National Representative System of Marine Protected Areas (NRSMPA), previously consisted of: 1) provincial structure of the shelf, 2) provincial structure of the slope, and 3) bathomic (depth related) structure of the slope.

Approach

The study makes use of recent taxonomic and distribution information, compiled from published literature and expert knowledge, on the distributions of more than 1500 demersal Australian fishes. The methods generally follow those developed for the bioregionalisation of the Australian slope using demersal fishes^{A4}.

Key findings

Depth ranges for the bathomes showed only minor variation around the Australian continental shelf, with the north-western region of Australia being more variable than other areas (Figure 2).

Bathomes need to be considered in the context of the provincial structure which influences the pool of fish available for each bathome. Thus, while the bathomes show consistent zonation patterns for demersal fish around Australia, these zones contain different suites of species in the different provinces and provincial transition zones.

The provincial structuring derived in this study is, in general, similar to that produced in the previous shelf bioregionalisation produced by CSIRO for the earliest IMCRA project^{A5}. However, there are several significant differences, such as the translocation of the Gulfs Province off South Australia, and uncertainties in the North West, in the Great Australian Bight and to the west of Bass Strait.

These differences may result in part from a potential loss of precision caused by combining the slope and shelf datasets. Additional work by the Hub shows a strong demarcation between shelf and slope faunas^{B22}. Continued use of shelf provinces as documented in the National Marine Bioregionalisation is therefore recommended^{A4}.

New knowledge and opportunities

The bathomic structuring demonstrated in this study is a first at this scale, and provides further opportunity to interpret and understand the patterns of faunal distributions within a hierarchical framework^{B19}. These results underpin other work undertaken within this Program, and more broadly in the Hub, and provide the basis for a better understanding of biogeography in the region. These results also provide greater confidence in marine bioregionalisation datasets as the basis of marine bioregional planning in Australian State and Commonwealth waters.

Converting the database to a georeferenced grid, rather than a 'string' parallel to the coast, would avoid the loss of precision for inshore species encountered in this study and would allow the retention of rich biological and physical detail, providing opportunities for novel analyses^{B26}.

Additional Hub results support a clear distinction between shelf and slope faunas^{B22}. The ongoing challenge for scientists and managers is to better understand the historical and current processes that have created and maintained these patterns of distribution. The fauna need to be further characterised into ancient or recent lineages. Such information will assist the management of units (whether geographic areas or species) based on their history, and their likely responses to future change.

The extensively updated database of fish distributions also provides a baseline against which to measure the southward extensions of species ranges being recorded in south-eastern Australia, and likely to be occurring to differing degrees elsewhere in the region^{B21}.

Bathomes of Australia's Coast and Shelf

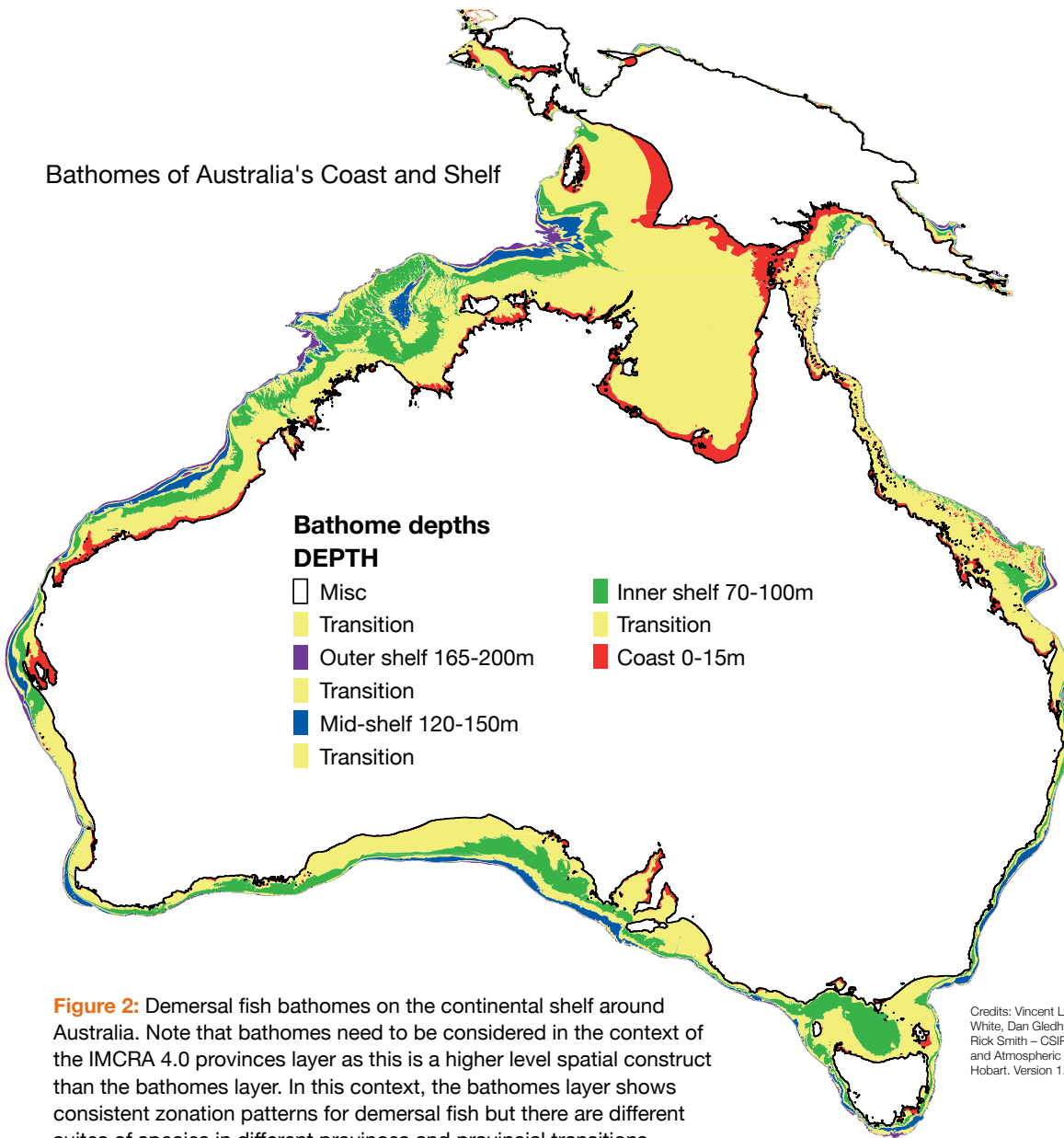


Figure 2: Demersal fish bathomes on the continental shelf around Australia. Note that bathomes need to be considered in the context of the IMCRA 4.0 provinces layer as this is a higher level spatial construct than the bathomes layer. In this context, the bathomes layer shows consistent zonation patterns for demersal fish but there are different suites of species in different provinces and provincial transitions.

Credits: Vincent Lyne, William White, Dan Gledhill, Peter Last, Rick Smith – CSIRO Marine and Atmospheric Research, Hobart. Version 1.0 June 2009.

Diversity and distribution of macrobenthos of the Western Australian continental margin

The continental margin of Western Australia is extensive and contains a highly diverse biota, but is largely unexplored, especially for those organisms comprising the bulk of marine biodiversity: the small invertebrates living on the seafloor (macrobenthos). Yet planning for conservation in Australia's deeper waters relies on understanding patterns of diversity as well as the processes underlying them. This need resulted in 'voyages of discovery' surveys involving researchers from Hub partners, CSIRO's Wealth from Oceans Flagship and Museum Victoria, in collaboration with Geoscience Australia and taxonomists from other Australian museums. These surveys spanned 23 degrees of latitude from Albany to Ashmore Reef, incorporated temperate, subtropical and tropical faunas, and sampled some 528 stations from 100–1100 m depth. This represents the first systematic sampling of benthic biodiversity at these depths along the WA continental margin. The species richness discovered will continue to be reported in taxonomic updates and revisions for years to come, but the major initial findings are summarised below.

Objectives

Spatial patterns of diversity and endemism were quantified for a variety of benthic infauna and epifauna on the continental margin and the physical and spatial variables that best explain patterns of distribution were determined. The adequacy of using the distribution of fishes as a surrogate for the highly diverse benthic invertebrate fauna was assessed.

Approach

The most abundant and diverse invertebrate groups encountered during the surveys – benthic crustaceans and polychaete worms – were selected for taxonomic identification. These were the groups for which the best taxonomic expertise and the best comparative data from elsewhere in Australia were available. Selective targeting of taxa was vital as the macrobenthos includes a diversity of marine invertebrate groups beyond the taxonomic expertise available in Australia. The selected taxa also comprise a significant fraction of infaunal benthic species richness (number of species); it is hypothesised that patterns based on these will be representative of the remaining fauna. Physical data used in the analyses were based on the combined physical and oceanographic datasets developed by the surrogates and prediction programs.

Key findings

The surveys generated 6800 records comprising more than 1600 species for the two target groups, including significant numbers of new species. Levels of endemism for invertebrates on the continental margin were high: about 27% of polychaete species were endemic to WA, and more than 39% of decapod crustacean species were endemic to southern WA. These results are similar to levels of endemism recorded for demersal slope fishes: ~30% in the south and 20% in the north of the region^{B22}. At this provincial scale, levels of endemism are inferred to be largely due to the evolutionary history of the faunas in different regions of the Australian continental margin. Results for tropical regions suggest the presence of a widely distributed tropical fauna. From the well-studied squat lobsters (families Galatheididae and Chirostyliidae) 40% of species from WA occur across the tropical Indo-west Pacific, with 18% of species reaching as far as the western Pacific Islands. Similar patterns occur in well-studied families of polychaetes.

A comparative analysis of data from fishes, crustaceans (decapods and tanaids), and echinoderms found broadly congruent geographic change in community structure along a latitudinal gradient for a single depth range. This correlation between community structure and latitudinal gradient lends support to Australia's existing bioregionalisation based predominantly on the distribution of fishes that forms the basis of marine bioregional planning. As this correlation was limited to a single depth-range, whether different taxa show congruent patterns along depth gradients remains relatively untested.

Although many species on the WA continental margin have wide latitudinal ranges, their depth distributions are narrowly defined (Figure 3). The distribution of species appears largely correlated with temperature, which is more highly correlated with depth than latitude. Along with temperature, depth is also correlated with changes in pressure, light and oceanographic currents, and a combination of these variables could determine the extent of a species range. Similar depth associated patterns occur in other invertebrate groups studied, confirming the importance of implementing bathymetric structure in Australia's bioregionalisation.

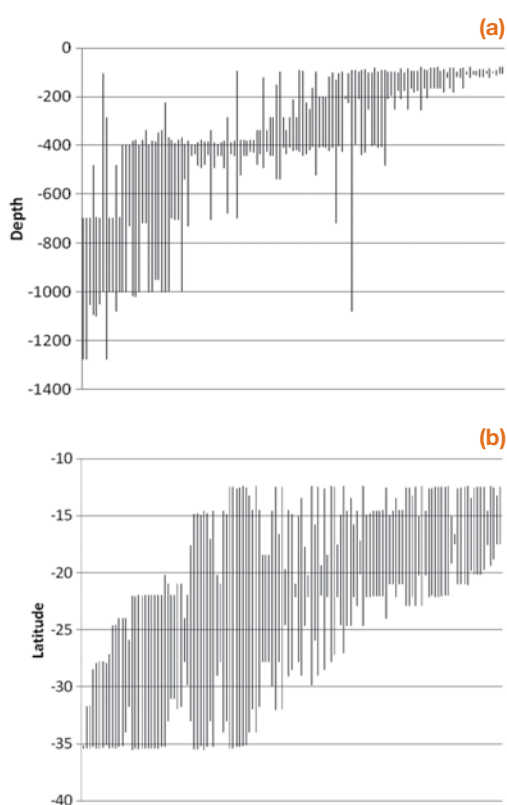


Figure 3: Most species occupy a narrow range of depth, illustrated here by the distributional range of 140 decapod crustacean species on the continental margin of Western Australia along a gradient of a) depth and b) latitude.

New knowledge and opportunities

The significant endemic component in the western invertebrate biota is quantified here for the first time, providing information for management, and confirming the need for significant fractions of the WA coast to be included in any representative national reserve system. We expect that the levels of invertebrate endemism reported here are not unique and similarly high levels remain to be described in other areas where information is lacking, in particular in Australia's north-east, including the Coral Sea. Ongoing expansion of the biodiversity databases established by the Hub will greatly improve the quality and breadth of data available to management.

Rare (and/or poorly sampled) species are prevalent throughout the Australian marine environment. The design of future surveys will need to be reviewed to better quantify endemism and other measures of province-level diversity. As this research used the most abundant and diverse invertebrate groups encountered during the surveys, future work that incorporates these apparently rare species to quantify endemism and province level diversity will require statistical approaches developed by the Prediction Program to represent this information in marine planning and management.

The discovery that many species on the WA continental margin are restricted to very narrow depth ranges agrees with findings for fish, but flags further gaps in national datasets^{A4}. Depths surveyed by the Hub on the WA margin encompass 100 to 1000 m, but few surveys over comparable depth ranges have been undertaken elsewhere in Australia. Depth often influences broad scale distributions in shallower waters. For example, the fauna of many coastal bays (Port Phillip Bay, Sydney Harbour, Moreton Bay) are distinct from those of the adjoining continental shelf. The systematic collection of quantitative data for a diversity of taxonomic groups encompassing broad bathymetric ranges on a national scale will strengthen the few existing datasets and better guide the management of the NRSMPA and potential future reserve establishment.

At least 30% of all species collected in this project are new to science. Among crustaceans and polychaetes alone, many hundreds of species now require formal taxonomic descriptions to ensure they remain accessible to researchers in perpetuity. Without formal taxonomic description species cannot be compared between areas and the data rapidly lose value. The Biodiversity Program has collaborated with projects such as the Census of Marine Life (which concluded its 10 year program in October 2010), and similar collaborations will be needed in the future.

Changes in Australia's marine fauna: learning from the origins of Australia's marine provincial bioregions

The largest units used in managing Australia's marine biodiversity – provincial bioregions – reflect the distributional ranges of narrowly dispersed demersal fishes. The historical processes leading to these distributions, however, have not previously been investigated. An improved understanding of similarities between marine biota in Australia and adjacent regions will identify interrelationships between provinces and their bathomes (depth related structure), and offer clues to their origins. A greater understanding of the past changes to marine biota, and the spatial relationships between them, will improve the prediction and management of changes in the marine environment.

Objectives

The faunal structure of broad-scale biogeographic units (provinces and bathomes) was determined and their affinities (relatedness) compared within and between provinces of the Australian EEZ and with neighbouring regions (ocean-basin scales). The evolutionary history of these units was investigated to determine how they may have developed, and how present-day processes maintain (or threaten) them.

Approach

All bathomes within Australian provinces were examined to 1000 m depth using contemporary fish data to determine affinities and patterns of distribution within Australia, and with surrounding ocean basins. Only demersal species were used as these are generally more informative for regional-scale biogeography than pelagic species^{A4}.

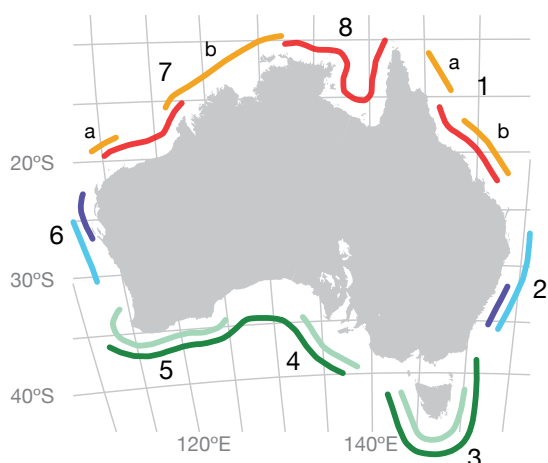


Figure 4: Affinities of demersal continental shelf and slope provinces determined by demersal fish distributions. Provinces were clearly delineated by latitude and depth, while shelf and slope provinces differed in each region. Differentiation in the north (1, 7, 8) was much greater than between southern provinces (3, 4, 5). The subtropical, central western province (6) grouped closest to the central eastern warm temperate province (2), but while they were substantially closer to the northern provinces on the shelf, they were well separated from both the southern and northern provinces on the slope.

Key findings

The complex biogeographic structure of Australia's marine fishes was confirmed, with latitude and depth having greater effect than 'ocean basins' at these scales.

- > Confirmation of previously delineated depth-related structuring in Australian marine demersal fishes. Assemblages in the seven bathomes were distinct and should continue to be managed as separate units.
- > There is strong evidence of major differences in fish fauna between provinces based on latitude, reflecting tropical and temperate elements of the fauna (Figure 4).
- > Australian endemic species are suitable to act as surrogates for the broader fish fauna providing confidence to managers in the use of this data to support marine bioregional planning.

New knowledge and opportunities

This study provides a better understanding of the structure and affinities of Australia's fish biota. It also highlights the importance of the provincial structure used for marine bioregional planning.

A deeper understanding is emerging of how the breakup of Gondwanaland and the later collision with South-East Asia has influenced Australia's temperate and tropical faunas.

A more robust picture of the historical processes that shaped present day biota can be achieved by combining these findings with phylogeographies, known changes in sea level, plate tectonics and palaeocurrents.

Present and future patterns of biodiversity can only be predicted using models based on present-day distributions and environmental variables. A better understanding of history and relationships will increase the power of these models to predict the responses of the fauna to present day pressures, including global warming.

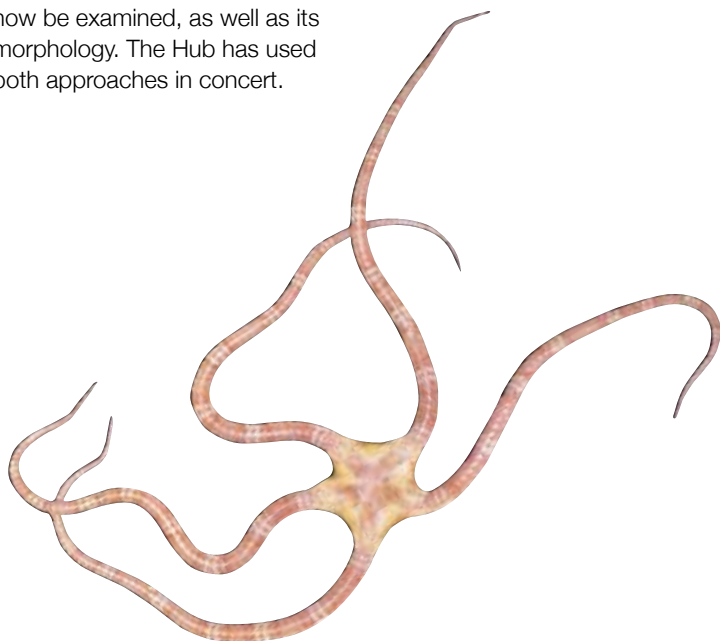
Where do Australian marine species come from?

Genes and bodies

Individual genomes, comprised of DNA, act as long-term storage compartments of coded instructions responsible (in interaction with the organism's environment) for species-specific traits. They also contain a record of the history of the species. The structure and composition of DNA evolves over time in response to natural selection and random genetic drift and may result in morphological modifications that characterise different species, and drive, given enough time, the evolution of distinct species. The fine detail of the DNA sequences in an organism can now be examined, as well as its morphology. The Hub has used both approaches in concert.

Very different forces

Large scale, slow (millions of years) geological episodes, such as continental drift, are a major cause of new species or evolutionarily significant lineages. Human-mediated changes such as heavy industry, rural development, landscape transformation, and recent global warming, are rapid, (tens of years), and account for species extinction. Species genetic variability is always open to change. Gene variants, once lost, cannot be recovered.



Phylogenetics and phylogeography

Morphological characters or DNA regions among species are commonly compared to infer a phylogeny, or 'family tree' showing the relatedness of organisms. Changes at the molecular level often are assumed to occur linearly over time. Given a robust phylogeny, and a reliably dated fossil of the most recent common ancestor of two species, the rate of changes over time can be used to estimate the time of major evolutionary events (such as rapid speciation, or mass extinctions) from within that phylogeny. Further, the rate of molecular change over time of a suitable DNA region, if known, can be used to approximate the timing of events not documented by fossils (such as ancient large scale geological events or dramatic sub-recent climate change episodes like glaciations). Such a DNA region, or 'molecular clock', must be used cautiously because DNA regions 'tick' at different rates over time and over different lineages. Phylogeography – the study of the historical processes leading to the contemporary geographic distribution of organisms – refers to the combination of all the above. The phylogeographic work in this Program has mainly studied the present geographic distributions of populations, species and genera, and their genealogical relationships. Work in progress is studying past distributions and processes of environmental change.

Changes in Australian marine fauna: explaining the origins of Australian marine invertebrate species

The distribution and diversity of marine biota on Australia's north-western continental slope are assumed to stem from a combination of historical climate change processes, significant geological episodes, and present day conditions. External conditions leave signatures on an organism, detectable at the molecular and morphological levels. Squat lobsters (families Chirostylidae and Galatheidae) constitute a robust model system for evaluating historical processes that may have shaped north-western Australian marine fauna. This is because Chirostylids and Galatheids are highly diverse and abundant on seamounts, continental margins and shelf habitats across a broad depth range. Most importantly, north-western populations are genealogically connected with relatives of south-west Pacific origin.

Objectives

Molecular and morphological differences in the deep sea squat lobster families Chirostylidae and Galatheidae were explored to understand the influence of climate change and geological episodes on the timing of observed patterns of biodiversity.

Approach

Squat lobsters collected across Australia's north-western continental margin were identified to genus and species morphologically, and DNA was sequenced from both mitochondrial and nuclear genomes. Thereafter, stable molecular phylogenies were computed and a molecular clock was calibrated against evidence from known squat lobster fossils (Cretaceous and Eocene; 144–65 million years ago (MYA), and 55–34 MYA respectively).

Key findings

- > Molecular techniques support species previously delineated by fixed morphological characters. New species or genetically distinct lineages were revealed and several cryptic species (not distinguishable by morphological means) were uncovered.
- > Monophyly is supported at the level of species and genus for the groups examined (all species within genera share a common ancestor).
- > Species within a number of squat lobster genera split early in their evolutionary history. This pattern has resulted in clustering of species within genera associated with geographic regions.

- > Preliminary molecular clock approximations suggest WA populations are significantly older than those from the south-west Pacific. Further support of these results, would provide robust insights into today's distribution patterns of squat lobsters, and suggest the direction and pathway for their colonisation of the region.
- > Genetic diversity within squat lobster species is high, consistent with their known high morphological diversity. A principal event that could have resulted in geographically associated populations within species in this region was the collision of the Australian continental land mass with Indonesia approximately 25 MYA during the Miocene.

New knowledge and opportunities

- > The distribution of cryptic species can be used to identify hotspots of rapid speciation and extinction events. Hotspots are potential model systems for monitoring and examining the influence of environmental stresses and change on present day biota and can provide guidance for targeted monitoring of biota and broader systems.
- > Improved knowledge of phylogenetic relationships in marine fauna will help realise the potential of using patterns in phylogenetic diversity to support marine planning and management. Phylogenetic diversity has been shown to be a more efficient measure for conservation planning in terrestrial systems.

Changes in Australian marine fauna: explaining the origins of Australian marine fish species

Historical processes have contributed to the diversity and distribution patterns of present day marine biota. These patterns are used to delineate bioregions, provinces and bathomes for Australian marine bioregional planning. Events such as glaciations, plate tectonics and changes in palaeocurrents can leave signatures in the genealogy of species. Time-calibrated molecular phylogenies can be used to identify rapid speciation or extinction events related to recent or sub-recent physical processes responsible for forming biogeographical barriers (such as recent climatic and oceanic changes, or sea level fluctuations).

Objectives

To better explain evolutionary events and identify historical processes responsible for present day patterns of marine biodiversity in southern Australia. These were interpreted in conjunction with the likely roles that vicariance (the splitting of the geographic range of a species into discontinuous parts, for example by climatic and/or geological events) and dispersal may have played in shaping the biodiversity of southern Australia.

Approach

Species of wrasse (endemic to Australia), leatherjackets and stingarees (Labridae, Monacanthidae, Urolophidae respectively) were selected as the model system. There is strong evidence of extensive recent radiation and vicariant evolution in these families related to the dynamics of the Australian tectonic plate and neighbouring seas. Specimens were morphologically identified to species, and DNA was sequenced from multiple mitochondrial and nuclear regions. A provisional molecular taxonomy was computed to explore cryptic genetic diversity within species. A multi-locus molecular clock was calibrated against independent fossil records for each family.

Key findings

- > Labridae: multiple sea-level changes occurred during the Pleistocene (about 1.8 MYA to present) following periodic warming and cooling events. A cooling episode was likely to have been responsible for the initial separation by the Bass Strait land-bridge of the once ancestral amphibassian population of *Notolabrus* species. Sequential heating and cooling events may have been responsible for the formation of the five *Notolabrus* species known today, all but one of which are still restricted to southern Australia.
- > Monacanthidae: Similar forces acted on the tropical to subtropical Australian Monacanthids and were responsible for the recent explosive radiation of this family during the Pleiocene (about 1.8–5.3 MYA).
- > Urolophidae: Divergence of main genera occurred following the progressive separation of Australia from Antarctica; the formation of modern stingarees took place contemporaneously in both western and east coasts during the last 10–20 MY.

New knowledge and opportunities

- > Identifying main refugia in which species persisted through the last glacial maxima and their colonisation routes would highlight areas likely to be important to conserving fish diversity through contemporary change.
- > Modelling niche evolution can be used to predict how ongoing climate change may influence local habitat and therefore drive future distribution of populations and major shifts in species composition. This information can assist marine conservation and management through identifying potential refugia, areas of endemism and improve predictions of species movement beyond simple shifting ranges in parallel to the shifting physical environment.
- > Protecting areas seen to be important in maintaining species diversity during previous climate events may contribute to species resilience to physical and chemical oceanographic changes associated with climate change.

Population connectivity in deep sea invertebrates: inferences from spatial genetic patterns

Deep sea habitats on seamounts, plateaux and continental margins harbour immense biological diversity likely to play crucial roles in ocean ecosystems. Deep sea fisheries can remove these biologically rich areas, and their recovery is not assured. Connectivity between impacted and unimpacted habitats is believed to be an important determinant of their recovery, yet their remoteness and wildness makes this very difficult to study.

The only known method for dispersal in these species is via their planktonic larvae, but little is known about how or where the larvae disperse. Because these coral-based habitats are under threat from a range of sources including fishing and possibly climate change, it is important to understand more about their larval dispersal to better predict their ability to recover and persist. Understanding the potential connectivity between these areas can also improve the management of deep sea fisheries to ensure their long-term sustainability (Figure 5).

Objectives

DNA variation in key species was identified to allow indirect estimates of the rates of biological exchange among seamount communities. These estimates were compared with model-based predictions of oceanographic connectivity to understand how ocean currents interact with reproductive ecology to determine population connectivity in the deep sea.



Figure 5: Understanding the potential connectivity between coral-based habitats is important to the management of deep sea fisheries.

Approach

Genetic markers were used to examine population connectivity over small (tens of km) and large (hundreds to thousands of km) scales in crustaceans, corals and echinoderms and examine the potential role of hydrodynamic processes in mediating connectivity in the deep sea through larval dispersal. The term 'population structure' is used here to mean that populations at different locations differ in their genetic compositions.

Squat lobster (*Munida isos*) and deep sea corals (*Desmophyllum dianthus*):

Squat lobsters and corals were chosen to examine local population structure. Microsatellites – a rapidly evolving DNA marker – were developed for these species and samples of 20–50 individuals were genotyped from seven seamounts south of Tasmania (Figure 6). The seamounts spanned two Commonwealth marine protected areas (MPAs), (the Huon and Tasman Fracture MPAs), the more distant Cascade Plateau, and in the case of squat lobster, Macquarie Ridge and Chatham Rise near New Zealand. Slower evolving DNA sequence markers which delineate population and species structure at larger spatial scales complemented the microsatellite analysis.

Deep sea corals are important habitat-forming species on seamounts and are likely to be severely impacted by anthropogenic influences including trawling and climate change^{A6, A8}. Earlier studies of genetic connectivity of deep sea corals suggest dispersal may vary among taxa, with some species having limited dispersal, while others show genetic homogeneity across thousands

of kilometres^{B32}. However previous genetic studies on Australasian seamount corals have used DNA sequencing of nuclear and mitochondrial markers which may not have provided sufficient resolution to detect patterns of genetic subdivision in corals which have a seemingly slow rate of mitochondrial DNA evolution^{A10}. Hypervariable microsatellite DNA markers were developed for two widespread and common seamount corals, (*Desmophyllum dianthus* and *Solenosmilia variabilis*), in order to determine the scale of population structure as well as the rate and directionality of gene flow among populations both at small (10s–100s of km) and large (>1000 km) spatial scales. For *D. dianthus*, eight microsatellite loci were developed and used to compare 19 populations sampled on 11 different seamounts from the Tasman Fracture MPA, Huon MPA, Cascade Plateau and Macquarie Ridge^{B16}.

For *S. variabilis*, 10 microsatellite loci were developed and corals from five of 17 sites across nine seamounts in the Tasman Fracture and Huon MPAs were given preliminary screening to assess the suitability of these markers to resolve population structure^{B16}.

Brittle stars: Ophiuroids are useful model organisms for the study of population connectivity at continental scales because of their abundant and frequent occurrence across a range of benthic habitats, and the variety of dispersal strategies they exhibit. These include planktotrophic (feeding, and usually long-lived) larvae, lecithotrophic (non-feeding, and usually short-duration) larvae (both of these are termed 'pelagic' larvae), viviparity (live birth) and asexual reproduction.

Variation in the mitochondrial gene was used to measure phylogeographic population structure in five widespread Indo-Pacific temperate species, including a dioecious brooding species, a circumpolar Antarctic species that broods its young, and a species with relatively large yolky eggs, indicative of a pelagic lecithotrophic larva. The reproductive habits of two species are unknown, but the relatives of one have planktotrophic larvae, and relatives of the fifth species, which is the shallowest occurring species we studied (50–650 m) predominantly have planktotrophic larvae.

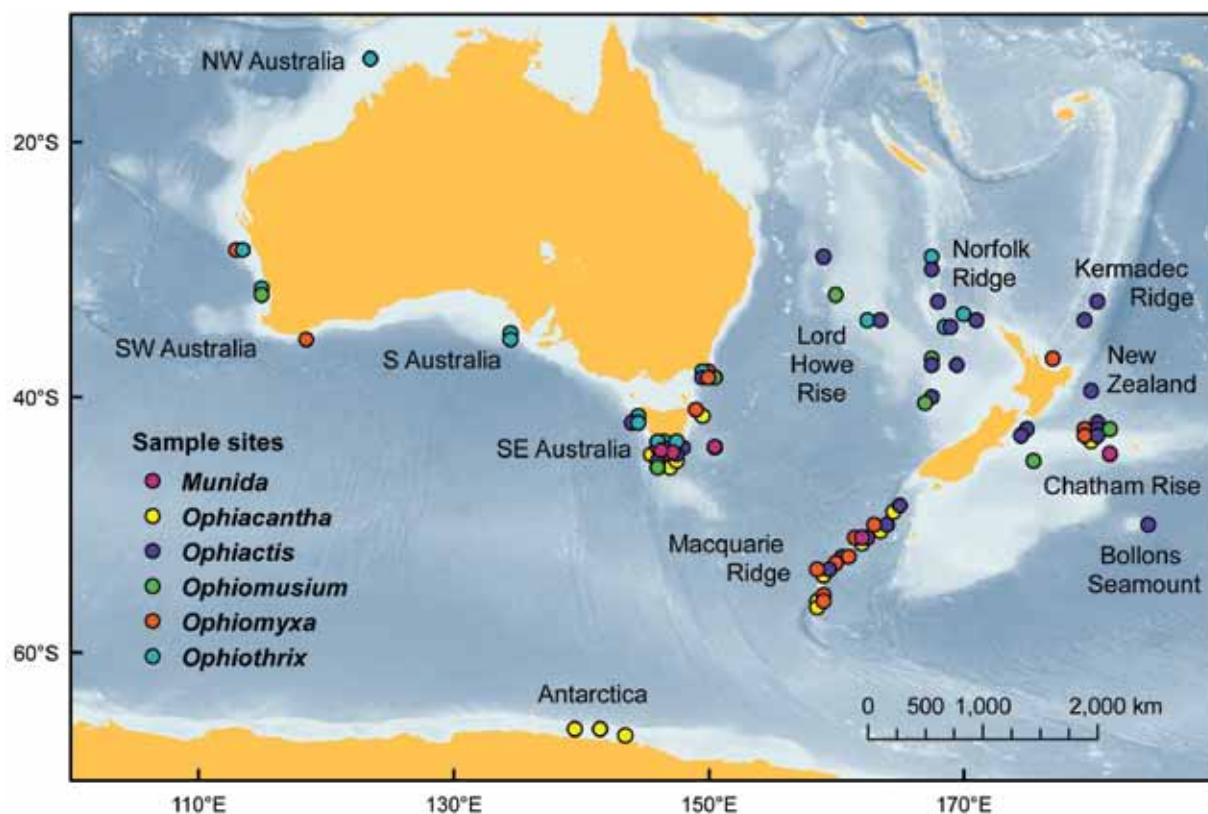


Figure 6: Sampling localities for deep sea invertebrates (brittle stars and squat lobster) used in this study.

Key findings

Squat lobster: Despite the apparently discontinuous distribution of *M. isos*, with coral habitats on seamounts separated by sediment covered valleys, no detectable population structure was evident at the scale of tens to several hundred kilometres in the vicinity of the Huon and Tasman Fracture MPAs. This indicates that migration (either of adults or larvae) among seamounts is sufficient to keep the populations effectively genetically homogeneous (for this level of genetic resolution) at this spatial scale. This is a striking result, as it contradicts the once-held view that seamounts are discrete biotic communities. Instead, populations of some seamount species exist as clusters of interconnected sub-units or demes that regularly exchange migrants.

However, at larger spatial scales, over hundreds of kilometres, populations of the Huon MPA, Cascade Plateau, Macquarie Ridge and Chatham Rise can be considered genetically distinct as a result of evolutionary divergence (random genetic drift) in the face of very low exchange of migrants.

Deep sea corals: In contrast to patterns found for *M. isos*, evidence was found of small-scale population structure in deep sea corals suggesting limited larval dispersal, even between sites on the same seamount that are separated by as little as a few hundred metres. For *D. dianthus*, there is a strong pattern of isolation with depth (between 600 m, 1000 m and 2000 m), consistent with findings based on DNA sequence data^{A13}. However, significant genetic subdivision was also detected among seamounts within MPAs (10s–100s of km) as well as between ridge and seamount systems (1000s of km); patterns that have not been detected based on DNA sequence data. Additionally, preliminary analysis for *S. variabilis* showed significant genetic variation among five



Figure 7: Regional and global ocean currents in the Australasian region. The Southern Ocean ‘supergyre’ may assist the long distance transport of pelagic larvae.

sites on a single seamount: 'Hill U' in the Huon MPA. Taken together, the genetic results for both deep-sea coral species are consistent with a pattern of local recruitment and limited larval dispersal. This matches predictions based on genetic studies of shallow-water corals^{A7,A11}. It also confirms the utility of microsatellite DNA markers to resolve population structure in deep sea corals.

Brittle stars: The population structure of the planktotrophic species at upper bathyal depths (600–1000 m) appears to be undifferentiated consistent with widespread dispersal in the Southern Ocean 'supergyre' current linking the southern Pacific and Indian oceans (Figure 7). In contrast, live-bearing or fissiparous species showed significant phylogeographic structure on a smaller scale, consistent with limited-distance dispersal.

Differences in population structure between planktotrophic and live-bearing or fissiparous brittle stars show the effects of life history strategies on population connectivity. This diversity in population structure will require a similarly diverse management approach given social and economic limits on potential coverage of the marine reserve networks. These findings support the view that deep sea communities are ecologically interdependent, which both constrains and provides opportunities for local and regional management.

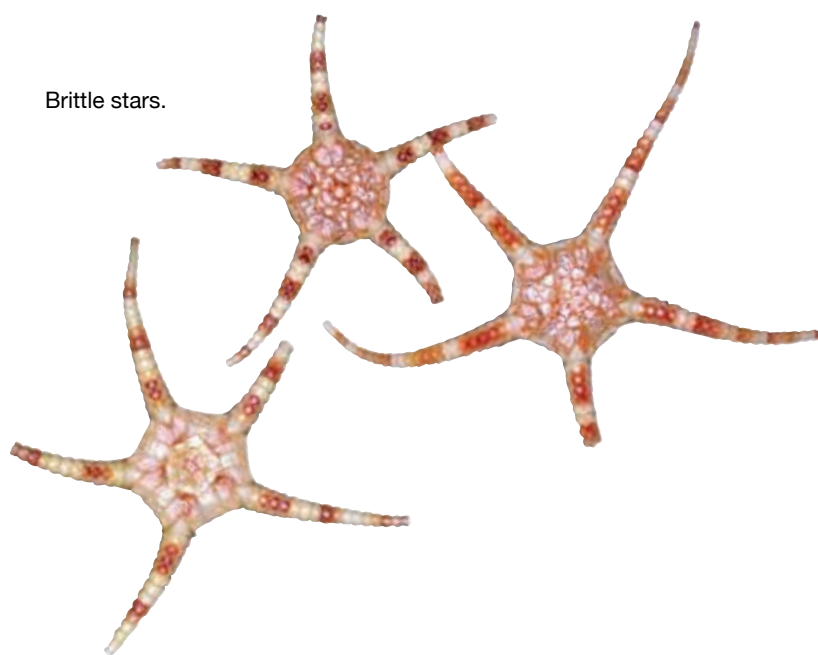
New knowledge and opportunities

Genetic data revealed cryptic patterns of population structure in organisms that are inherently difficult to study and sample, from one of the last truly unexplored habitats on earth. DNA-based analysis of deep sea organisms linked with oceanographic modelling offers the most effective way of characterising their spatial distribution and identifying cryptic species biodiversity.

Seamounts are not simply isolated 'islands' in the deep sea but contain some species which are highly interconnected and others that are effectively isolated. These contrasting patterns of connectivity across a variety of taxa indicate some species will be more vulnerable than others and provide challenges to future management.

For species such as corals that have effectively closed populations, management will need to protect existing adults to ensure adequate supply of recruits for population maintenance. Conversely, for those species that have connected and highly ecologically interdependent populations, management of the network including on- and off-reserve areas will be important.

Brittle stars.



An aerial photograph of a river delta, likely the Colorado River, showing a wide expanse of green water meeting a brown, arid landscape. The water is a vibrant green, while the land is a mix of brown and tan, with some lighter patches. The river flows from the top left towards the bottom right, where it branches out into a delta. The overall scene is a natural, somewhat desolate landscape.

Surrogates Program

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Brendan Brooke

Surrogates Program

Improving Australia's capacity to map biodiversity

Physical surrogates offer a cost-effective way to understand biodiversity distribution in Australia's vast marine territory. Existing biodiversity surrogates have made a valuable contribution to marine bioregional planning in Australia. This program has tested existing surrogates and developed new ones based on intensive biophysical surveys in temperate and tropical waters.

Objectives

The Surrogates Program collated existing marine physical environmental data and developed new data with national coverage (Figure 1). These data enabled seabed habitat and biodiversity modelling, including predictions of biodiversity undertaken by the Prediction Program. This included deriving new national maps of ecological disturbance regimes on the continental shelf.

A second objective was to increase confidence in the surrogates approach, and its management effectiveness, by testing the utility of a suite of physical environmental variables as surrogates for seabed biodiversity. This was the first attempt in Australia to rigorously test surrogacy relationships across diverse seabed environments. The surrogacy analysis was expected to help identify ecological processes that link physical environmental attributes to the distribution of seabed biota. This systems understanding is essential to selecting appropriate surrogates.

Approach

The program fostered collaboration between partner agencies in the review of literature on physical surrogates of biodiversity, the collation and management of data, the collection of new data, and the development of new field and data analysis approaches. National-scale marine environmental data were updated, new variables were developed, and the data were formatted to enable key tasks in the Prediction and Surrogates programs. A literature review of this work was published. The collective knowledge of the partners was used to select four survey areas representing a useful range of seabed habitat types in the Australian marine estate (Figure 2). Close collaboration and additional in-kind contributions by the partners enabled the acquisition of accurately co-located physical and biological data, a prerequisite for the robust testing of surrogacy relationships. Oceanographic modelling of inshore and shelf environments was employed to test the utility of seabed exposure as a biodiversity surrogate and to develop a model of ecological disturbance regimes on the continental shelf.

New approaches were developed to ensure quality and consistency in the collection and analysis of seabed multibeam acoustic and video data across the survey areas. In particular, the robust analysis of co-variance between physical and biological attributes required fine-scale multibeam data and advanced spatial analysis and statistical modelling techniques, following the lead of the Prediction Program.

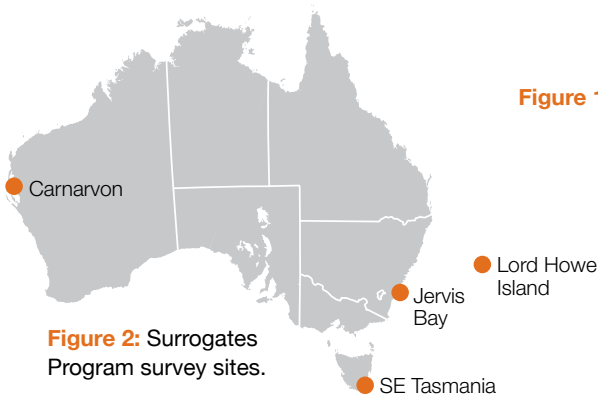


Figure 2: Surrogates Program survey sites.

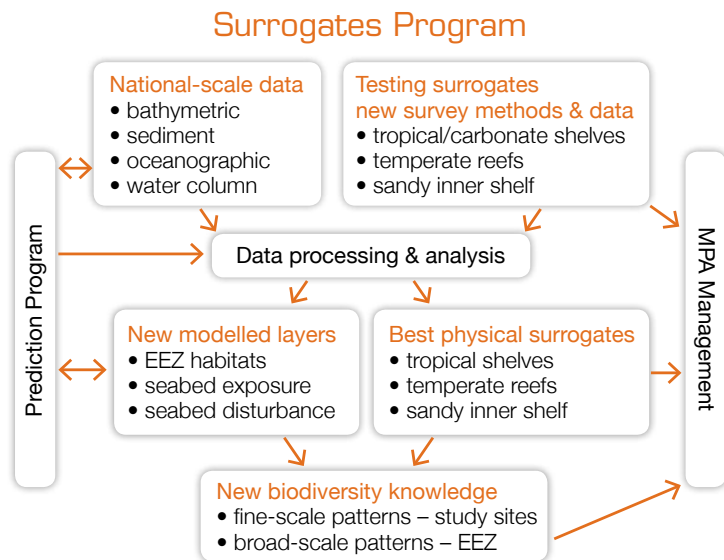


Figure 1: Work flow and linkages for the Surrogates Program.

Outputs

Outputs of the program contribute to a better understanding of surrogacy. They are useful for managing the marine estate and will enable further research into biodiversity patterns, key ecological processes and features. They include:

- > New and updated national-scale marine physical environmental datasets delivered to Marine Hub partners to develop new national biodiversity maps to support marine bioregional planning.
- > National datasets provided to the Environmental Resources Information Network (ERIN) of the Department of Sustainability, Environment, Water, Population and Communities (DSEWPaC) to support the prediction of distributions of listed species, and an online report on the data.
- > Accurately co-located seabed physical and biological data for the survey areas (Table 1), with data managed by relevant institutions and provided to managers of the marine parks and marine planning regions surveyed.
- > New seabed exposure and fetch models for the inner shelf of south-eastern Australia and the Carnarvon Shelf, and exposure and ecological disturbance regime models for the entire continental shelf.
- > Archived seabed biological specimens, including new infauna and epifauna species, lodged with museums.
- > Peer-reviewed online reports and papers in scientific journals. These include a review of physical surrogates of biodiversity and the results of testing physical surrogates of seabed biodiversity on the tropical north-west shelf, south-eastern temperate rocky reefs and a sandy embayment, and a mid-ocean carbonate shelf.
- > Visualisations of the seabed survey areas, media pieces, Hub newsletter articles, technical workshops, national and international conference presentations and special sessions on surrogacy research.

Outcomes

The new knowledge of surrogates and seabed ecological processes directly supports the management of the marine estate and places Australia at the forefront of this research. Key outcomes to date are:

- > Improved predictions of marine biodiversity around Australia.
- > Greater confidence in the effectiveness of a surrogates approach for biodiversity mapping and modelling.
- > A template for national inter-agency collaboration in surrogacy research.
- > New data and knowledge of the distribution of seabed biodiversity have helped to guide the review of marine park zoning at Jervis Bay and Lord Howe Island.
- > New information on the distribution of habitats and communities on the Carnarvon Shelf and south-eastern Tasmanian shelf to support marine bioregional management.

Table 1: Co-located physical and biological data collected at the four survey sites.

Survey site	Multibeam sonar (km ²)	Sediment and (infauna) samples	Epifauna samples (sorted)	Underwater video (km)	Seabed exposure (grid size)
Carnarvon Shelf	1090	265 (144)	226 (110)	61	150 m
South-eastern Tasmania inshore and shelf	308	25 (0)	–	69	1 km
Lord Howe Island Shelf	420	36 (33)	6 (0)	0.5	-
Jervis Bay	50	76 (74)	–	40.5	140 m

National data and data management: supporting a national picture of biodiversity

Marine physical environmental data were required in a consistent scale and format for national-scale seabed habitat mapping and biodiversity predictions in the Marine Biodiversity Hub.

Objectives

The objective was to collate and develop useful marine data layers with national coverage. The data were required in a common format and with comprehensive metadata to enable sharing by Hub partners and the wider marine science community. The new survey data collected by the Surrogates Program also requires appropriate management.

Approach

ArctInfo Grid and ESRI shapefiles were chosen as the primary spatial data storage and delivery formats because of their widespread use by research and management organisations. To ensure compliance with the Spatial Information Council of Australia and New Zealand (ANZLIC) standards and DSEWPaC data requirements, the ERIN metadata entry form was used. Data managers at Geoscience Australia (GA) and CSIRO have overseen the data management, including data quality control and formatting. The datasets will be linked to the Australian Ocean Data Network (AODN) for discovery and sharing.

Data were obtained by updating the existing set of national marine data (initially compiled for the National Marine Bioregionalisation in 2003) and new data were derived from the existing layers where needed (such as uncertainty for water column attributes: Figure 3). The new dataset is described in a peer-reviewed report available online and the

data have been delivered to DSEWPaC. The new survey datasets collected by the Marine Biodiversity Hub are being managed by the partners to ensure they are appropriately formatted, archived, fully described in metadata, provided to the department and discoverable via internet portals such as the AODN.

New knowledge and opportunities

- > Collation and distribution of 37 national marine environmental data layers that fall into five categories: bathymetry and geomorphology; seabed sediment; seabed exposure; bottom-water nutrients and physical chemistry; and surface water parameters.
- > Data discoverability and access have been enabled through compilation of comprehensive metadata and by listing the data in the AODN and websites at CSIRO and GA.
- > New survey data are appropriately managed in corporate databases by partners and museums: multibeam sonar, sediment, exposure (GA); video/still images (Australian Institute of Marine Science (AIMS), GA, University of Tasmania); infauna samples, sponge and other epifauna samples (WA Museum; Australian Museum; Museum of Victoria).

Management agencies such as ERIN now have access to new and updated national datasets of a range of marine environmental parameters. These data can support existing modelling of protected species habitat and guide the environment, assessment and approvals process. They also provide the foundation for future data collection initiatives to monitor change in the marine environment.

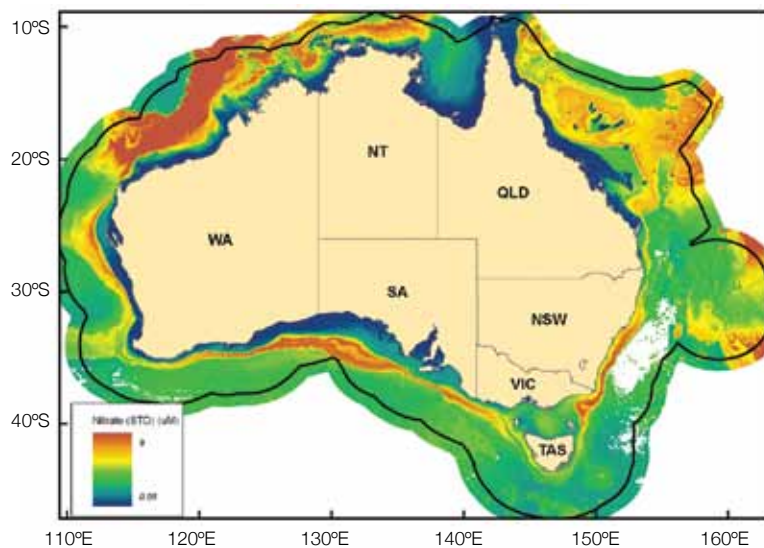


Figure 3: One of the new national data products: bottom water nitrate level, standard deviation.

Seabed exposure and disturbance: new measures for predicting biodiversity

An important influence on the biodiversity of the continental shelf and coast is the exposure of the seabed to shear stress produced by waves, wind, tides and ocean currents. Several exposure models were developed to test exposure as a surrogate for benthic biodiversity and estimate where exposure results in seabed disturbance.

Objective

To test the influence of exposure on seabed biodiversity and its utility as a surrogate for biodiversity patterns.

Approach

Seabed exposure parameters were produced using oceanographic and fetch models for the four study areas, including coastal south-eastern Australia. The parameters were tested as surrogates of community and genera-level algal diversity in Tasmania, where there is a wide range of wave exposure conditions, and for infauna species richness and abundance at the other study sites (Lord Howe Island, Jervis Bay, Carnarvon Shelf). At the national-scale, shelf exposure parameters and an ecological disturbance regime index were produced using the GEOMACS hydrodynamic model to understand the influence of seabed exposure on broad-scale patterns (10 km grid) of biodiversity on the continental shelf. These exposure parameters for the entire shelf were also required by the Prediction Program.

Key findings

For the coasts of Tasmania and south-east Australia, the wave and fetch models provide grids of exposure indices with a resolution of approximately 1 km (Figure 4).

The indices were tested as surrogates for macroalgal diversity patterns in Tasmania. They explain up to 18% of community level patterns and up to 37% of variance in the occurrence and cover of algal genera. At Lord Howe Island, exposure parameters for

representative points on the shelf proved useful surrogates of infauna diversity, especially species richness. For Jervis Bay and the Carnarvon Shelf, exposure parameters for typical wave regimes produced using the shallow-water SWAN model (150 m grid resolution), were generally less important than seabed morphology and sediment variables as predictors of infauna diversity.

At the national-scale, the GEOMACS modelling indicates that disturbance regimes are likely to occur on about 20% of the Australian shelf, most extensively in the Gulf of Carpentaria, sections of the north-west shelf, eastern Great Australian Bight, northern Bass Strait and southern Great Barrier Reef. These areas may have relatively high levels of seabed biodiversity.

New knowledge and opportunities

The new shelf exposure parameters better express the distribution of seabed shear stress. These data and the new coastal relative fetch indices have been used in broad-scale seabed biodiversity modelling tasks in the Prediction Program. The national seabed disturbance model is quantitative examination of the likely distribution of disturbance regimes on the shelf. The utility of the disturbance index as a surrogate for broad-scale biodiversity can now be tested using field data. This work identified broad-scale ecological processes that shape the distribution of biodiversity on the shelf.

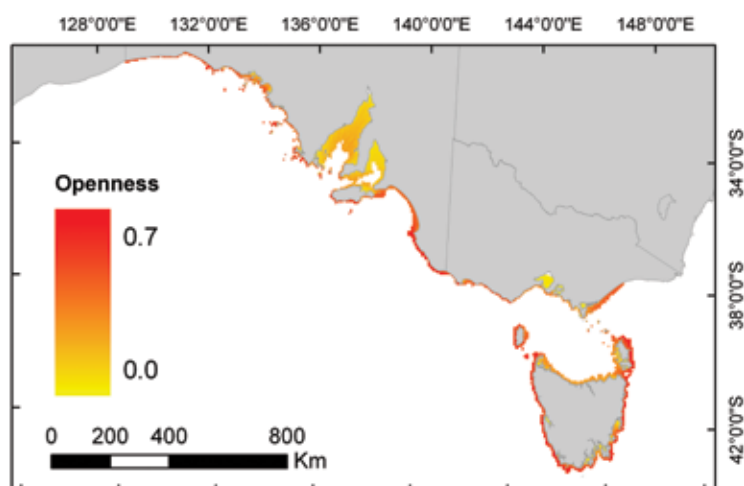


Figure 4: Extent of the wave exposure grid calculated for shallow temperate waters of south-east Australia. Values shown are of the fetch-based index 'openness', the unweighted sum of fetch in all directions from a gridpoint.

Cost effective methods for discovering and monitoring biodiversity: developing a national approach

A key element of the Surrogates Program was the adoption and development of field and data analysis approaches that could be applied widely to support nationally consistent marine environmental discovery and monitoring. Multibeam acoustics and underwater video/still images were identified as cost-effective methods of obtaining field data at large spatial scales. These were optimised for measuring seabed biodiversity and testing surrogacy relationships.

Objectives

The collection and analysis of accurately co-located multibeam acoustic data, towed underwater video footage and seabed still images.

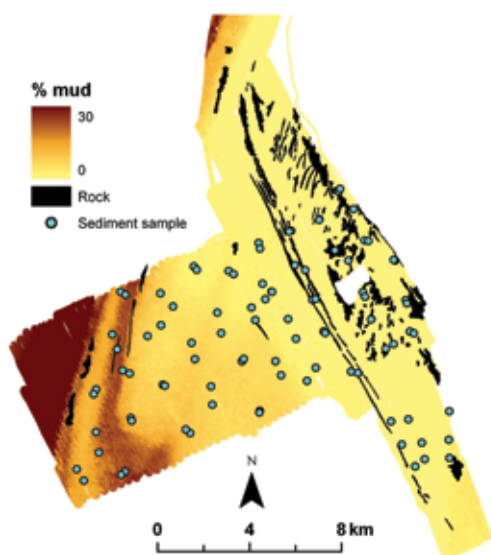


Figure 5: Seabed sediment modelling using multibeam sonar data, showing predicted mud content (%) and sample locations for Point Cloates on the Carnarvon shelf.

Approach

Two advanced multibeam sonar systems (Simrad EM 300 and 3002) were used to acquire high-resolution continuous coverage bathymetric and backscatter data layers for the surrogacy research. Seabed morphological and textural variables derived from the multibeam data were tested as surrogates of benthic biodiversity. These derived data were also used to predict continuous layers of seabed sediment properties based on sediment sample point data using machine learning models (Figure 5). Multibeam backscatter processing procedures and algorithms were developed in collaboration with Curtin University of Technology to provide high quality remotely sensed seabed textural data.

To capture key elements of biological diversity, AIMS, UTAS, GA and the University of Sydney combined their expertise in underwater video and autonomous underwater vehicles (AUV) to develop video survey plans and data collection and analysis methods. New approaches to video/AUV surveys were also discussed at Hub workshops and national conference special sessions that have helped develop a national approach to mapping seabed biodiversity.

New knowledge and opportunities

Multibeam sonar systems provide the key enabling data layers for surrogacy research. Multibeam bathymetry and backscatter data and their derivatives were useful surrogates for seabed biodiversity in all the environments examined at scales ranging from metres to hundreds of kilometres. Multibeam sonar data delineated key physical features of seabed habitats, enabling efficient collection of seabed biological samples. They also provided the essential bathymetric grid for hydrodynamic modelling.

In the Tasmania study, backscatter data were classified into substrate types with an associated level of uncertainty, while multibeam data formed the geospatial grid on which to precisely locate repeat AUV surveys. These new approaches support the monitoring of benthic ecosystems, and research on monitoring marine protected areas. Multibeam data and seabed images have also been used to build accurate and visually appealing three dimensional fly throughs of the survey areas.

Marine bioregional management will benefit from effective monitoring of ecosystem health and the performance of management interventions, including marine reserves. This developing national approach to biodiversity discovery and monitoring – which includes new technologies and their integration through a collaborative inter-agency approach – will support that need.

Testing surrogates of biodiversity: case studies of representative systems

> Carnarvon Shelf

The Carnarvon Shelf is representative of tropical shelf systems that characterise the central western shelf sector of the North-west Marine Region. Surrogacy relationships and biodiversity mapping is important in this region to support natural resource management in the face of rapidly expanding oil, gas and tourism industries.

Objectives

The case study aimed to identify the best physical surrogates of benthic biodiversity for a large geographic area by analysing a range of co-located physical and biological data. It also sought new insights into ecological processes on this shelf that link physical environmental variables with biodiversity patterns.

Approach

The collaborative Carnarvon Shelf research (GA, AIMS, WA Museum) collected unique, comprehensive co-located seabed biophysical data to identify benthic environments off Ningaloo and enable robust analysis of biodiversity surrogates, patterns and processes in north-western Australia. The research complements state-based work (AIMS, University of WA, Curtin University) in Ningaloo Marine Park and provides new environmental information and biodiversity data for the North-west Marine Region.

The survey area extends across the continental shelf offshore Ningaloo Reef and encompasses 1038 km² of Ningaloo Marine Park (state and Commonwealth waters). An additional 52 km² was mapped north-west of the Muiron Islands in the mouth of Exmouth Gulf. The collection of data was designed to enable robust testing of physical surrogates for a range of measures of

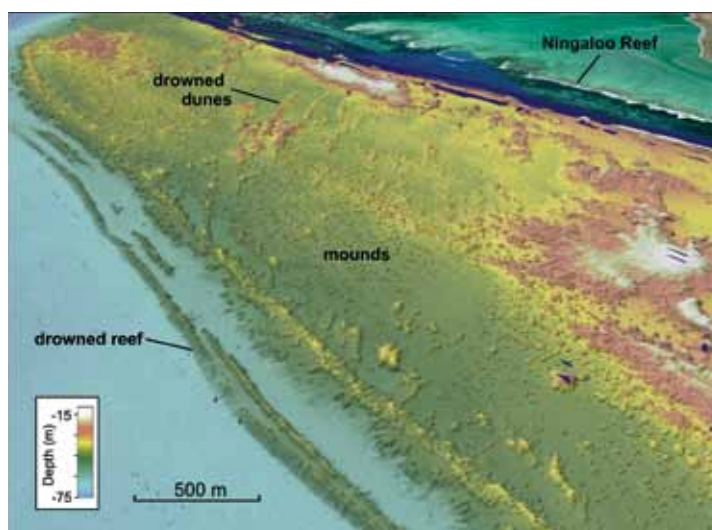


Figure 6A: Perspective image of Carnarvon Shelf at Point Cloates with geomorphic features indicated.

seabed biodiversity (benthic habitats, epibenthic and infaunal species and assemblages) across a range of typical north-west shelf seabed environments (coral reef, sponge gardens, sand waves and flats). Surrogacy relationships were tested using a machine learning model (Random Forest Decision Tree).

The physical data include multibeam sonar bathymetry and backscatter, oceanographic records and model outputs (such as shelf currents; bed shear stress) and sediment characteristics from 265 samples. Biological data comprise records of infauna from 144 grab samples, epifauna from 110 epibenthic sled samples, and seabed characterisations of habitat and epibenthos derived from underwater towed-video footage (and still images). The new biological records will be integrated with collections from other parts of the north-west shelf to provide a regional database.

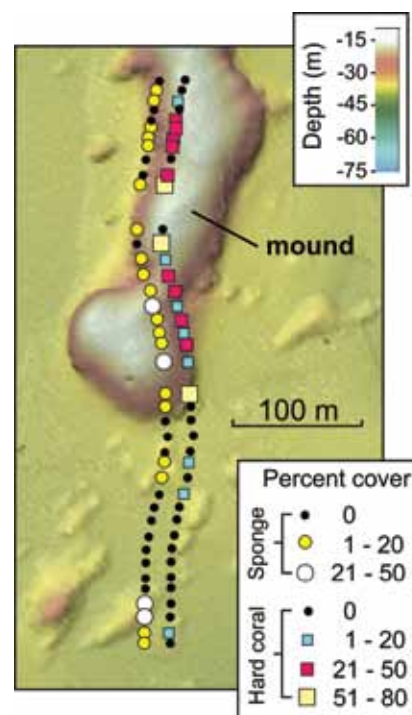


Figure 6B: Observed occurrence of corals and sponges along a 500 m video transect at Point Cloates.

Key findings

A total of 1090 km² of multibeam bathymetry and backscatter data was collected, processed and gridded at 3 m spatial resolution. Seabed geomorphic features derived from these data were useful broad-scale surrogates of benthic habitats of the Carnarvon Shelf (Figure 6A). For example, in the northern half of the Marine Park, relict shoreline ridges and drowned cemented coastal dunes are preserved on the shelf and support modern coral reefs and sponges (Figure 6B). In contrast, most (~90%) of the seabed across the Carnarvon Shelf is covered by bedforms of sand and gravel that support diverse infauna but few epibenthic organisms.

The best surrogates for sediment infauna biodiversity (Figure 7) are the percentage of gravel, seabed roughness, and depth. However, the most useful surrogates and their predictive power vary along the shelf. In the south (Gnaraloo) where the shelf is broadest, the strongest surrogate for infauna diversity is percentage of gravel while in the north, where the shelf narrows, (Mandu, Pt Cloates), seabed morphological parameters are also useful surrogates, but have lower predictive power.

Epifaunal samples collected in epibenthic sleds from low-lying rock outcrops recorded the highest biomass and diversity of sponges, as defined by species richness (number of species) and abundance and high numbers of large branching and massive growth forms. Significantly, sponge gardens are clearly identified in towed video footage, often as small patches in areas with low-relief reef. These results show that towed video footage is an effective non-intrusive method of identifying a key element of benthic biodiversity on this shelf.

Detailed mapping and sampling on the Carnarvon Shelf has enabled the development of a new robust method of producing continuous physical data layers (such as seabed morphology and sediments) that incorporates machine learning models. This new approach will enable more reliable biodiversity predictions because it provides more accurate estimates of seabed parameters beyond sample points than previous interpolation techniques. These new layers can be used as surrogates for biodiversity across an area of interest.

New knowledge and opportunities

A major new sponge database has been developed for the Carnarvon Shelf (678 specimens; 266 species/112 genera) and a digital catalogue will be available on the AIMS website. The Carnarvon data are housed with that relating to other collections of sponges from the north-west shelf held by museums. These data will enable the regional mapping of sponge diversity for assessing the utility of sponge diversity as a surrogate for general seabed biodiversity (such as other epifauna, infauna and fish).

The Carnarvon Shelf field survey has characterised the influence of seabed morphology and sediments on infauna and sponge biodiversity on the shelf of the North-west Marine Region. This new knowledge can be used to examine the adequacy of MPAs and the significance for marine biodiversity of Key Ecological Features in this region. An understanding of these features can guide the sustainable use and protection of these systems.

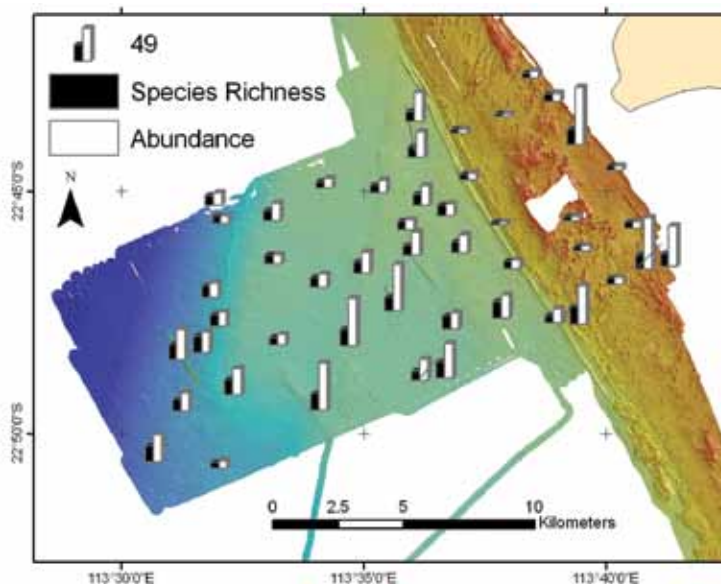


Figure 7: Diversity of sediment infauna across the Carnarvon shelf at Point Cloates, represented by number of species and total abundance in each sample.

> Lord Howe Island Shelf

This mid-ocean subtropical shelf is thought to be little impacted by human activities, making it a useful site to analyse relationships between seabed biota and physical attributes and provide new insights. Its physical environment is representative of other remote tropical shelf systems, and the results are potentially transferable to locations such as Norfolk Island and the Queensland Plateau.

Objectives

The survey was undertaken to determine habitat information that could be derived from multibeam sonar mapping and sediment sampling of the shelf around Lord Howe Island and to test surrogates of infauna diversity using variables that represent shelf morphology, sediment and exposure.

Approach

Multibeam sonar, sediment and infaunal samples were collected on a Marine National Facility (RV *Southern Surveyor*) survey in collaboration with the University of Wollongong (led by Prof. Colin Woodroffe). Multibeam bathymetry data were integrated with shallow-water bathymetry derived from a satellite image (QuickBird). The Lord Howe Island Marine Parks managers helped to design the survey plan which complemented video surveys by NSW Department of Environment and Climate Change. Co-variance of the physical and biological data was tested using machine-learning models (Boosted Decision Tree and Generalised Regression Neural Network).

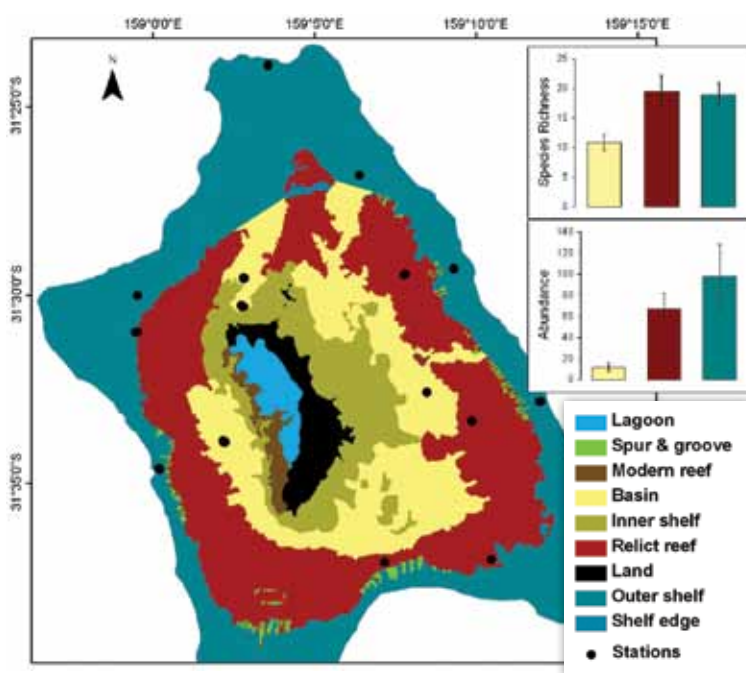


Figure 8: Geomorphic features of Lord Howe Island Shelf and summary of infaunal diversity (species richness and abundance) for basin, relict reef and outer shelf habitats.

Key findings

High-resolution bathymetric data covering 420 km² at 4 m grid resolution reveal the complexity of the shelf morphology which is dominated by a relict barrier reef (~35 m depth; 7000 years old) around Lord Howe Island. The relict reef is 20 times larger than the modern coral reef and shows that a relatively minor change in past climate had a major impact on coral reef growth. This record provides a useful context for assessing the potential impacts on coral reefs of future climate change.

The relict reef produces significant variation in seabed exposure and sediment characteristics across the shelf. Infauna diversity (163 operational taxonomic units recorded in 2139 individuals from 33 samples) changes in concert with these physical variations (Figure 8). Sediment sorting, shelf morphology and seabed exposure are important predictors of infaunal species, and effective surrogates of infaunal assemblages.

Infaunal abundance and species richness increased offshore, with high abundances on the relict reef and outer shelf. Most species were rare (47% of species had ≤ 2 individuals), several new species were discovered, many species appear to be endemics, and assemblages were dominated by five species that made up 55% of all infauna. High numbers of suspension feeding infauna on the outer edge of the relict reef indicate a reliance on oceanic currents for food.

New knowledge and opportunities

This work demonstrates the physical complexity and associated biodiversity pattern that may exist on mid-ocean shelves and provides an approach for rapidly and accurately mapping shelf habitats and biodiversity. It has provided marine park managers with a more comprehensive understanding of this shelf system, including the ecological processes that link seabed morphology, sediments, exposure and infauna biodiversity.

> South-eastern Tasmania temperate shelf bedrock reef

Australian temperate rocky reefs are poorly understood with respect to their cross-shelf distribution, overall extent, physical complexity and associated biodiversity. As planning for conservation of biodiversity is limited by this lack of knowledge, new approaches are needed. The bedrock reefs of south-eastern Tasmania are likely to be representative of temperate reef systems known to occur along the continental shelf of south-eastern Australia. The survey region incorporates reefs located across various shelf depths and degrees of wave exposure, from outer shelf to harbours and estuaries, enabling comprehensive testing of a range of physical attributes as surrogates of reef biodiversity.

Objectives

The primary objective was to identify the best physical surrogates of benthic biodiversity on bedrock reefs in a temperate shelf setting, with a focus on habitats and epibenthic assemblages. A second objective was to develop new approaches to seabed mapping that are optimised for surrogacy analysis. This involved testing and integrating new survey technologies (multibeam sonar, underwater video, AUV imagery) for mapping Tasmanian bedrock reef and adjacent shelf habitats, and developing these approaches for establishing baselines for monitoring reef ecosystem health. It was also expected this work would yield initial insights into shelf processes driving biological patterns on bedrock reefs.

Approach

Research in south-eastern Tasmania was a collaborative effort involving GA, the Tasmania Aquaculture and Fisheries Institute and the Australian Centre for Field Robotics (University of Sydney). Surveys were undertaken to collect co-located multibeam sonar bathymetry and seabed video and images from five locations along the south-eastern coast and shelf of Tasmania, including reefs inside and outside state and Commonwealth marine reserves. Approximately 300 km² of multibeam bathymetry and associated acoustic backscatter data were collected, processed and gridded at 2 m spatial resolution. A wide range of seabed morphological and textural parameters were derived from the multibeam data. Video footage was used to identify benthic habitats and epibenthic assemblages, while species level identifications were undertaken using high-resolution finer-scale underwater images (Figure 9).

A key aspect of this project was the development of methods for deriving seabed morphological and textural parameters from multibeam sonar data, and seabed substrate and species identifications from high resolution seabed images (video, AUV). These fine-scale, co-located biophysical data were required to accurately map seabed features, identify useful surrogates and predict patterns of biodiversity on reef areas beyond the video and AUV-image tracks. Seabed parameters derived from the multibeam sonar data were used to predict the distribution of benthic substrata (identified in AUV images) throughout the study areas using a range of machine learning models. Boosted Regression Tree models and Species Archetypes analysis (developed in the Prediction Program) were then used to identify useful surrogates and predict the occurrence of key taxa or species groups onto predicted reef substrates across the study area.

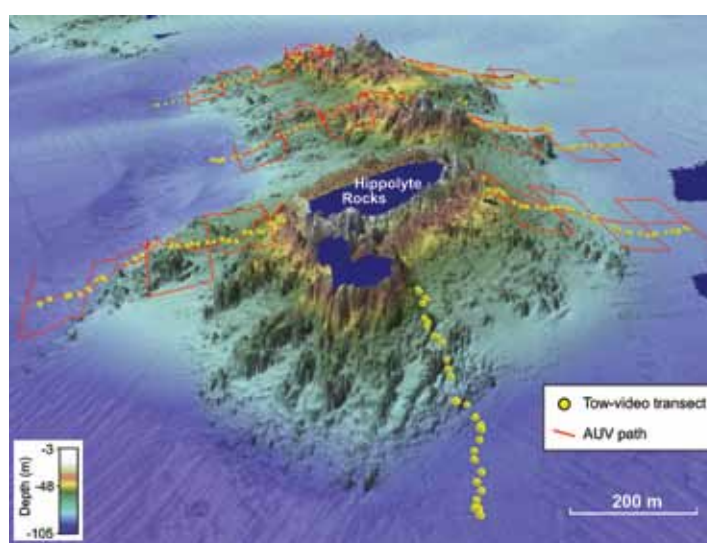


Figure 9: Multibeam sonar image of Hippolyte Rocks, Tasman Peninsula showing survey lines for underwater video and AUV.

Key findings

Bedrock reefs cover 60 km² of the survey area with 30% of these reefs in <45 m water depth and dominated by macroalgal (kelp) assemblages (Figure 10). The remaining 70% of reef area is below 45 m and covered in diverse sponge gardens. Water depth, substratum type and geomorphology (including seafloor curvature and aspect) were often correlated with reef biota and therefore these multibeam derivatives are identified as potentially effective surrogates of reef biodiversity in this setting. Statistical predictions of seabed type (including reefs) with accuracies of up to 66% were achieved, demonstrating that quantification of seabed morphology based on multibeam sonar data can be used to derive robust products of seabed complexity.

Variables derived from multibeam sonar data were found to be useful predictors of the spatial distribution of benthic biota on bedrock reefs. Results of Boosted Regression Trees analysis show depth and predicted substratum are important variables determining the distribution of canopy algae, which was more likely to be found on reef and boulder substrates and only to depths of up to approximately 50 m. Variables derived from multibeam bathymetry and backscatter data were also important for predicting the distribution of benthic invertebrates. For example, soft corals were more likely to occur where the seafloor is relatively steep and has greater topographic complexity.

By integrating sonar data with video and AUV images we have been able to determine the representativeness of seabed habitats found in Commonwealth Marine Reserves (CMR). For example, the Huon CMR area we mapped (south Friars) is representative of habitats, assemblages, and commercially important species that occur in similar water depths outside the reserve (e.g. north

Friars). These off-reserve areas can therefore be used as reference sites for monitoring the effectiveness of protection afforded by the Huon CMR using the techniques developed in this program. This integrated approach also resulted in an improved understanding of the distribution of the invasive screw shell (*Maoricolpus roseus*) in Tasmanian shelf waters. In particular, extensive beds of screw shells have accumulated around the less exposed reefs along Tasman Peninsula to provide a 'new' substratum for sponges and other invertebrates, effectively extending their natural distribution. In contrast, areas disturbed by waves and currents (e.g. The Friars) are mostly devoid of screw shells.

New knowledge and opportunities

Opportunities exist to make use of data sets of this type in areas where rocky reefs have yet to be evaluated for their conservation status. In addition, the survey techniques and integrated data analysis developed here can be employed for monitoring reef ecosystem health in MPAs, especially the integration of multibeam sonar and underwater optical technologies.

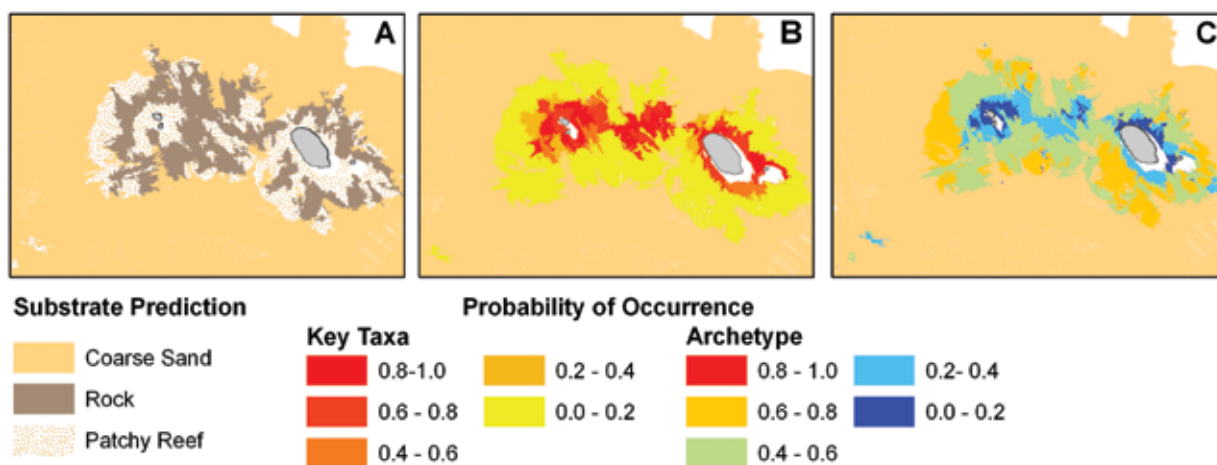


Figure 10: Model results for the Hippolyte Rocks, showing: A) Predicted substrate using Support Vector Machine Model; B) Predicted probability of occurrence of canopy algae using BRT; C) Predicted probability of occurrence of dominant corals using Archetype analysis.

> *Jervis Bay sandy inshore habitats*

The Jervis Bay study area is representative of temperate sandy nearshore to inner shelf habitats in south-eastern Australia, including areas managed as MPAs. A wide range of seabed environmental parameters were able to be tested as surrogates of infauna biodiversity at fine spatial scales.

Objectives

To identify the best physical surrogates of biodiversity in a temperate sandy inshore environment, with a focus on describing the ecological processes that link the physical environmental variables with observed patterns in infaunal biodiversity.

Approach

A field program collected co-located seabed data across sandy habitats typically found in temperate inshore waters. The area included Commonwealth waters of Booderee National Park and part of Hyams Beach and Point Perpendicular-Crocodile Head Sanctuary Zones. Physical data include ~50 km² of multibeam sonar bathymetry gridded at 5 m resolution, oceanographic records at five mooring stations, plus sediment and geochemical samples at 74 stations. Biological data include infauna records from the sediment samples, plus habitat descriptions and epifauna characterisations recorded from underwater video footage. Surrogacy relationships were tested using machine learning models. Re-sampling was undertaken at select stations for sediments, geochemistry and infauna to analyse the stability of surrogacy relationships over time.

Figure 11: Jervis Bay benthic habitats derived from underwater video.

Key findings

Five habitat types with distinct epifaunal assemblages were readily identified from video with 267 species identified from more than 13,500 specimens (Figure 11). The best physical surrogates of this infauna diversity (species richness) were seabed roughness, mud and chlorophyll a concentrations in seabed sediments and benthic mineralisation rates (indicative of reactive organic matter). Biological processes are also locally important, with mounds of tube worms forming a distinct habitat that has low infaunal diversity but high epifaunal diversity. The mounds appear restricted to areas less exposed to wave energy. Sandy habitats adjacent to these mounds have higher infauna diversity, suggesting a synergistic relationship.

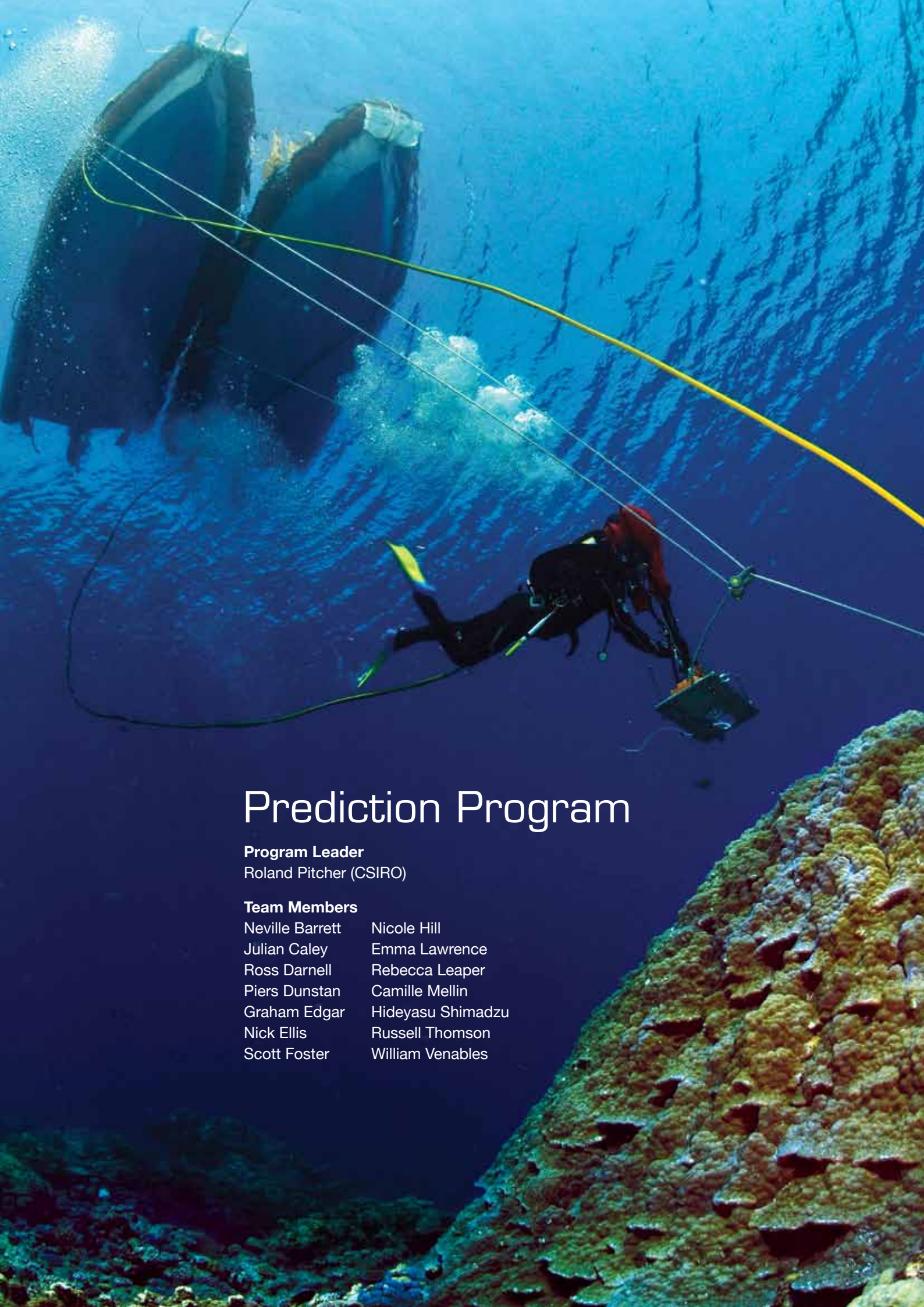
Detached and drifting macroalgae accumulate in the nearshore, forming dense thick mats (up to a metre deep) that cover the seabed. This drifted material dampens sediment re-suspension and oxygen transfer to the sediments, leading to patches of anoxic sediments and low infaunal diversity. In contrast, deeper habitats are more exposed to waves and are characterised by coarser sand that is worked into bedforms, providing habitat for a diverse and abundant infaunal assemblage dominated by crustaceans. This illustrates how the mapping of sediments and their geochemistry can uncover the processes that drive ecological patterns, and act as a surrogate for infaunal diversity in the extensive areas of south-eastern Australia where algal drift accumulates.

The input of organic matter was a major source of spatial and temporal heterogeneity in Jervis Bay sediments, generating a dynamic mosaic of potentially limiting resources and by-products (including total sulphur).

New knowledge and opportunities

In 2009, managers of Jervis Bay Marine Park (NSW DECC) used the new high-resolution multibeam data to map areas of inner shelf reef within a Sanctuary Zone and assist with a review of park zoning. The new understanding of spatial co-variance between sediment infauna and physical factors can also support the monitoring of sandy inshore ecosystems and assist in the design of management strategies.





Prediction Program

Program Leader

Roland Pitcher (CSIRO)

Team Members

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Roland Pitcher

Prediction Program

Predicting national marine biodiversity: tools for marine conservation management

Provincial bioregions were validated and depth biomes defined in the Biodiversity Program. Biodiversity patterns at these scales are used to develop a comprehensive national marine reserve system. Locating representative marine reserves within these provinces and bathomes requires a finer scale classification of marine biodiversity. Existing marine biological survey data alone are insufficient for mapping biodiversity patterns at this finer scale. Surrogates for biodiversity patterns must therefore be drawn from more broadly available environmental data. This program has used the surrogates approach to develop national maps of predicted marine biodiversity, and associated uncertainty, for grids of approximately 1 km² around Australia. Resulting maps have been used by marine bioregional planners in reserve design.

Objectives

The primary objective of the Prediction Program was to quantify relationships between marine biodiversity and environmental surrogates at a scale useful to marine planners. Models were developed that predicted patterns of marine biodiversity from environmental data. This was done at large regional scales in four major marine biomes: the continental shelf, the continental slope, tropical coral reefs and temperate rocky reefs.

Approach

Areas of coexistent broad scale biological and environmental data were used to develop methods of modelling predicted biodiversity patterns in data-poor areas. Investigations included:

- > the explanatory performance of models and confidence of predictions;
- > the importance of different environmental surrogates for prediction;
- > the scales at which different surrogates have predictive value;
- > the sensitivity of predictions to uncertainty in the interpolated surrogates; and
- > the extent to which selected taxa (such as fishes) were biological surrogates for biodiversity patterns in other taxa (such as invertebrate groups).

The program began by collating broad geographic and environmental biological survey data to match environmental data from the Surrogates Program. 'Biodiversity' in this instance was defined as patterns in the numbers, distribution and abundance of species and their communities. These patterns were defined by structure, composition, and co-occurrence (species-groups).

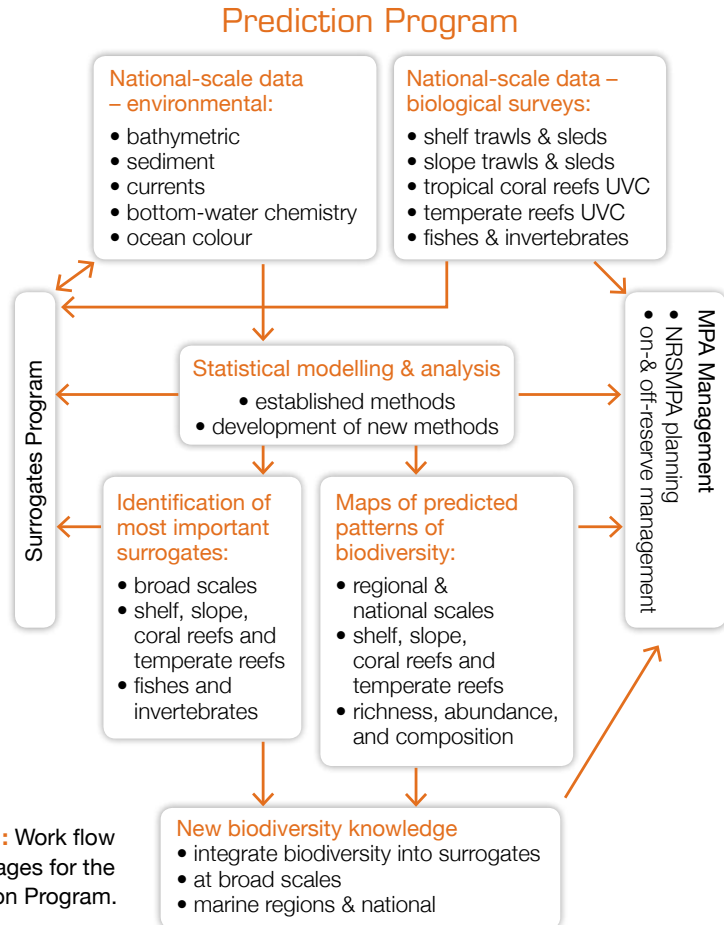


Figure 1: Work flow and linkages for the Prediction Program.

Outputs

New methods and models were developed to predict biodiversity structure, composition, and species-groups. Prediction performance ranged from ~10% to ~80% depending on the variation in the data. Important predictors included temperature, nutrients, depth, sediments, oxygen, salinity, exposure, irradiance, bedstress, and chlorophyll. The relative importance of these predictors varied for different biota, regions and spatial scales.

Biodiversity indices (such as richness) were used to aggregate species-level variation. These indices tended to be predicted with less uncertainty than composition, which includes species-level variation.

Predictions can be highly sensitive to interpolation uncertainty in the surrogates, and the impact of this sensitivity on management decisions should be considered.

Within provincial bioregions and across a limited depth range, the biodiversity patterns of fishes (or any other group) were poor surrogates for biodiversity patterns in other taxa. This contrasts with the finding in the Biodiversity Program that fish were good surrogates for other taxa at the broader provincial level.

- BI: benthic irradiance
- CH: chlorophyll A (average)
- DP: depth
- MD: % mud
- no: nitrate (std dev)
- NO: nitrate (average)
- o2: oxygen (std dev)
- O2: oxygen (average)
- SI: silicate (average)
- SN: % sand
- st: sea surface temperature (std dev)
- TM: sea bed temperature (average)

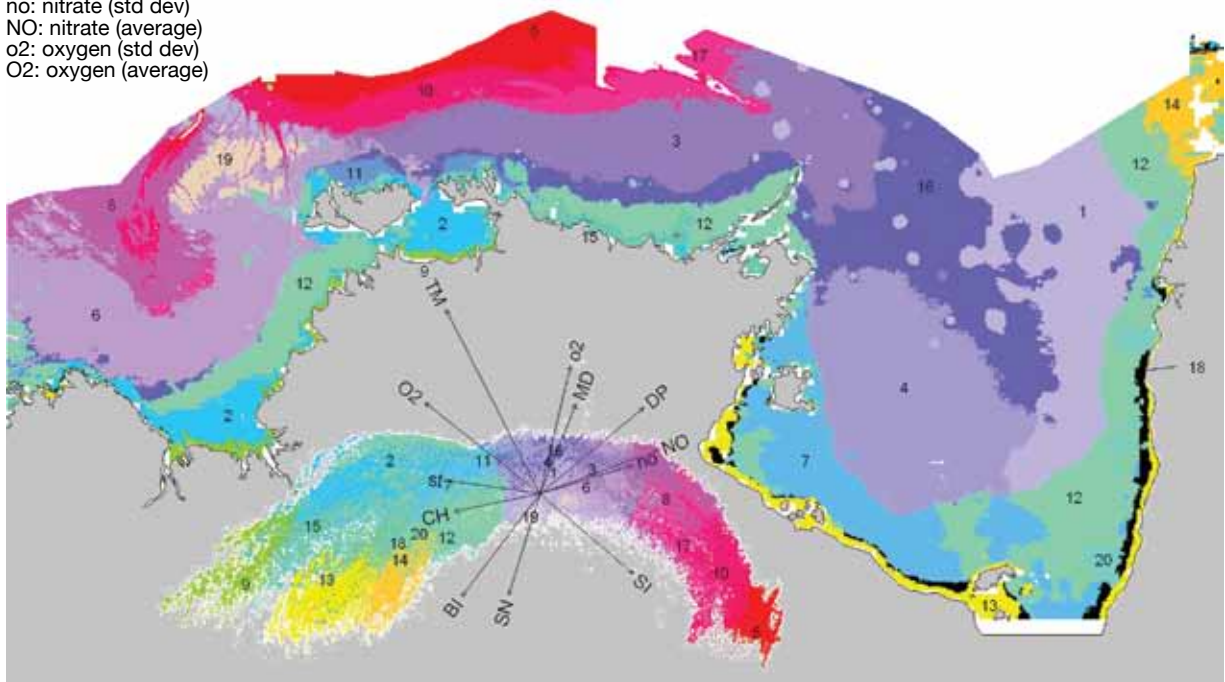


Figure 2: Predicted seabed biodiversity assemblages of the North Marine Region Marine Biodiversity Hub Product Description (2009).

New knowledge and opportunities

The Hub has predicted patterns in marine biodiversity from environmental surrogates and produced the first ever national maps of biodiversity to support marine bioregional planning (Figure 2). These were provided to the Department of Sustainability, Environment, Water, Population and Communities (DSEWPaC) for the south-west, north-west, north and east marine regions, and to states for coastal waters planning. The maps demonstrate the usefulness of combining environmental and biological datasets through predictive models and will support the transition from planning to management, including detection of future change. However, surrogates do not account for the major proportion of pattern in marine biodiversity. Biological and environmental data are sparse for large areas of shelf and deep water, and surveys of invertebrates and plants are only few and localised. These data gaps, and ongoing statistical challenges, provide opportunities for further research.

Patterns, varieties and groups of biodiversity

Structure

Structure is the numeric patterns of species at sites, including the number of species (species richness), the total number of individuals, and of each species (abundance), and the relative distribution of abundance among species (evenness). Species may be relatively even in abundance, or some may be numerically dominant. Biodiversity structure may be jointly represented by rank-abundance-distributions (RADs), an ordering of the observed counts of species at a site from most abundant to least abundant. Species identities are not retained. These attributes at sites are sometimes referred to as alpha diversity.

Composition

Composition relates to the identity and variety of species at sites, and is measured as changes in the mixture of species identities and abundances between sites in a region. A relatively homogeneous mix of species and their abundances over an area is sometimes called a 'community'. This term typically implies that composition is organised by interaction among the constituent species; the term 'assemblage' is often used in preference. Species identities are important in composition, and several assemblages may be present in a region if composition changes appreciably among sites. The contribution to biodiversity of changes in composition over an area is sometimes referred to as beta diversity.

Species groups

Some species may consistently co-occur at high and low abundances, and be co-absent, at locations in a region. This is another type of compositional pattern where species identity is important, and such species with a common spatial pattern in their abundances may be called a 'species-group'. Several such species-groups may occur in a region.



Biological survey datasets: the basis of biodiversity prediction

Large-scale environmental and biological data were provided from which to predict patterns of marine biodiversity distribution for Australia.

Objectives

- > Scope available biological survey datasets, and assess and acquire those suitable for biodiversity prediction.
- > Reformat datasets into a structure suitable for matching to the environmental layers from the Surrogates Program, and for prediction analyses.

Approach

Candidate biological survey datasets were sought from marine research agencies, metadata was acquired and suitability for prediction was assessed. Suitability criteria included broad spatial scale, broad coverage of environment space (wide contrast in surrogates), broad coverage of taxa, representative sampling methods, and availability. The suitable data were acquired, loaded into a relational database, re-formatted to a standardised structure, and matched to a 0.01° grid of environmental data layers. These formed the basis of the biodiversity prediction analysis tasks. Additional datasets were obtained for biodiversity predictions to support DSEWPaC's marine bioregional planning process.

Key findings

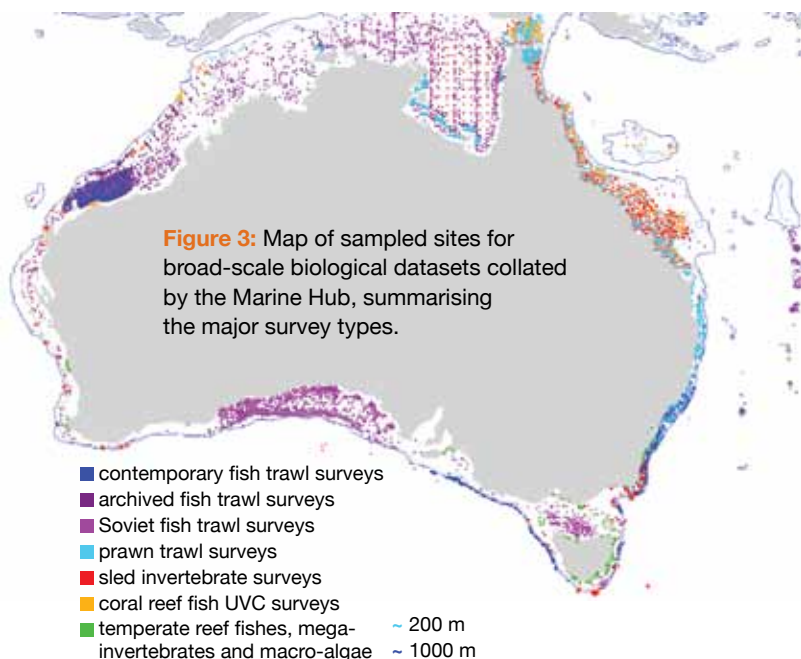
Biological survey datasets from the continental shelf and upper slope, and tropical and temperate reefs, comprised primarily fishes, with only a few including invertebrates and marine plants^{P45}. Most suitable datasets were provided by Hub partners, and by NSW and Queensland fisheries agencies.

The broadest datasets were shelf and slope fish trawl surveys from CSIRO. The most extensive were archived Soviet fish surveys from the 1960s and 1970s. These had a relatively limited suite of larger fishes and numerous taxonomic issues. Small fishes and discrete invertebrates sampled by prawn trawl surveys were restricted to northern and eastern Australia. Comprehensive surveys of invertebrates were localised. Visual surveys of coral reef fishes were available for selected reefs across tropical Australia, and those for temperate rocky reef fishes, mega-invertebrates and macro-algae were patchily distributed across southern Australia.

This collation of datasets enabled the prediction and mapping of biodiversity in support of marine bioregional planning (Figure 3). Data-poor areas included seabed deeper than ~1500 m, large areas of shelf, and the sampling of invertebrates, smaller fish species, and tropical and temperate reefs.

New knowledge and opportunities

The utility of collating contemporary and archived datasets to predict patterns in marine biodiversity and their value to DSEWPaC and state government agencies has been demonstrated by the contribution of the biodiversity predictions to marine planning. This standardised collation of datasets is a unique asset that underpins Australia's leadership in marine science and management. It will continue to support the transition from marine bioregional planning and MPA establishment to management and implementation, including monitoring and 'off-reserve' management. However, critical gaps remain in geographic and taxonomic coverage, as well as sampling methods. These gaps need to be prioritised by the need for management decisions and conservation planning, and by the likelihood of biodiversity discovery.



Biodiversity structure: species richness and abundance

The number of species and their abundance sampled at survey sites are among the fundamental attributes of alpha diversity. They incorporate all species and individuals counted in samples, including rare species, but without information on species identities. These attributes were analysed separately in models that aimed to predict their spatial patterns from the mapped environmental surrogates.

Objectives

- > Identify the environmental drivers of species richness and abundance.
- > Incorporate possible spatial effects such as spatial dependence between contiguous sites.
- > Assess regional differences and ecosystem specificities regarding relationships between species richness or abundance, and environmental data.
- > Predict and map species richness and abundance from environmental surrogates.
- > Map these predictions across different marine systems around Australia.

Approach

Generalised linear models were developed to define the relationship between species richness (abundance) and the environmental surrogates. In addition to the environmental variables, these models included spatial information both at large scale (geographic position) and at small scale (spatial dependence)^{P41}. A range of indices were used to quantify model performance and accuracy, allowing the identification of the most important predictors of species richness and abundance. The predictions included estimates of uncertainty which were mapped to indicate on the reliability of the predicted attributes.

Key findings

Maps from predictive models identifying areas of high alpha diversity (expected species richness and abundance) for a variety of taxa were produced for coral reefs in the Great Barrier Reef (GBR) and Torres Strait and for temperate reefs in South Australia (Figure 4). Physical predictors were ranked based on their predictive ability and goodness-of-fit. Typically, sea surface temperature, salinity and nitrate concentrations were important for fish on the GBR and in the Torres Strait. In South Australia, exposure, sea surface temperature, salinity and oxygen concentrations were important for fish, and the minimum and seasonal range of sea surface temperature were important for algae. Spatial autocorrelation, or the spatial dependence that characterises contiguous sites, was important in models of coral reef fish species richness and abundance (for GBR and Torres Strait), but not significant in models predicting the species richness or abundance of fish, algae and invertebrates on temperate reefs in South Australia. This is the first time algal diversity has been modelled at this scale and extent for Southern Australia which is known for its diverse algal communities and high levels of endemism. Predictions show significant heterogeneity in species richness across the region and several diversity hotspots.

New knowledge and opportunities

Maps showing the predicted species richness or abundance are a useful tool for marine bioregional planning and management. Estimates of uncertainty associated with these maps indicate their reliability. These elements combined with predictions of assemblage composition can assist in the prioritisation of habitat for protection, environmental assessment and the approvals process. The approach can also be used to model the abundance of a single taxon, which may be useful to determine distribution patterns of iconic, protected or commercial species.

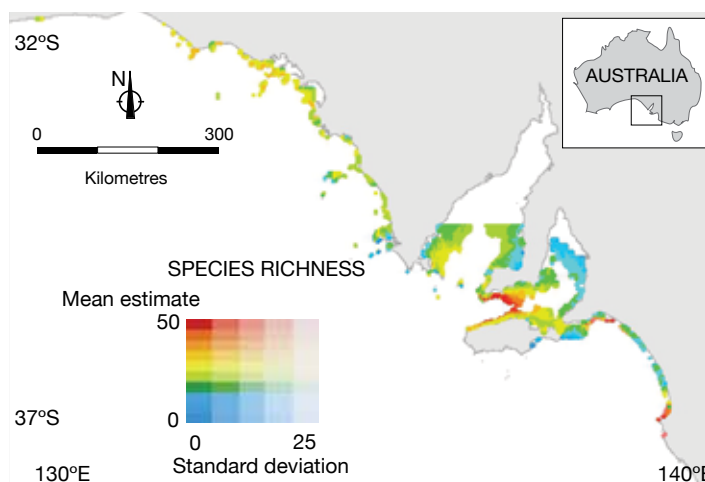


Figure 4: Spatial Generalised Linear Mixed-Effect Models in South Australia explained 43.4% of deviance in algae species richness with a mean prediction error of 12.6%^{P34}.

Biodiversity structure: rank abundance distributions

Marine surveys frequently collect many rare species that are found at only one site, and managing the resulting data is beyond the capability of most analytical techniques. Advice provided to marine planners is therefore based only on information from the most abundant species. Rank Abundances Distributions (RADs) are the ordered abundances of all species found, from the most to the least abundant, and describe all species found in a community, including the rare ones. They provide additional information on the distribution of biodiversity.

Objectives

- > Develop statistical methods that use all species contained in samples, including rare species.
- > Analyse community structure (such as the number and relative frequency of species) instead of characterisations such as community composition (requiring species identities).
- > Fit models to RADs using physical surrogates and use the models to predict RADs at new locations.

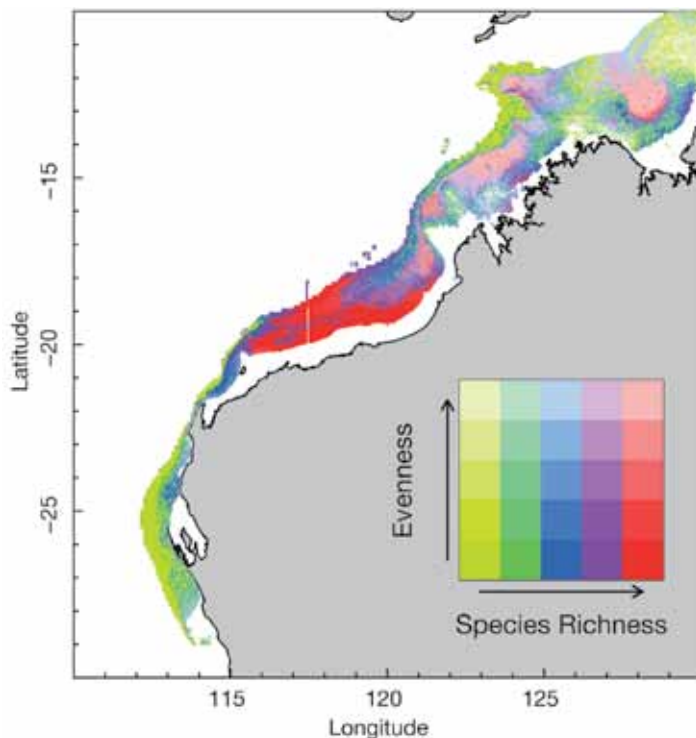


Figure 5: Changes in community structure in the North-west Marine Region can be used to identify rare community types. Biodiversity was analysed and predicted using rank abundance distributions on communities collected from the continental shelf and slope to 1500 m. Trawl sampling of demersal fish communities found 475 species: 25% at only one site and 62% at five sites or less. The complex community structure reflects average sea surface temperature and its variability, irradiance and turbidity. Rare community structure can be identified by examining changes in richness and evenness.

Key findings

The analysis allows predictions with estimates of uncertainty for three key attributes of biodiversity: the total number of individuals (N), the total number of species (S) and the evenness of the community (η). The evenness of a community is the relative abundance of all the species found, and forms the basis for the RAD. Models have been fitted for the south-west, north-west, north and east marine bioregional planning regions, for both the continental shelf and slope, and for temperate reefs to 10 m depth in South Australia, Victoria and Tasmania. The relationship between RADs and environmental gradients changes with location and species. The model predictions are used to identify biodiversity hotspots with rare combinations of species richness and evenness (Figure 5).

Approach

RADs are used as the fundamental building block for analysis. Species identities are discarded. Because they are based on ranked species, (most to least abundant), and are not dependent on species identity, community structure can be compared across multiple communities with very different species compositions. Predictions are accompanied by estimates of uncertainty. Maps of uncertainty rate the reliability of predictions and can provide a key element of management and planning.

New knowledge and opportunities

The identification of hotspots has supported significant conservation planning in recent decades. This approach adds an understanding of abundance and evenness to existing knowledge of biodiversity hotspots. Understanding which areas are characterised by rare community structure is important in conservation management. This approach has been recognised by the Global Ocean Biodiversity Initiative, an international partnership that builds on scientific criteria agreed under the Convention on Biological Diversity to identify ecologically or biologically significant areas. Australia has an opportunity to lead the continued refinement of these tools for marine planning and management.

Biodiversity composition: assemblages

The distribution of assemblages is a key input to marine regional planning. Typically they have been derived from the unguided clustering of either physical or biological samples into groups with similar attributes. These groups were then used to interpolate or predict groups for areas where no samples were available. The Prediction Program tested improved approaches to characterise and predict assemblages based on their combined physical and biological attributes. There is no single best approach to characterising and predicting assemblages; by testing and comparing different methods we can provide more consistent advice to marine planners.

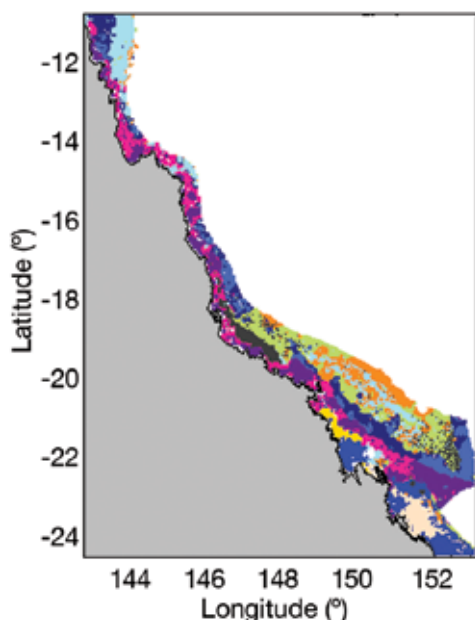


Figure 6: Bagged MRT was used to characterise assemblages of the 1213 species that occurred at more than 10 of the 1189 sites sampled by sled in the Great Barrier Reef. Five hundred bootstrap samples were generated.

Objectives

- > Apply recent improved methods that jointly relate multiple species to the environmental variables to analyse data at the community level.
- > Predict and map the expected assemblage patterns based on environmental variables.
- > Test the consistency of assemblage prediction approaches.

Approach

Multivariate Regression Trees (MRT) was used to identify and predict assemblage groups. This involved partitioning the sites by splitting site data along gradients of the environmental variables to maximise differences in species compositions between groups, and minimise differences within groups. It is a type of constrained classification analysis because the classification of sites into groups is constrained to conform to a structure that can be explained by the physical variables. The mapped partitions are categorical groups representing species assemblages with differing environmental specifications. An issue with partitioning tree methods is instability: small changes in the data can result in a very different sequence of splits and grouping of sites. We tested bootstrap aggregation (bagging), which involves taking many random selections of the data, as an extension of the MRT method. The output is the proportion of times each pair of sites appears in the same site-group: a result that can be clustered and mapped (Figure 6).

Key findings

Measures of overall model performance in terms of variation explained by the physical surrogates were available, but prediction uncertainty cannot be estimated. This is a drawback of this method. Fitting consecutive MRT models to subsets of data resulted in inconsistent tree structures, confirming the need for more robust bootstrapping methods. Bootstrap aggregation results were more stable, consistently assigning a large proportion of sites to equivalent assemblages.

New knowledge and opportunities

Community-level modelling such as the boosted MRT approach is a practical option to identify marine assemblages in locations with thousands of species (Figure 6). The benefits include an increased power to detect shared patterns of response to environmental gradients and an enhanced capacity to synthesise large amounts of information into interpretable forms. Increased confidence in the type and location of marine assemblages will help to identify appropriate conservation zones within existing marine reserves.

Biodiversity composition: patterns of β diversity

Marine bioregional planning requires maps of biodiversity composition patterns across large regional scales. Existing methods for predicting these patterns require single, internally consistent datasets, usually from a limited number of comparable surveys. To achieve large regional scale coverage, however, information from multiple, often disparate, datasets must be synthesised. Further, full coverage requires predicting from environmental data layers, the ranges of which are rarely fully explored by biological surveys, thus confounding predictions. An alternative approach to mapping biodiversity composition patterns called 'Gradient Forest' was developed. The approach calibrates physical environmental surrogates against biological responses, rather than directly predicting compositional patterns. This work assessed the performance of surrogates and their relative importance and contributed to producing the first national maps of patterns of marine biodiversity for Australia's marine bioregional planning.

Objectives

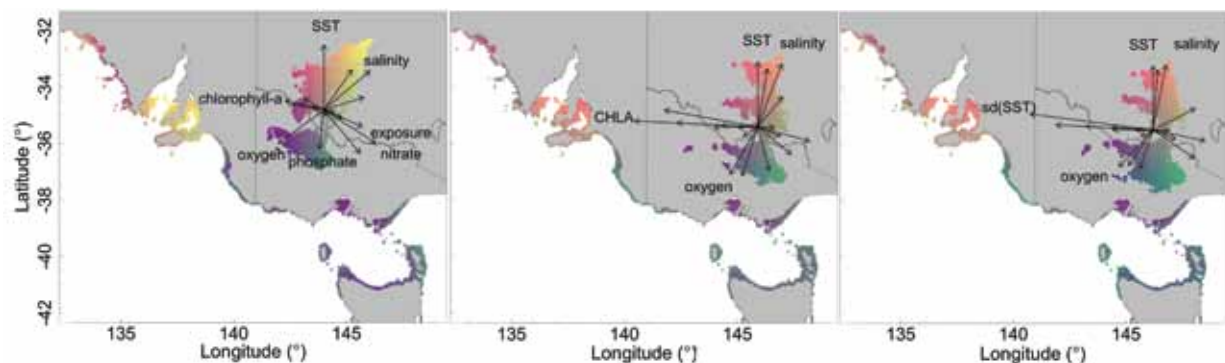
- > Quantify the magnitude and shape of changes in biodiversity composition (species presence and abundance) along gradients of environmental surrogates, and synthesise this information across multiple disparate survey datasets.
- > Use this data-based evidence to transform all the environmental surrogate layers to a common biological importance scale, to provide a regional multi-dimensional environment space calibrated to represent biodiversity composition.
- > Map the multi-dimensional biological response back into geographic space to represent predicted spatial patterns of biodiversity composition.
- > Apply the method in large marine planning regions around Australia to support the identification of areas for further assessment for the National Representative System of Marine Protected Areas.

Approach

The approach is based on modification of the statistical method 'random forest', a partitioning tree method that forms a forest of hundreds of trees for each species that occurs with sufficient frequency. The new modification collates the tree split values along each physical gradient where species abundance changes and by how much. These split values are collated across all species, trees and forests, and presented as cumulative distributions of compositional change along each environmental gradient. These distributions represent patterns of biological change response along gradients for each environmental variable and are used to transform the available environmental layers to provide continuous maps of expected patterns of compositional change of marine biodiversity. If required, the continuous representation of beta diversity patterns can be clustered to represent assemblage groups.

Another contemporary method that can predict patterns of compositional biodiversity change is generalised dissimilarity modelling. Comparisons between these technically different methods were made for the Great Barrier Reef (GBR) and southern Australia.

Figure 7: The species abundance and biomass of demersal fish communities sampled on shallow rocky reefs (<10 m) across the coast of Southern Australia.



Key findings

The Gradient Forest method integrates biological information into the use of surrogates for bioregionalisation by calibrating environmental layers with species survey data and transforming them into a biodiversity response. Importantly, data from multiple surveys, even with different sampling methods and abundance measurements, can be utilised because the units of biodiversity response used are common, thus maximising the value of existing data holdings. The key outputs include identification of the important environmental variables and their biodiversity response curves, including thresholds. Typically, compositional changes along gradients were non-linear, showing that not all portions of gradients are equally influential. Different variables have been important in different regions and for different types of biota, indicating it is unwise to extrapolate the use of surrogates in one region to another or among different types of biota, and that biological data for calibration are needed.

Overall, across many species, the available physical surrogates have predicted about 10–50% of the variation in biodiversity patterns, indicating that other processes are responsible for the majority of variation in species abundance composition. Even so, the explained variation is useful for mapping and the maps represent the most important patterns in biodiversity composition more closely than uncalibrated raw environmental surrogates alone. The approach has been applied to shelf and slope in the south-west, north-west, north and east marine regions, and the GBR; to coral reefs in the GBR and Torres Strait; and to temperate reefs in South Australia and the South-east Marine Region (Figure 7). The results and predictions of the Gradient Forest method were congruent with those of generalised dissimilarity modelling (GDM).

New knowledge and opportunities

Management applications of this approach have been completed for the south-west, north-west, north and east marine regions, and in South Australia. The outputs, including maps of the expected patterns of seabed assemblages, have been provided to DSEWPaC (Figure 8). Similar outputs for temperate reefs guide marine planning in South Australia. The approach also forms the basis of a Census of Marine Life (CoML) collaboration between the Marine Hub and scientists from Canada and the United States to compare environmental drivers of compositional patterns between different regions, and to assist marine planning in those countries. The Census collaborators also contributed to the development of the method. Further applications of this approach are planned for temperate rocky reefs in other southern states, for the shelf and slope in the South-east Marine Region, and for the Chatham Rise and Challenger Plateau of New Zealand.

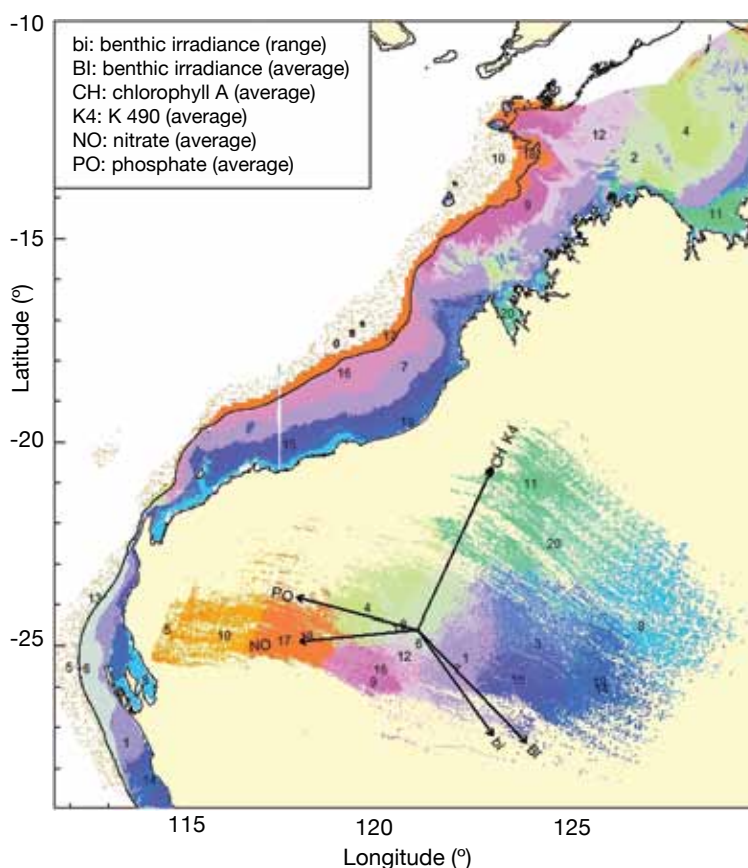


Figure 8: Clustered patterns of biodiversity composition along environmental gradients, quantified using the Gradient Forest method for samples collected by six trawl surveys and one sled survey conducted in the past 50 years, on the continental shelf and slope in the North-west Marine Region.

Biodiversity composition: species archetypes

Marine biodiversity is comprised of thousands of individual species. Most marine species are distributed over large areas, so any species can belong to multiple assemblages. The assemblage found at any one location is a mixture of all the species that could be present there. The species archetype approach was developed to identify coherent groups of species that share similar physical environmental preferences, rather than identifying membership of a particular assemblage. This alternative focus on species distribution can be useful in marine planning and zoning, and in identifying species of particular concern.

Objectives

- > Identify groups of species (archetypes) from large collections of species surveys that share a similar environment.
- > Simultaneously group species and predict the distributions of the groups using environmental data.
- > Identify which species belong to which archetype and how the species archetypes are distributed.

Approach

Species archetypes is a model based grouping of species presence for prediction across environmental gradients. Finite mixture models are used to simultaneously allocate the species to archetypes and estimate the responses of the archetypes to the environment. Statistical criteria can be applied to the models to determine an appropriate number of archetypes. Prediction of the probability of presence is obtained for each archetype with an associated measure of uncertainty.

Key findings

Many species have similar environmental requirements and hence response to measured environmental gradients. Species with similar responses can be modelled as a single entity without significant information loss. Each species group represents the response of its member species to the environment, with the number of members in each group potentially ranging from one to the number of species analysed. Prediction of multiple species simultaneously has significant advantages over many single species predictions. Each species in a group contributes information to the model and improves predictions. Consequently, the method can predict the distributions of species which are ubiquitous, and those with restricted distributions. Predictions from environmental gradients provide the probability of presence of the species group, and the uncertainty of that prediction.

New knowledge and opportunities

The species archetype approach reduces management complexity and can be applied in spatial management, such as identifying the areas where key species (groups) are found. It has been applied on the GBR, to south-eastern Australian demersal fish, and to invertebrates from temperate coastal reefs in South Australia, Victoria and Tasmania (Figure 9). Further development will allow the use of count or biomass data and the identification of 'habitats' based on species archetypes.

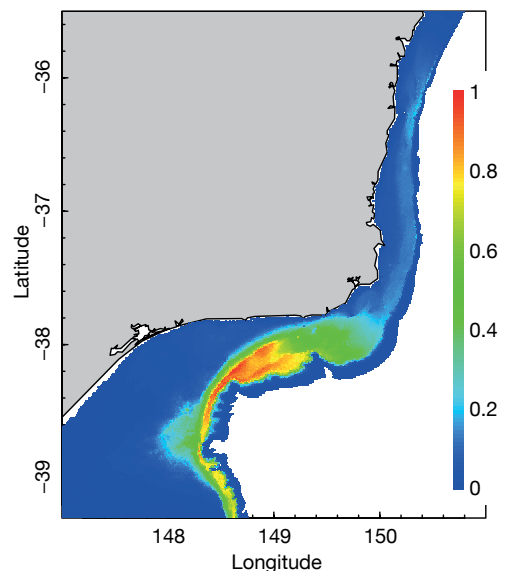


Figure 9: Species archetypes were calculated for demersal fish communities on the continental shelf and slope off Victoria and New South Wales. One hundred common species were split into 10 species archetypes. This figure shows the distribution of a group of species found on the deeper shelf including Latchet, sawsharks, Red Cod and Crested Flounder.

Influence of spatial scale in predictive biodiversity models

The scale at which a system is considered influences the relative importance of different predictors. For example, depth could be a major driver of the structure of fish assemblages when considering a single reef, whereas latitudinal gradient in sea surface temperature could be more important at a regional scale. A novel procedure was developed to investigate spatial scale (local versus regional scales) effects on the performance of distribution models and on the relative importance of different model predictors. This work has important implications for the use of predictive biodiversity models for management of the marine environment.

Objectives

- > Develop a method to use in conjunction with a range of modelling techniques to investigate spatial scale effects; test and validate the method on artificial datasets.
- > Apply the method to existing models developed for Australian regions and assess cross-systems differences.
- > Recommend the best scale and resolution to consider when developing predictive models of marine biodiversity.

Approach

The approach is based on spatial weights that simulate an increasing spatial scale around a focal point. Predictor importance at each spatial scale was compared after fitting statistical models such as generalised linear models or boosted regression trees as examples. The method was developed and validated using an artificial dataset and then applied to two real example datasets of marine fish species richness data from tropical Australia (GBR and Torres Strait).

Key findings

The method proved effective to detect spatial scale effects in the artificial dataset^{P43}. The application on real datasets showed consistent patterns between regions and response variables, such as the importance of spatial predictors appearing at a medium scale (20 km) only, below which local variation in environmental variables provided better predictors of species richness (Figure 10).

New knowledge and opportunities

The approach can be combined with a range of modelling techniques to determine the optimal scale and resolution of future predictive models, the scale at which physical variables have influence (Figure 11). It can contribute to the design of future surveys. These results highlight the importance of ensuring that the useful predictive scale of models of biodiversity is relevant to the particular management question.

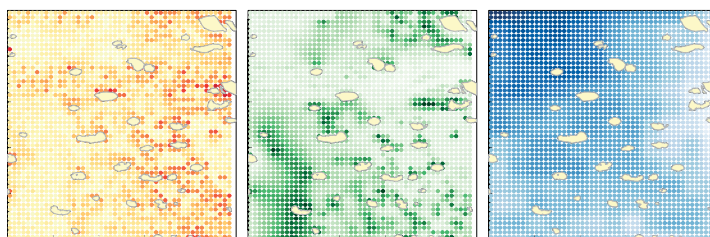


Figure 10: Dataset used for validating the method, including physical covariates varying at fine (A: left), medium (B: middle) and broad (C: right) spatial scales and extracted from datasets of the Torres Strait.

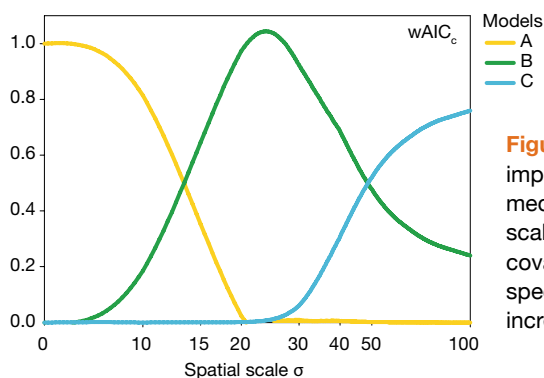


Figure 11: Relative importance of the fine, medium and broad scale environmental covariates in predicting species richness with increasing spatial scale.

The effect of interpolating physical variables on their value in explaining biodiversity

The central premise underpinning the work undertaken in the Prediction Project is that biodiversity can be explained by physical variables. The statistical methods used in this task all assume that the biological data and the physical data are measured at the same sampling sites. This is rarely true and typically the physical variables at the biological site are estimated by interpolating between the nearby measurements of the physical variables. The effect of using interpolations of the physical variables rather than actual measurements has been investigated.

Objectives

- > Investigate the effect of ignoring interpolation uncertainty on model performance. This uncertainty arises from interpolating (not measuring) physical covariates.
- > Develop a statistical model that incorporates interpolation uncertainty.

Approach

A commonly used class of models, generalised linear models, was studied. Analytical approximations were obtained for key aspects of these models. The approximations indicate the circumstances in which ignoring prediction uncertainty will be important and what problems will arise. Simulation experiments based on the data from the GBR demonstrate the problem. In these experiments synthetic surveys were created by degrading the GBR data, essentially re-creating the sampling and modelling process^{P31}.

Key findings

Treating the interpolated physical variables as though they were observed variables will affect the analysis. There will be biased predictions that are overly confident, and biased models that may distort the true relationship with physical variables. These problems can be overcome using suitable statistical models.

The severity of bias will increase with any of the following three factors: greater influence of the environmental variables on patterns of biodiversity; greater interpolation uncertainty; and greater non-linearity of the relationship between biodiversity and the physical variables.

A dataset from the GBR lagoon shows that the difference between models that do (and do not) incorporate uncertainty associated with interpolating physical variables can be substantial and could affect management decisions (Figure 12). In particular, patterns in the distribution of diversity are likely to be less distinct, and areas likely to appear more similar than is actually the case. This would lead to underestimating the extent of spatial management required to reach a particular level of protection.

New knowledge and opportunities

The results imply that current modelling strategies have shortcomings unless interpolation uncertainty can be removed/reduced or accounted for in the modelling process. In practice this means that either more physical data is required, or interpolation uncertainty should be included in the models. Substantial statistical challenges need to be addressed to account for prediction uncertainty in a wide selection of model types. Finally, interpolation variance needs to be routinely supplied with interpolated datasets.

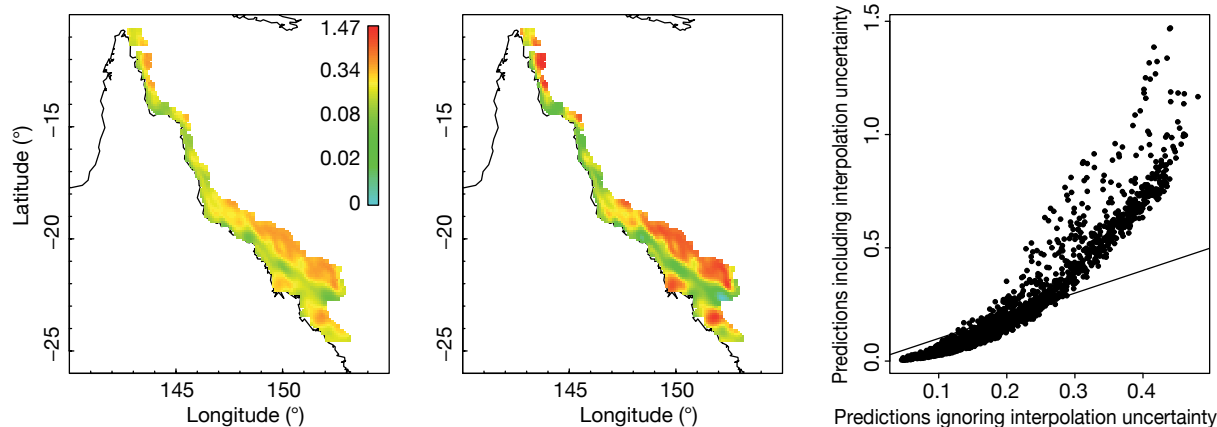


Figure 12: Predictions of richness from models that do not (left) and do (centre) account for covariate interpolation uncertainty. Interpolation uncertainty is non-ignorable as the maps are not identical and the predictions depart from $y=x$ line (right).

Biological surrogates

At a national scale, Australia's marine biodiversity is known only for fishes, as the most extensive data available come from fish trawl surveys^{P45}. Sampling of invertebrates and flora has been patchy and localised. As a consequence, the national marine bio-regionalisation (IMCRA 4.0) was based largely on an analysis of the fish distributions. There was an implicit assumption that other biota had similar patterns. The Biodiversity Program found that fish were consistent surrogates for key invertebrate taxa at the provincial scale. Here fish are tested for their value consistent surrogates for other taxa within a biogeographic province.

Objectives

Examine the extent to which compositional/assembly patterns and biodiversity indices of selected taxa (such as fishes) are biological surrogates for other taxa (such as invertebrate groups) within a biogeographic province.

Approach

Datasets from the GBR and Torres Strait Seabed Biodiversity Project were selected as they are among the few available that adequately sampled multiple taxonomic groups for this analysis. Both included up to 12 major phyla encompassing fishes, invertebrates and marine plants, sampled by both epibenthic sled and prawn trawl. Correlations between Bray-Curtis dissimilarity matrices of different taxonomic groups from the scale of sampled sites^{P42}, up to sub-regional scales. Also calculated were pair-wise similarity indices between assemblage clustering patterns of the

different phyla, again at a range of scales^{P64}. The two approaches were then used to examine whether biodiversity patterns determined at higher taxonomic levels (genus, family, order, class, phylum) reflected patterns determined at the species level (Figure 13).

Key findings

Patterns of species richness were sometimes reasonably well correlated for a few biotic groups, such as red and brown algae or green algae and seagrasses. This result was not consistent, however, and richness of most groups was poorly correlated. For patterns of compositional diversity and assemblages, cross-phyla surrogacy was typically poor and nested taxonomic levels (for example, genus and family), were little better and declined with coarser taxonomy. In some analyses there were indications that biological surrogacy improved slightly at coarse scales, but again this result was not consistent.

New knowledge and opportunities

Within biogeographic provinces, the evidence suggests that different biotic groups have different patterns of biodiversity, and that patterns determined with coarse taxonomy inadequately reflect those at the species level. This indicates that marine planning at sub-provincial scale should be precautionary when based on limited taxonomic groups or poor taxonomy; it cannot be assumed that biodiversity patterns for fishes reflect those for other biota. The lack of correspondence between different biotic groups also emphasises the great need for more comprehensive data on the distribution and abundance of marine biodiversity across a wide range of biota.

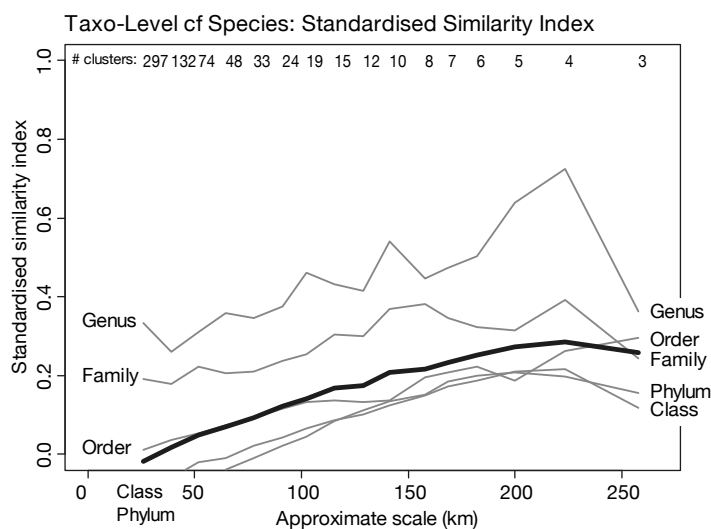


Figure 13: Similarity of patterns of assemblage clustering of nested taxonomic levels, relative to species level, at a range of spatial scales (numbers of clusters) for GBR seabed epibenthos. Black line: average similarity. Similarity decreased with coarser taxonomic levels and at finer spatial scales.



Off-reserve Management Program

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Chris Wilcox

Off-reserve Management Program

Developing new options for managing marine biodiversity

This program explores alternative approaches to managing the effects of marine activities on biodiversity. The Department of Sustainability, Environment, Water, Population and Communities (DSEWPaC) employs a range of measures to manage marine activities under the *Environment Protection and Biodiversity Conservation Act 1999* (the EPBC Act). These measures, which include marine reserves, species conservation programs, strategic fisheries assessments and other environment and approvals processes, provide varying levels of protection for biodiversity assets. As the scope and intensity of activities in and out of marine reserves grows, however, so does the need for new options to protect and sustain marine biodiversity.

Recent changes in the management of Australia's pelagic tuna fishery, particularly the Eastern Tuna and Billfish Fishery (ETBF), offered an opportunity to explore the use of market based measures to improve conservation outcomes. Incidental capture of seabirds in the fishery is regulated by a threat abatement plan (under the EPBC Act) that requires spatial closures to fishing. The fishery is also experiencing increasing pressure to reduce its impacts on turtles, with significant leeway for policy development due to the absence of regulation. Finally, the fishery has incorporated spatial incentives in its management plan. This system allows fishery managers to reduce the fishing effort allocated to operators that fish in undesirable areas. The confluence of these drivers and the availability of data on the species capture and operations of fishers provides a unique opportunity to evaluate alternative management approaches.

Objectives

The Off-Reserve Management Program explored the use of incentives to influence the spatial overlap between biodiversity impacts and assets, and the incorporation of biodiversity offsets to reduce the complexity of spatial management. The specific objectives were to:

- > Deliver a system for evaluating triple bottom line outcomes of spatial management in the tuna fishery and demonstrate its use in the evaluating scenarios selected with industry and managers.
- > Explore the application of biodiversity offsets, providing background research and potentially demonstrating an implementation using marine turtles.

Off-reserve Management Program

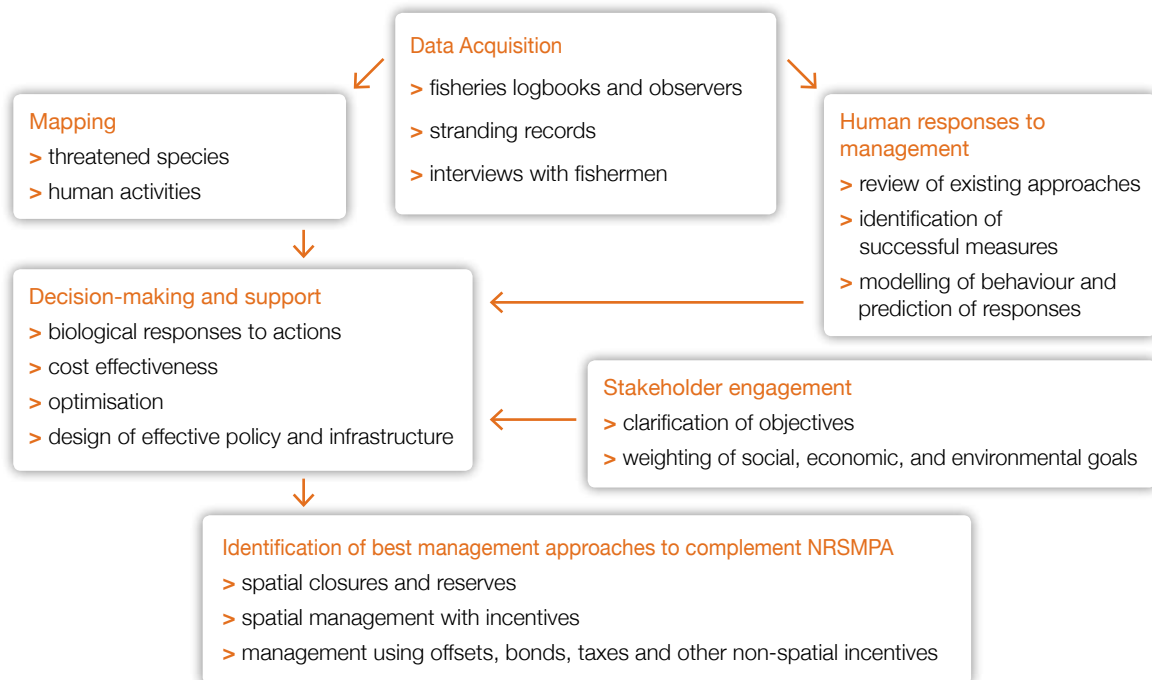


Figure 1: Work flow and linkages for the Off-reserve Management Program.

Approach

Project I: Spatial management of marine activities using incentives

This project focused on exploring incentives as an alternative to spatial closures to achieve the objectives of the threat abatement plan for the incidental capture of seabirds during longline operations. Simulation modelling was used to predict the outcomes of management scenarios. Expected economic, social and biodiversity outcomes were then compared using performance relative to stakeholder identified criteria for each outcome. The outcomes were compared separately, and also in an integrated way using multi-criteria decision analysis.

A range of statistical and mechanistic models were developed to predict spatial distributions of target and threatened, endangered and protected (TEP) species. These models incorporated spatial structure explicitly, allowing prediction in areas where sampling is relatively sparse. Non-traditional datasets, such as strandings data on turtles, were also used along with mechanistic models to reconstruct species distributions from these datasets. Two approaches were used to model the response of fishers to incentives: one based on a statistical model parameterised on past behaviour, and a second mechanistic model that incorporates opportunity cost. Finally, stakeholders were consulted in a structured approach to assess the relative importance of economic, environmental, and social objectives. These results, along with predictions of fishing behaviour and species distributions, were used to evaluate the triple bottom line performance of existing approaches to managing fisheries bycatch and alternatives that employ both mild and strong incentives.

Further to this work, DSEWPaC requested an evaluation of the cost of MPA designs using the MARXAN software for the East Marine Region. Market-based instruments were also evaluated as a tool for reducing the number of incompatible fisheries, and thus the cost of implementing the National System of Representative Marine Protected Areas.

Project II: Biodiversity offsets applied to marine species

This project complemented Project I by developing tools that enable the use of biodiversity offsets to manage the impacts of marine activities on threatened species and habitats. A literature review on biodiversity offsets and their application in harvested systems included auditing systems, measurement of credits, and other relevant issues. DSEWPaC's interest in this work led to an expanded scope that included other market based approaches to conservation including market access, taxes, performance bonds and cap and trade systems. The IUCN threat database and surveys of expert opinion were used to provide a global analysis for turtles and seabirds to identify cases in which offsets might be useful. A potential case study was identified for species affected by the Australian tuna fishery and discussed with stakeholders in DSEWPaC, the Australian Fisheries Management Authority, recreational fishers, fishing industry representatives and conservation NGOs. Ongoing work is developing this case study as a basis for developing a trial offset program.

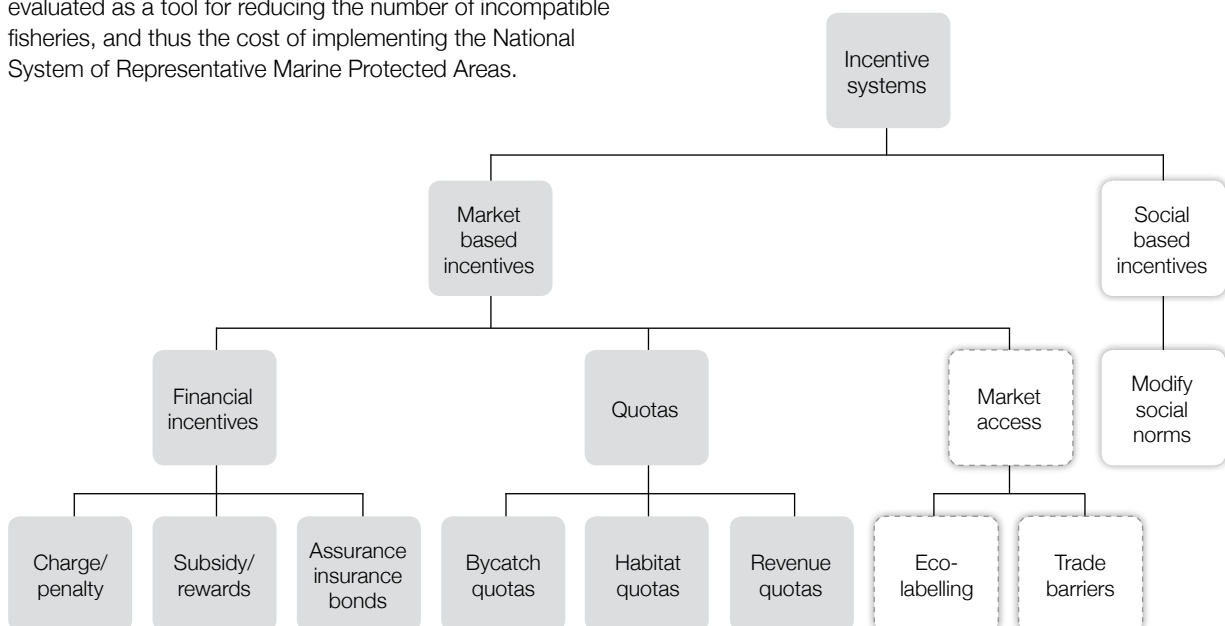


Figure 2: Possible incentives contributing to managing fisheries bycatch of threatened species.

Outputs

Environmental impacts vary widely among fishing operators. This variation suggests that narrow targeting on high impact operators is likely to produce larger benefits than industry-wide regulation.

Reviews of market-based incentives suggest they can be highly effective at relatively low cost to industry and government. For instance, environmental bonding in the United States mining sector has resulted in compliance rates above 99.5% even when bond values are relatively low.

Expert elicitation can quickly assess risk to species across a range of taxa, locations, and threats, and can provide semi-quantitative results.

Spatial incentives can reduce environmental impacts from fishing to the same extent as closures, but with much less cost. Mild incentives are sometimes more effective than either strong incentives or closures.

Responses by fishers to closures or incentives are difficult to predict, and depend on both the returns from fishing in other locations, and how other fishers react to new regulatory conditions. This implies that predictions of costs and benefits from simple approaches, such as historic catches in a region, are likely to be inaccurate.

Life history parameters are available for at least some members of all seabird families, and at least some parameters are available for all marine turtles. These can be used with a simple rule of thumb to evaluate the cost-benefit ratio of conservation actions, providing a basis for prioritising investment or further investigation.

Offsets provide a valuable tool for marine conservation. In some circumstances they can provide conservation benefits more efficiently than other approaches when used either as interim measures to support the realisation of aspirational conservation objectives, or as a longer term solution.

Outcomes

The results of this program demonstrate that market based instruments may be a useful and cost-effective addition to existing measures for managing activities in the marine environment. Opportunities exist for the use of market based instruments to reduce the compensation costs to industries displaced by marine reserves and as cost-effective options for regulating activities outside reserves that affect DSEWPaC responsibilities under the EPBC Act.

Incentive based spatial management can provide a tool for integrating many management objectives into a single management system. A variety of complex objectives can be represented in a single map with varying requirements or penalties for each location representing the risk associated with operating in that region. This can provide a means for managing industries that affect multiple assets, without requiring complex regulations and the resulting administrative and compliance issues with industry.

Expert elicitation could provide a tool for obtaining semi-quantitative information to support decision-making. For example, elicitation could help to prioritise those protected species most threatened, and provide threat rankings for species on the list of species proposed for protection, thus optimising limited resources.

Market-based instruments offer the opportunity to shift from threat abatement plans and other regulatory approaches in which DSEWPaC bears the cost and burden of proof to one in which these costs are realised as part of doing business. This approach would require shifting to a more outcome-based approach to management (away from defined procedures), and has the potential to increase the effectiveness of regulatory approaches while reducing the cost.

While the potential for offsets in marine applications is rapidly expanding, there is a need for further policy development in this area. Development of clear standards for exchanges, mechanisms for ensuring offset integrity, and other policy clarifications could determine whether the approach has a net benefit, or results in ongoing losses.

Predicting species distributions to support conservation management decisions

Developing spatial management strategies in the marine zone requires understanding the distribution of species affected by human activities.

Objectives

This project developed methods for making rapid, inexpensive predictions of the distributions of marine species from widely available data. The ability to make predictions in areas where sampling was sparse was particularly important.

Approach

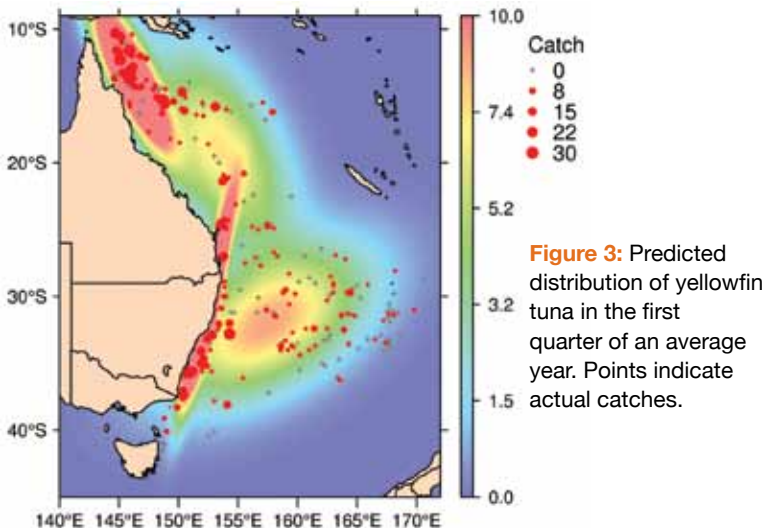
Three methods for predicting distributions were used, each tailored to the available data. Logbook catch and effort data were used to estimate the distribution of species targeted by the fishery using a hierarchical Bayesian statistical model that accommodated sampling bias, environmental effects on distributions, and seasonal migrations^{R30}.

The distribution of marine turtles was estimated using the only large dataset available, that of dead turtles that have drifted onto beaches. A physical model of ocean currents and wind and a statistical model to correct for variation in reporting and mortality were used to estimate at-sea distribution of live turtles.

A generalised additive model was used to estimate the distribution of seabirds encountered from fisheries observer data^{R40}. This model provides a smooth fit to the data, but limits unrealistic predictions at the periphery where data are sparse.

Key findings

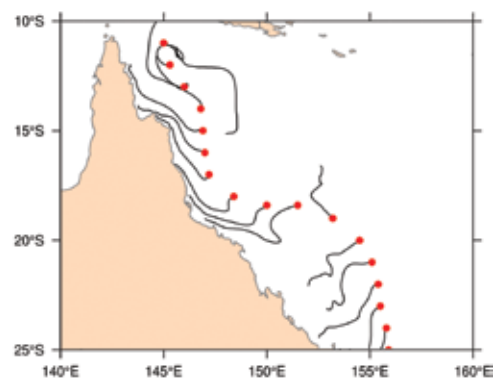
- > The Bayesian model for target species distribution provided a good representation of tuna and billfish distribution in this highly dynamic system. Seasonal and temporal variations were captured and enabled conservative predictions in areas with sparse sampling (Figure 3).



- > Model predictions of the distribution and abundance of four target species, and the pattern of variation among years and seasons, were consistent with literature based on logbook and tagging studies.
- > Modelled drift paths of beached turtles were relatively consistent with the observations at sea and with expert opinion on species distribution (Figure 4). The analysis identified parts of the tuna fishery as potential source areas, confirming the potential for stranding data to contribute to the analysis of at-sea distributions of turtles caught in the tuna fishery.
- > Environmental drivers had a strong effect on the distribution of seabird species, but most of the variation in the pattern was explained by the location of the observation. This suggests relatively static patterns of distribution for the common albatross, petrel and shearwater species in the Coral-Tasman Sea region.

New knowledge and opportunities

The approaches used here can predict species distributions from sparse datasets: a characteristic of many datasets for TEP species. This provides opportunities for DSEWPaC to implement market-based mechanisms and other regulatory approaches in the absence of extensive datasets.



Incentives as an alternative to reserves: greater conservation benefit at a lower cost?

Spatial management tools such as marine reserves can be expensive to establish, monitor and manage. Incentives may offer an alternative or supplement to marine reserves, achieving similar conservation outcomes while reducing the cost of establishment and industry compliance.

Objectives

The objective of this project was to evaluate the response of fishing operators to different spatial management approaches, including changes in expected revenue, cost, and bycatch rates.

Approach

Two models were developed to estimate the effects of introducing spatial management approaches on the spatial and temporal distribution of fishing effort in the fishery^{R9-11}. The first was a statistical model that estimates the probability of a fisher operating in a given area based on its characteristics (for example, average revenue per unit effort, distance from port) and those of the fisher^{R23}. The model assumes historical effort allocation choices are representative of future decision-making (Figure 5).

The second model used dynamic programming to determine an optimal effort allocation based on revenues, costs and the opportunity cost of using up the effort quota each trip (something ignored by the first model). This model is less reliant on historical effort patterns, and more responsive to changes in conditions. The impact on economic performance was considered by estimating the proportional changes in total fishery revenue and operating cost. The changes in bycatch were estimated based on changes in overlap between the distribution of bycatch species and fishing effort.

The models were used to compare several management scenarios for the tuna fishery (Figure 6)^{R37}. First, incentives (in this case reductions in the total amount of effort a fisher is allowed, as per the ETBF Management Plan) were evaluated as an alternative to closures used under the Threat Abatement Plan for the Incidental Capture of Seabirds During Longline Operations^{R15,R38}. Secondly, incentives and closures were evaluated for managing incidental capture of marine turtles off the Queensland coast^{R27}. Finally, project staff collaborated with DSEWPac to evaluate the expected cost of proposed reserve designs developed using the MARXAN software for the East Marine Region.

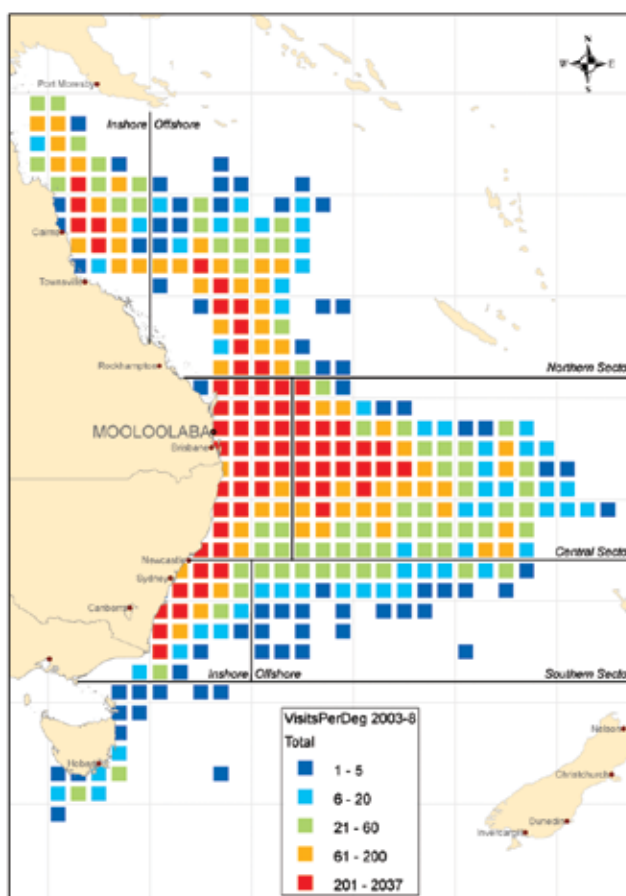


Figure 5: Distribution of total fishing days, Eastern Tuna and Billfish Fishery, 2003–08.

Key findings

Overall, for both models, introducing an incentive resulted in reduced fishing effort in the management area, and the magnitude of this reduction generally increased with the strength of the incentive.

The economic and conservation outcomes of strong and weak incentives or closures varied according to year and incentive level, as well as by port and management area. This variability is a consequence of the high spatial and temporal heterogeneity of the fishery.

The response of fishers to incentives based on profits alone would be non-linear and complex, and, in some instances, counter-intuitive. Given this complexity, it is necessary to evaluate any management system individually.

Reserves that are designed with cost in mind, in addition to conservation value, were less expensive than those designed based on conservation alone. However, there was significant cost variation among reserves designs considered to have equivalent costs based on historic fisheries landings. This illustrates the effect of adaptation by fishing operations to changes in spatial management, indicating that in-depth analysis of fishing responses could yield savings of up to 20% in terms of lost fishing revenue.

A key advantage of an incentive-based spatial management system is that the pattern and strength of the incentives can be fine tuned during the season in response to unexpected spatial shifts in both the target and bycatch populations. This reduces the burden of having to establish reserves based on uncertain predictions of cost and biodiversity benefit, which may result in sub-optimal outcomes.

New knowledge and opportunities

This project demonstrates the potential for managers and researchers to develop management tools for marine activities that can provide improved conservation outcomes at a reduced cost. The results also show that management solutions need to be tailored to suit specific scenarios.

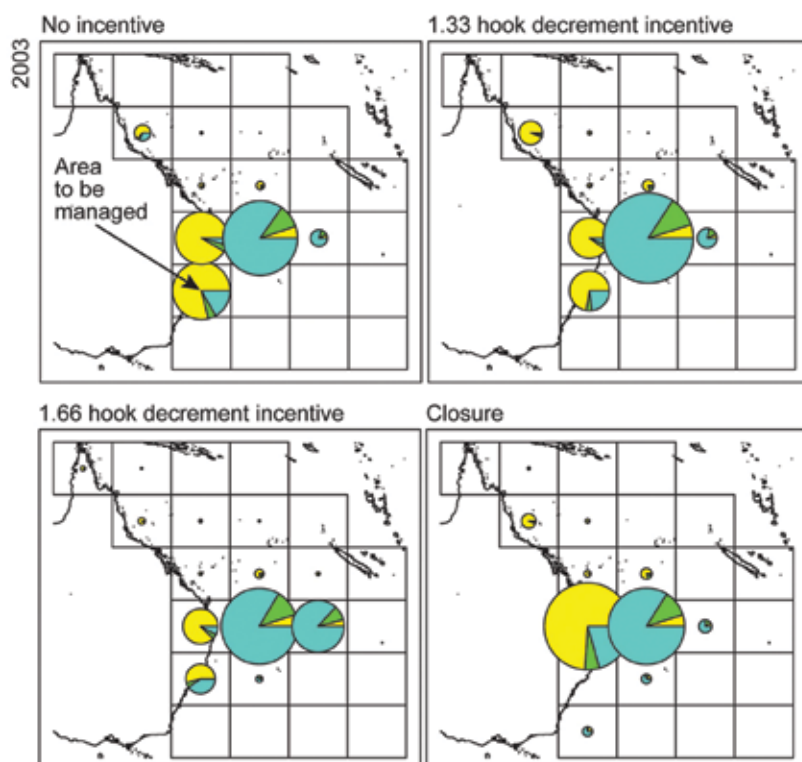


Figure 6: The distribution of fishing effort with increasing incentives. Circle size is proportional to effort in a cell. Colours represent target species catches (yellow: yellowfin; blue: albacore tuna; green: swordfish).

Measuring the benefits of spatial management by integrating social, economic, and environmental criteria

Including social, economic and environmental criteria is central to assessing how a policy, project or resource allocation will meet agreed objectives. However, providing consistent advice can be difficult where proposed options perform differently against the criteria and the stakeholders weight the criteria differently.

Objectives

This project developed a framework for comparing the total benefit of alternative policies across fundamentally different values (such as economic return, cost, environmental performance, and impacts on other users)^{R22}. The framework was then applied to evaluate spatial management and alternative approaches under the Threat Abatement Plan for bycatch of seabirds.

Approach

The differences in management objective preference between stakeholder groups active in shaping Australian fisheries management were surveyed to elicit weightings (preferences) for a range of different objectives (Figure 7)^{R24}. In a follow-up interaction, respondents were presented with a summarised version of the objective rankings and asked to re-evaluate their preferences.

These weightings were then used in a multi-criteria evaluation of different spatial management options for the tuna fishery^{R29}. This stage used predictions from the species distribution and fleet dynamics models developed earlier in the spatial management project to estimate the economic, environmental and social impacts of the management alternatives.

Several management scenarios were developed in discussion with ETBF stakeholders for evaluation based on the stakeholders' objectives. These scenarios were based around the ongoing closures in the southern region of the fishery to protect seabirds. Management responses of no action, a weak incentive, a strong incentive, and the existing closure approach were compared^{R29}.

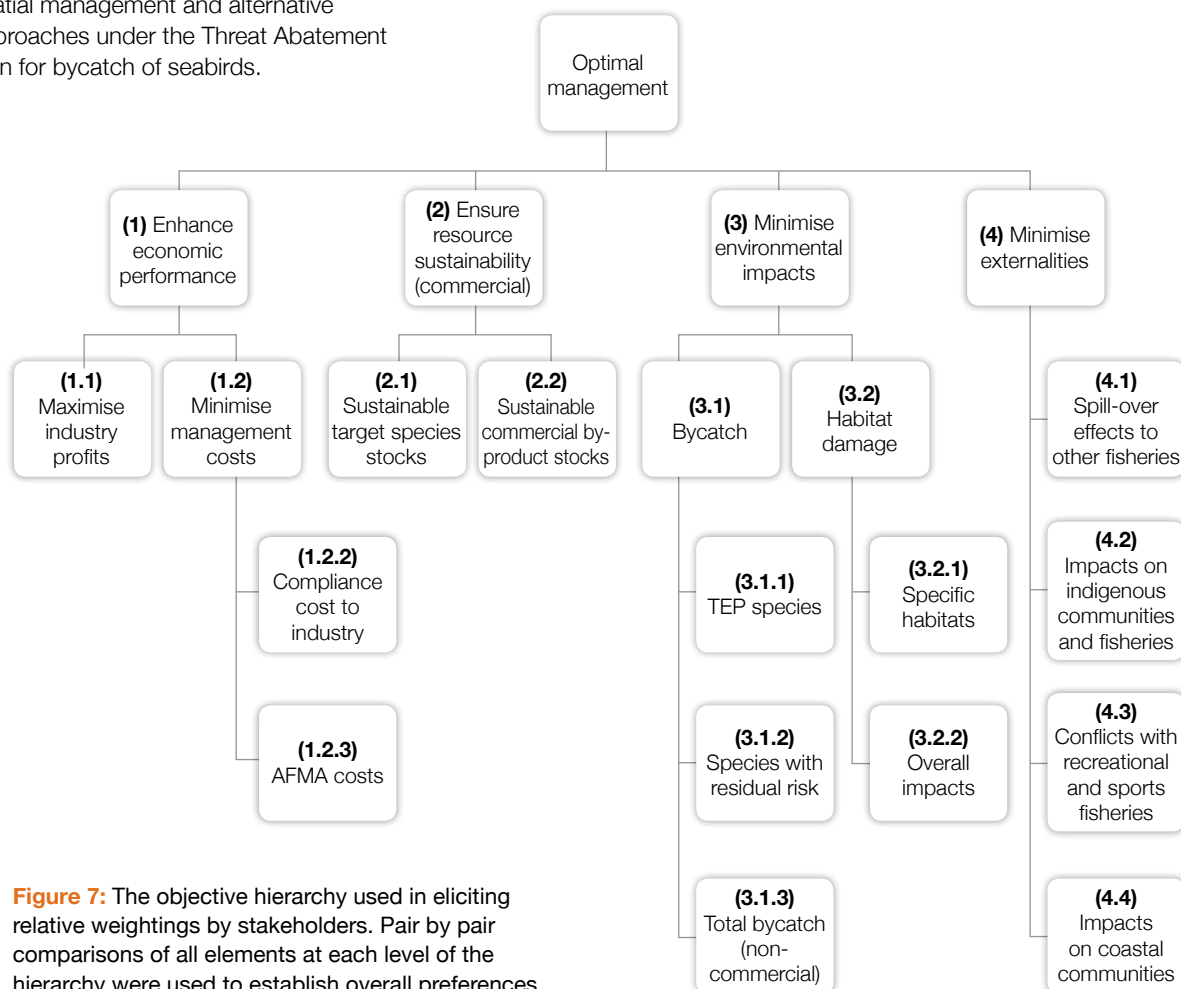


Figure 7: The objective hierarchy used in eliciting relative weightings by stakeholders. Pair by pair comparisons of all elements at each level of the hierarchy were used to establish overall preferences.

Key findings

Responses from stakeholders vary within and between stakeholder groups, but generally stakeholders expressed preferences for objectives that aligned with their sectoral interests and/or professional responsibilities. For example, managers and industry preferred profit-based objectives; scientists and economists preferred objectives that incorporated all costs (externalities); and NGOs preferred objectives based on all costs and environmental impacts (Figure 8).

All stakeholders placed some importance on all objectives, however, even those activities that might be in conflict with their primary objective.

Stakeholder groups were in general agreement when considering the relative importance of broader issues related to economic performance, stock management, conservation and externalities, but less in agreement with regard to the sub-categories (such as bycatch reduction versus habitat protection under the broader conservation objective).

When stakeholder objectives were considered, weak incentives performed best in the evaluation. In a large part, this is due to their ability to deliver environmental benefits at low cost. However, the effects of the different management strategies were highly variable between years due to the dynamic nature of the fishery.

New knowledge and opportunities

Agreeing on a clear set of objectives is a key step in developing effective management options. The formal elicitation process used here showed that despite different stakeholders emphasising their own sectoral interests, there was broad agreement on the primary objectives of all groups. This provided the basis for comparing management options against their ability to meet those objectives. Implementing marine bioregional plans will lead to many situations in which formal elicitation processes could assist stakeholder engagement.

Differences in stakeholder responses within particular sectors show the importance of identifying and then including a broad cross-section of these sectors in planning discussions.

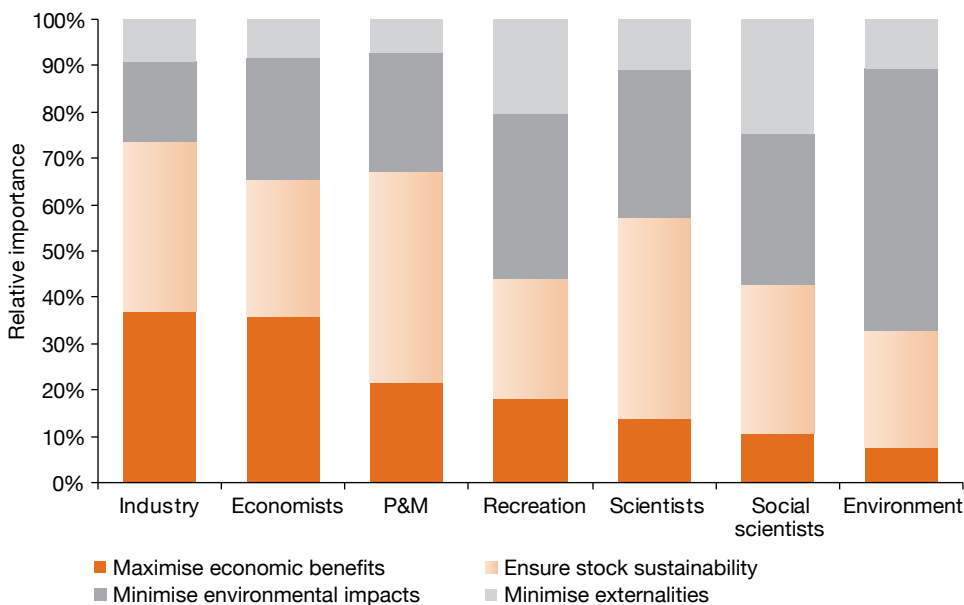


Figure 8: Stakeholder weighting of relative importance for the highest level objectives in the hierarchy^{R24}.

How can market based instruments ease the cost of MPA establishment?

In the context of costing the establishment of the NRSMPA, DSEWPaC queried the use of market-based instruments to increase the compatibility of fishing and other economic activities associated with marine reserves.

Objectives

This project evaluated the ability of market based instruments to cost-effectively make a fishery (or other marine related activity) more compatible with identified and generally non-commercial conservation values.

Approach

The potential benefits and limitations of alternative market-based instruments and their use in marine biodiversity management were assessed by reviewing the performance of previous applications^{R13, R14, R16, R39}. Market based instruments aim to mitigate the undesirable impacts of activities by better aligning operator incentives with management objectives. They have been applied in terrestrial settings, but their application has been limited in the marine environment. The measures considered in this work are listed in Figure 9.

The review focused on how alternative market based instruments could reduce negative impacts associated with commercial fishing. Several fishing methods and their associated impacts were considered. These instruments could also apply to other marine related activities.

Key findings

- > Market-based instruments can improve the performance of existing management measures by reducing undesirable impacts without undue economic cost.
- > Market-based instruments can reduce the costs imposed on industry by allowing them to develop solutions to mitigate undesirable impacts.
- > Seabird bycatch in longline fisheries varied widely between operators, with higher profit operations most frequently having a lower environmental impact.
- > Market-based instruments must be carefully tailored to suit the individual circumstances of the problem at hand.
- > Advances in technology (such as GPS tracking and video monitoring systems) are revolutionising the monitoring and enforcement of fishery regulation.
- > Within the context of fisheries related impacts there is a strong relationship between the frequency with which the issue occurs, and the appropriate management response (Figure 10).

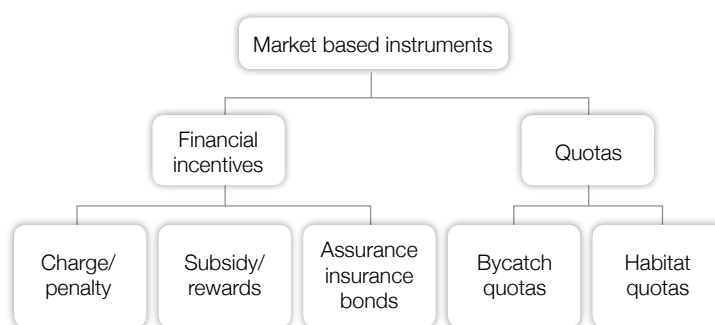


Figure 9: Hierarchy of market-based fisheries management systems for reducing environmental damage.

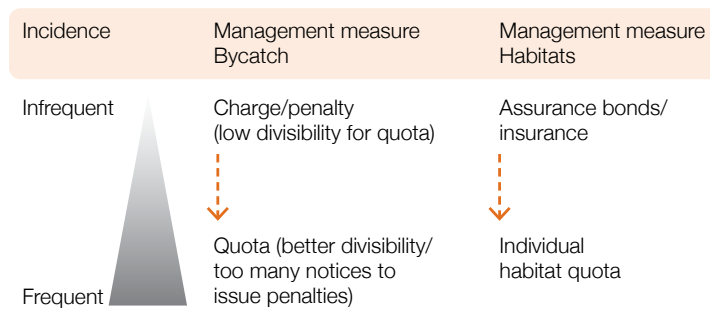


Figure 10: Relationship between frequency of occurrence and appropriate market based instrument.

Creating a practical basis for biodiversity offsets approaches to marine conservation:

understanding threats, developing options and supporting decision making

Implementing cost effective conservation options presents a number of challenges. It is essential to understand the range of threats affecting a particular species or system. Choosing which threat to focus on requires an estimate of the impact of reducing any given threat. Furthermore, the expected impact needs to be converted into a common currency to allow comparison among potential options. This project developed simple rules of thumb for deciding between options.

Objectives

The objective of this work was to develop an approach to guide investment and evaluate market based approaches, including offsets. Marine turtles and seabirds were the primary focus as these taxa have declining populations due to the impact of human activities. Species of marine turtles and seabirds are protected under the EPBC Act and are the focus of DSEWPaC management efforts.

Approach

An essential first step in developing offsets in particular was to understand the range of threats faced by a given species. While global analysis has been conducted by the IUCN for seabirds, no similar analysis exists for turtles. This shortcoming was addressed by developing a semi-quantitative expert elicitation procedure covering all turtle species and threats^{R8}.

A second step in developing an offsets policy was to understand the effect of reducing a threat as an offset for another action that will affect a species. For seabirds, removal of invasive predators from breeding sites might be an efficient offset^{R33}. A review of IUCN data and other literature found invasive predators to be the most common threat across seabird species and that their removal results in a 27% increase in breeding success^{R3, R19}.

Offsets are available and their population effects can be estimated, but these estimates need to be expressed in a common currency that can be readily evaluated. One method is to estimate the effect each action would have on extinction risk. A literature review was used to assemble the necessary population rates for such an analysis across all turtle and seabird species for which data was available^{R20}. A simple rule of thumb was developed for evaluating the cost-effectiveness of potential conservation actions for their cost-effectiveness (offsets must have a better cost to effect ratio than direct remediation to be viable). This rule of thumb was illustrated using a worked example with a southern ocean albatross^{R20}.

Once a decision has been made to invest in a particular conservation action, either as an offset or as a direct investment, questions may remain about how best to invest funding. A set of optimisation tools was developed to guide investment in restoration actions, (such as beach protection or eradication of invasive predators), across a subset of possible sites with varying benefits^{R4, R17}. This method was then applied to restoration efforts in an archipelago off western Canada.

Key findings

Formal surveys of experts can provide useful information on threats to species, and with appropriate statistical analysis it is possible to control for bias and produce semi-quantitative estimates of risk (Figure 11).

Adequate biological information exists for most marine turtle and seabird species to evaluate offset options, at least on an approximate basis. The primary limitation appears to be finding information on the cost of conservation actions.

Simple rules of thumb, such as the ratio of expected population benefit per unit cost between alternative conservation actions, can provide a useful tool for making decisions between conservation actions. Moreover, approximate rules of thumb can facilitate the elimination of options unlikely to provide adequate benefits.

Using optimisation tools to support decision-making can substantially increase the impact of conservation investment on realised outcomes. This is a clear result both at the level of choosing between alternative conservation actions and in choosing among potential sites for implementing a given conservation option.

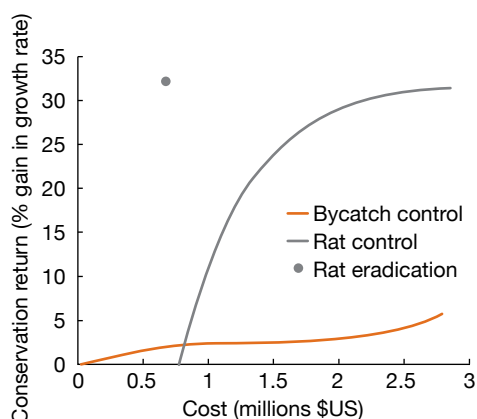


Figure 12: Increase in population growth rate with investment in three alternative conservation actions for shearwaters around Lord Howe Island^{R33}.

New knowledge and opportunities

With increased use and management of the marine environment, decision-makers are faced with the challenge of choosing among management options, often with limited knowledge of their effectiveness. Despite limited information, expert elicitation together with available biological information will often be sufficient to develop simple rules of thumb to choose between conservation options.

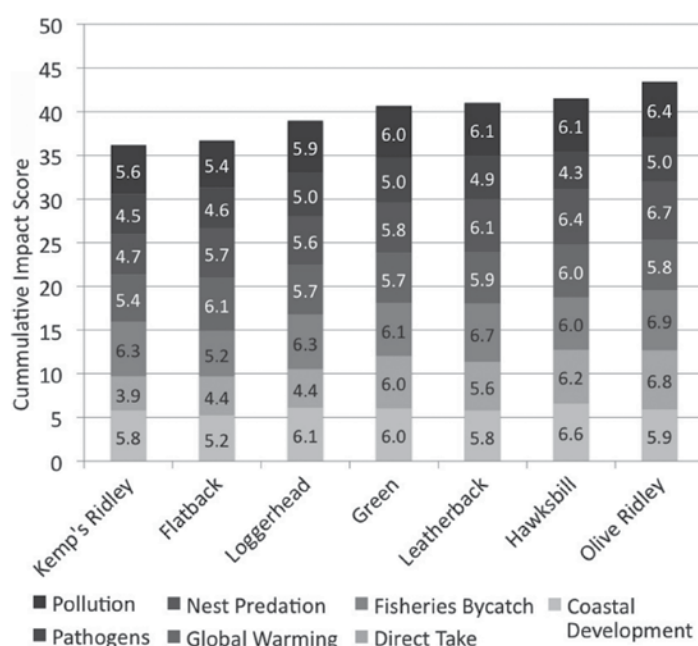


Figure 11: Predicted cumulative impact scores for each hazard type pooled across geographic regions for each sea turtle species. Impact scores follow International Conservation of Nature/Birdlife International scheme: 0-2 no or negligible impact; 3-5 low impact; 6-7 medium impact; 8-9 high impact^{R7}.

The use of biodiversity offsets in managing fisheries and other marine industries

Biodiversity offsets have been widely applied in terrestrial systems but their application in marine systems is limited. Fisheries and aquaculture are key marine sectors in which offsets may be applied to minimise potential impacts and achieve improved economic and conservation outcomes.

Objectives

This research area explored the use of biodiversity offsets specifically for fisheries impacts. The objectives were to:

- > Develop several fisheries-offset case studies, including a comparison of biological benefits and economic costs.
- > Address the potential complexities arising in the use of offsets.
- > Propose at least one case study for a fisheries impact that could be addressed with offsets.

Approach

The application of biodiversity offsets for managing fisheries bycatch was explored using bioeconomic models applied to two case studies: one for Southern Ocean albatross affected by high seas fisheries and a second for Tasman Sea shearwaters affected by Australian fisheries^{R20,R26,R33}. For the shearwaters, one of the analyses explored the use of offsets as an interim solution to reduce extinction risk in the short term^{R26}. One of the fundamental points that arose in the debate over offsets was that they did not reduce the underlying problem: incidental catch of non-target species. This analysis addresses that issue, exploring the use of offsets as an interim measure while improved fishing methods are developed.

Finally, a discussion paper was developed for the implementation of a biodiversity offset for incidental capture of marine turtles in the ETBF, a Commonwealth managed pelagic longline fishery^{R32}. The underlying concept was included in an early draft of the Australian Fisheries Management Authority (AFMA) draft policy on longline catch of marine turtles.

Key findings

Confusion over how biodiversity offsets might be used in the scientific and economic literature is widespread. In particular, there is a difference in opinion as to whether they should result in a net gain or simply be equivalent to the impact caused by an industry. Two published papers from this work sparked a lively debate in the literature^{R3, R33}. In total, this debate included six full length publications and four letters in peer reviewed journals, covering the most salient points relevant to offsets from an ecological and operational perspective^{R2, R3, R5, R33, R34, R35, R36}.

Biodiversity offsets are sometimes more cost effective than other measures, such as marine reserves and fisheries closures, in addressing bycatch impacts^{R26}.

Offsets are particularly useful as an interim measure to reduce fisheries impacts while fishing methods are improved that result in sustained reduction in fisheries impacts. If they are funded by a levy on the fishery, one would expect offsets to hasten the pace of development of lower impact fishing methods. They should also reduce the net impact of bycatch in a more cost efficient manner than other approaches and provide lasting benefits not achievable through other methods such as fisheries closures.

Opportunities for management

Inexpensive conservation options could be explored as biodiversity offsets in a simple pilot program designed to minimise impacts on marine turtles.

Exploring the use of market based instruments in marine conservation

The use of market-based instruments to create incentives for sustainable resource use in the marine environment is relatively new, with the exception of a few applications in fisheries. This project examined the extension of their use to additional marine conservation issues.

Objectives

This research area had three objectives:

- > To develop several proposed approaches to offsets to a level where they could be considered for conservation management.
- > To explore existing applications of market based instruments.
- > To develop opportunities for new applications of these approaches.

Approach

Using ecological and economic modelling, examination of case studies, and literature review, the project team explored three potential approaches to marine conservation. These were the development of a microloan based alternative to conservation payments; the use of offsets for managing technological improvements in fisheries bycatch; and a technology exchange between fisheries to offset bycatch. An essay that argues the case for considering financial incentives in conservation was also written^{R1}.

Outcome-based payments are becoming a common tool for conservation. A combination of literature review and case studies was used to explore an alternative to payments: the use of

a community run perpetual trust fund to make very small loans on a short-term basis to resource users who agree to make conservation concessions. This approach could address some of the shortcomings of payment programs and would apply in areas such as the Coral Triangle where conservation problems coincide with low levels of economic development^{R6, R21}.

A bioeconomic model was developed to examine whether biodiversity offsets could provide an interim management measure for fisheries bycatch while accelerating development of longer term solutions^{R25, R26}.

The third market-based instrument investigated was the use of technology transfer between fisheries as a means of developing offsets for fisheries bycatch. This is based on a case study in which a high value US fishery was providing technology transfer to a Mexican fishery to help reduce bycatch of a shared turtle stock. The Mexican fishery bycatch rate was 100 times higher than the US rate. Inexpensive investments therefore resulted in very large reductions in bycatch. Colleagues from the US have been deeply involved in this program, and have documented both the costs of the program and its outcomes in terms of conservation^{R28}.

Key findings

Newer approaches to linked conservation and development programs can address some of the shortcomings of existing approaches, including the need for ongoing government or philanthropic financial support.

Multiple avenues exist for the use of offsets, ranging from investments in management of a species, (as in the case of habitat restoration based offsets), to investments in the reduction of impacts from other industries, (as in the case of offsets based on technology transfer between fisheries).

Reviews of the use of market-based instruments in other contexts indicate that in some cases they can be effective at altering behaviour at very low cost. Performance bonds appear to be one of the most promising instruments for application to marine environmental problems.

New knowledge and opportunities

Advice and input was provided to both DSEWPaC and AFMA on the use of market-based instruments for marine conservation. A proposal was developed for a pilot offset program for fisheries bycatch of marine turtles^{R32}. A contribution was made to recent Commonwealth policy developed for the bycatch of turtles, and a review examined the effectiveness of six types of market based instruments relevant to the marine context^{R39}.

Publications

Biodiversity Programs: improving biodiversity management through understanding its origins, structure and dynamics

- B1** Ah Yong, S.T., Baba, K., Macpherson, E., Poore, G.C.B. (2010). A new classification of the Galatheaidea (Crustacea: Decapoda: Anomura). *Zootaxa*, 2676:57–68.
- B2** Andreakis, N., Ah Yong, S., Poore, G. (in prep). Taxonomy, phylogeny, comparative phylogeography and origins of the squat lobster family Galatheaidea in the Indo-Pacific.
- B3** Andreakis, N., Ah Yong, S., Taylor, J. (in prep). Systematics, Phylogenetics, morphological evolution and phylogeographic patterns in Munidopsids.
- B4** Andreakis, N., Gledhill, D.C., Rowe, D.L., Puckridge, M., Innes, B.H., White, W., Butler, A., van Oppen, M.J.H., Last, P.R. (in prep). Signatures of speciation, and the origins of Australian Labrids, Monacanthids and Urolophids.
- B5** Andreakis, N., McCallum, A., Poore, G. (in prep). Galathean species from Western Australia: origins and evolution inferred by multilocus nuclear phylogenies.
- B6** Andreakis, N., McCallum, A., Poore, G. (in prep). Molecular phylogeny, phylogeography and morphological evolution of the squat lobster family Chirostylidae.
- B7** Barrett, N.S., Buxton, C.D., Edgar, G.J. (2009). Changes in invertebrate and macroalgal populations within Tasmanian marine reserves in the decade following protection. *Journal of Experimental Marine Biology and Ecology*, 370(1–2):104–119.
- B8** Butler, A.J. (2010). Précis for managers: understanding the past to predict the future. Report to Department of the Environment, Heritage, Water and the Arts, CSIRO Wealth from Oceans Flagship, Hobart, Australia.
- B9** Butler, A.J., Rees, T., Beesley P., Bax, N.J. (2010). Marine biodiversity in the Australian region. *PLoS ONE* 5(8):e11831.
- B10** Carpenter, K.E., Livingstone, S.R., Abrar, M., Aeby, G., Aronson, R.B., Banks, S., Bruckner, A., Chiriboga, A., Cortés, J., Delbeek, J.C., DeVantier, L., Edgar, G.J., Edwards, A.J., Fenner, D., Guzman, H.M., Hoeksema, B.W., Hodgson, G., Johan, O., Licuanan, W.Y., Lovell, E.R., Moore, J.A., Obura, D.A., Ochavillo, D., Polidoro, B.A., Precht, W.F., Quibilan, M.C., Reboton, C., Richards, Z.T., Rogers, A.D., Sanciangco, J., Sheppard, A., Sheppard, C., Smith, J., Stuart, S., Turak, E., Veron, J.E.N., Wallace, C., Weil, E., Wood, E. (2008). One third of reef-building corals face elevated extinction risk from climate change and local impacts. *Science*, 321:560–563.
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Surrogates Program: improving Australia's capacity to map biodiversity

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*Note: In 2010, the University of Tasmania established the Institute for Marine and Antarctic Studies which includes the Tasmanian Aquaculture and Fisheries Institute (TAFI)

Financial statements

Funds distribution and in-kind contributions summary

	Contribution (\$)	Distribution (\$)
CERF Grant	6,000,000	
UTas contribution	350,000	
MV contribution	15,000	
AIMS		727,068
CSIRO		2,179,013
GA		1,094,208
MV		226,248
UTAS		1,303,463
Field Surveys		360,000
Hub Operations (Administration, Communications, Knowledge Broking)		475,000
Total	6,365,000	6,365,000

In-kind contributions to June 2010

Partner	In-kind \$ budget to end June 10	In-kind \$ actual to end June 10	Actual vs budget to end June 10
AIMS	1,093,853	1,228,974	12%
CSIRO	3,252,258	3,445,678	6%
GA	2,925,471	4,311,069	47%
MV	1,063,150	833,570	-22%
UTAS	2,571,483	2,827,136	10%
Total	10,906,215	12,646,427	16%

Note that Hub work has continued past June 2010 and all partner in-kind contributions will meet budgeted amounts.

In-kind FTE personnel contributions to end June 2010

Partner	Project 1 Biodiversity	Project 2 Surrogates	Project 3 Prediction	Project 4 Mgt Tools	Administration	Total FTE
AIMS	2.34	2.10	2.37	-	-	6.81
CSIRO	4.76	1.24	5.67	2.59	-	14.26
GA	0.40	10.39	0.70	-	-	11.49
MV	6.39	-	-	-	-	6.39
UTAS	0.30	4.90	5.98	-	2.94	14.12
Total	14.18	18.63	14.72	2.59	2.94	53.07

Image credits

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The Marine Biodiversity Hub is funded through the Commonwealth Environment Research Facilities Program (CERF), administered through the Australian Government's Department of Sustainability, Environment, Water, Population and Communities. The key aim of CERF is to provide sound advice to inform environmental public policy objectives and to better the management of Australia's unique environment. (Our stakeholder partners are: AFMA, APPEA, CFA, DAFF, DSEWPac, the Sustainable Tourism CRC, and WWF Australia)