

GREAT AUSTRALIAN BIGHT RESEARCH PROGRAM

RESEARCH REPORT SERIES

Great Australian Bight Benthic Biodiversity Characterisation

Final Report GABRP Project 3.1

Williams A, Tanner J.E, Althaus F, Sorokin S, MacIntosh H, Green M,
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GREAT AUSTRALIAN BIGHT RESEARCH PROGRAM

The Great Australian Bight Research Program is a collaboration between BP, CSIRO, the South Australian Research and Development Institute (SARDI), the University of Adelaide, and Flinders University. The Program aims to provide a whole-of-system understanding of the environmental, economic and social values of the region; providing an information source for all to use.

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EXECUTIVE SUMMARY

The Benthic Biodiversity Theme, Project 3.1 in the Great Australian Bight Research Program (GABRP), has undertaken the first detailed study of benthic biodiversity in the deep (200-3000 m) waters of the Great Australian Bight (GAB). Data were generated during two large-scale surveys [[Section 2](#)] that, to date, are the deepest systematic surveys for benthic biodiversity undertaken in Australia's marine jurisdiction.

The surveys were designed to sample over two gradients along which ecosystem characteristics were expected to vary: depth and east-west (longitude). Sampling was in 6 depth strata – 200 m (shelf break), 400 m (upper continental slope), 1000 and 1500 m (mid-continental slope), 2000 m (lower continental slope), and 3000 m (continental rise) along 5 north-south transects (T1 to T5) at increasing meridians of longitude (i.e. a total of 30 sites). Additional samples came from a topography-based survey – where sites were also on sediments but mostly within or adjacent to potential brine-seep zones (SZ), volcanic seamounts (VSM), and areas with outcropping rocky bottom (OR). These samples were collected by a parallel program - the Great Australian Bight Deepwater Marine Program (GABDMP), a CSIRO led research program sponsored by Chevron Australia.

To provide a background for the survey collections, a full suite of environmental co-variate data were generated and compiled to use in the biodiversity analyses [[Section 3](#)]. The project also compiled historical benthic biodiversity data from the GAB from a comprehensive inventory of museum records for the GAB [[Section 4](#)].

Survey collections were used to generate quality assured species-level taxonomic identifications for the major elements of the benthic fauna [[Section 5](#)]; these data acted as a foundation for detailed analyses of composition, diversity, distribution, abundance, assemblage structure and biogeography of infaunal invertebrates [[Section 6](#)], epifauna [[Section 7](#)] and fishes [[Section 8](#)]. Historical (museum) collections from the GAB were also analysed for biogeographic patterns [[Section 9](#)].

Comprehensive sampling of a large poorly known area such as the deep-sea in the GAB is not realistically feasible. Therefore the use of physical surrogate (covariate) data available at broad scales (remotely sensed oceanographic, hydrographic or acoustic data) is attractive for generating predictive maps of biodiversity and habitat distributions so that spatial extents and changes in them can be used as indicators of ecosystem status. The project explored two different leading-edge methods of predictive modelling: species distribution (habitat suitability) modelling [[Section 10](#)] and gradient forest assemblage mapping [[Section 11](#)]. These analyses demonstrate what is presently

possible for the GAB. The density, quality and relevance of physical covariate data available for the region is yet to be fully evaluated, and further analysis of the project data will be helpful to fully understand the utility of the data sets currently available for predictive mapping.

Project data aimed to provide the basis for understanding how indicators and metrics derived from benthic fauna may contribute to an ecological monitoring program to assess the potential future impacts of oil and gas exploration and/or production on the deep-sea ecosystem of the GAB [Sections 12]. Accordingly, there was relatively high sampling density in the region of the Great Australian Bight Commonwealth Marine Reserve (GAB CMR) and within active oil and gas lease areas. This work included a review of current management arrangements and objectives for the GAB [Section 13].

Project data from baseline (unperturbed) sites provides the basis to evaluate indicators and metrics in future comparisons – a reference-site monitoring approach. We identified several opportunities to develop indicators and metrics by considering the data at both species- and assemblage-level. Many of the opportunities are underpinned by the robust (consistent species-level) taxonomic foundation for the collections taken during this and other studies. This is essential to generate robust metrics for species and assemblage level indicators, and to subsequently develop knowledge about community structural and functional changes (including recovery) in response to disturbance. Data resolved to species-level enable a variety of assemblage-level (composite) metrics (e.g. richness, diversity, distinctness) to be derived, and this is possible across several major taxa collected from the GAB.

The project team has provided selected summaries of benthic biodiversity information to ecosystem models for the GAB being developed by Theme 7 within the GABRP.

1 INTRODUCTION

1.1 Overview

Benthic ecology is a foundation element in any system-level study of the marine environment. Benthic communities are typically composed of a highly diverse fauna that variously influences system productivity, provides structural habitat, alters the physical and chemical condition of the sediment and sediment-water interface, and transfers energy to higher trophic levels. The benthic fauna is composed of infauna (the invertebrate fauna that exist within, or closely associated with, marine sediments) and epifauna (animals living on the surface of the seabed, either attached to the substrate itself (e.g. sponges and corals) or living freely upon it (e.g. crabs, echinoderms, molluscs, fishes). Infauna form part of a key pathway for primary productivity, via detritus from surface waters, to enter the food chain of most deep ocean waters, and ultimately provides the food sources that the benthic assemblage requires, as well as forming the basis for much of the food chain that supports a wide range of economically and socially important species.

Where human pressures on benthic ecosystems are planned to increase, it is necessary to establish a baseline characterisation to assess and understand the extent to which the composition and function of benthic ecosystems may be affected. Oil and gas exploration in the Great Australian Bight (GAB) may increase significantly in the next decade, and will accelerate and expand the need for scientific understanding of the region's marine ecosystems. Despite the high conservation significance of the region's benthic ecosystems (e.g. high expected levels of faunal endemism are protected in a Marine Park and Benthic Protection Zone and by Key Ecological Feature status), characteristics of the deep GAB benthic environment and fauna are largely inferred from knowledge of GAB shelf fauna, and deep fauna off south-east Australia. Virtually nothing is known of the GAB mid- and lower continental slope depths in which oil and gas exploration will be focused – only one site at 1000 m and one at 2000 m depth have been sampled for infauna and epifauna (Currie and Sorokin, 2011).

The proposed baseline benthic characterisation of the GAB is an essential component of research during the early phase of expanded oil and gas-related activities because there are virtually no existing data, because conservation values are untested on the mid- and lower continental slope and continental rise, and because the oil and gas lease areas extend across the GAB Marine Park. Thus, this project is needed (1) to determine a baseline characterisation, including by identifying metrics that may be relevant to monitoring the potential future impacts of oil and gas exploration on benthic

communities in the deep GAB, and (2) to help establish requirements for future ecological monitoring.

This project is one of two complementary projects to determine composition and function of benthic communities. This project (3.1) will provide metrics established from 'traditional' morphometric taxonomic approaches, while the second project (3.2) will evaluate and implement leading-edge molecular methods. The strength of the combined approach is the provision of results and strategies that are familiar and immediately comparable with similar studies in other world oceans (this project), together with results that promise new insights and greater cost-effectiveness for ecological monitoring.

This project provides data that considerably increase our understanding in relation to the following 3 knowledge gaps identified in the literature review by Rogers et al. (2013):

- 1) Benthic infauna are proven indicators of pollution events associated with oil and gas developments, however, virtually nothing is known about the diversity, distribution and ecology of the infaunal assemblages inhabiting the GAB shelf, slope and abyssal plain.
- 2) It is largely uncertain what levels of epifaunal biodiversity and endemism are currently represented on the GAB shelf, slope and abyssal plain. Little information is also available on most aspects of their ecology, including their trophic significance and distributional responses to environmental conditions.
- 3) The types and distributions of abyssal benthic habitats and biodiversity in the GAB are unknown.

1.2 Objectives

1. Quantify spatial patterns in the physical environment, and composition and abundance of benthic fauna, in BP leases and adjacent continental slope areas of the GAB, to provide baseline metrics that may be relevant to monitoring the potential future impacts of oil and gas exploration on benthic communities.
2. Contribute to determining requirements (including identifying potential indicators and metrics), and identify suitable control regions, for future ecological monitoring in the GAB – especially to detect and quantify ecological impacts from oil and gas exploration on benthic communities of the GAB Marine Park (MP).
3. Contribute data and results to models of ecosystem-level structure and function for the GAB developed in Theme 7.

2 Field surveys

Four field surveys contributed data to the benthic biodiversity characterisation presented here: in 2013 the Marine National Facility (MNF) RV *Southern Surveyor* voyage (SS2013_C02) and the Fugro vessel *Southern Supporter* (FU201301), and in 2015, the MNF RV *Investigator* voyages (IN2015_C02 and IN2015_C01). Two of these surveys (SS2013_C02 and IN2015_C02) were conducted under the GABRP, sampling benthic biota at six depth strata (200 m, 400 m, 1000 m, 1500 m, 2000 m and 3000 m) on five north-south transects (T1-T5). The biological sample collection was supplemented with opportunistic collections of macrofauna samples from a BP funded geological survey conducted by Fugro (FU201301), and the GAB Deepwater Marine Program (GABDMP 2016) survey targeting topographically distinct sites. The study area covered by the four surveys is shown in Figure 2.1.

2.1 Survey 1 – RV Southern Surveyor

The MNF vessel RV *Southern Surveyor* was chartered for collecting geological as well as benthic and pelagic biological samples for the GABRP from April 3 to 22 2013. The survey plan, science highlights and summary for voyage SS2013_C02 are available from the MNF website at

<http://mnf.csiro.au/Voyages/Southern-Surveyor-schedules/Plans-and-summaries/Southern-Surveyor-2013.aspx>.

2.2 Survey 2 – Fugro vessel Southern Supporter

The Fugro vessel *Southern Supporter* was chartered by BP to undertake geological sampling in the GAB from April 9 to May 8 2013. Sampling included the opportunistic collection of macrofauna from 8 multicorer deployments which were provided to the GABRP Project 3.1. The FUGRO geology report from this survey is commercial in confidence.

2.3 Survey 3 – RV Investigator (GABRP)

The MNF vessel RV *Investigator* was chartered for collecting benthic and pelagic biological samples for the GABRP from November 29 to December 22 2015. The survey plan, science highlights and summary for voyage IN2015_C02 are available from the MNF website at

<http://mnf.csiro.au/Voyages/Investigator-schedules/Plans-and-summaries/2015.aspx>.

2.4 Survey 4 – RV Investigator (GABDMP)

The MNF vessel RV *Investigator* was chartered for collecting geological and benthic biological samples for the GABDMP from October 25 to November 25 2015. The survey plan, science highlights and summary for voyage IN2015_C01 are available from the MNF website at

<http://mnf.csiro.au/Voyages/Investigator-schedules/Plans-and-summaries/2015.aspx>.

2.5 Permits

Biological collections were conducted under the permits listed in Table 2.1

Table 2.1 List of permits acquired for biological collections during the four surveys listed above

Permit Type	Survey	Permit reference
Australian Department of the Environment and Energy		
Access to biological resources in Commonwealth area for non-commercial purposes	SS2013_C02	AU-COM2013-186
	IN2015_C01 and IN2015_C02	AU-COM2015-284
Commonwealth Marine Parks and Reserves – Scientific research	SS2013_C02	005-APR-130301-01 File # 2013/03282
	IN2015_C01 and IN2015_C02	CMR-15-000344
		File # 2015/00169
Australian Fisheries Management Authority		
AFMA Scientific Permit	SS2013_C02	# 1002443
	IN2015_C01 and IN2015_C02	# 1002838
BP		
Animal Ethics approval - nekton sampling	All surveys	Date: 23 May 2014
Animal Ethics Committee (Department of Primary industries Parks, Water and Environment)		
Animal research approval certificate	SS2013_C02	AEC Project 16/2012-13
	IN2015_C01 and IN2015_C02	AEC Project 19/2014-15

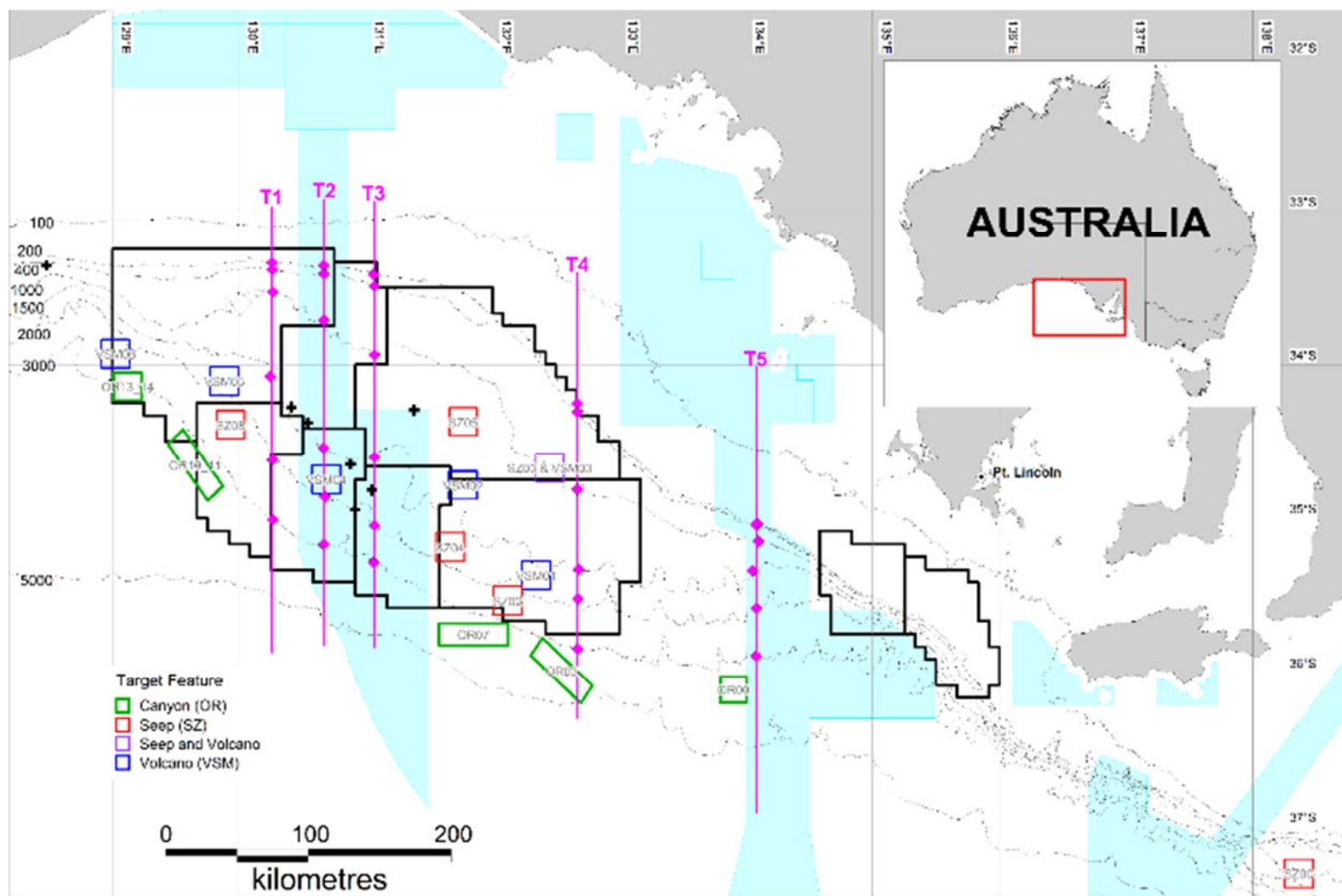


Figure 2.1 Overview of the study area showing the GABRP transects (T1-T5) with depth stratified sampling sites (pink diamonds), the opportunistic macrofauna samples (black crosses), and the GAPDMP topography sites (rectangles - SZ, OR and VSM, see key). Also shown: relevant isobaths (labelled); proclaimed Commonwealth Marine Reserves (shaded light blue); active oil and gas lease blocks (black boundaries). The Inset: study area in relation to Australia.

3 Physical environmental data for the central GAB

Nick Ellis¹, Franziska Althaus¹, Jason E. Tanner² (CSIRO¹ and SARDI² project team)

Surface sediments collected during the recent surveys using corers and sediment grabs were analysed for grain size composition and carbon content (organic, inorganic and total). In total, 38 samples were successfully analysed for carbon content and 37 for grain size composition. These data contributed point records of environmental data for multivariate analyses in Section 6.

A set of broad-scale environmental data layers used for the biophysical analysis, modelling and mapping of biodiversity were collated and spatially assigned to a 0.01 degree grid from a variety of sources (Table 3.1) (Pitcher et al. 2016 and references therein). These include:

1. Bathymetry DEM: depth, slope, aspect — the model bathymetry is based on several sources. The data set uses the Geoscience Australia (GA) GA2009 250m bathymetric product as a background (Whiteway, 2009). The WA state's official coastline (mean tide) was used to define 0 depth and islands. Commercial partners provided bathymetric data based upon LiDAR/LADS surveys and CSIRO and GA provided surveys based on acoustic systems. Australian Hydrographic Service (AHO) and the Western Australian Department of Primary Industries (WA DPI) provided historical soundings. These were integrated and processed in swath mapper processing software by Gordon Keith (CSIRO) into a 0.01 degree gridded product.
2. Sediment: gravel, sand, mud, carbonate — Data sourced from the Australian MARine Sediments Database (MARS), Geoscience Australia (Passlow et al., 2005).
3. Bottom water attributes (annual average and seasonal range): temperature, salinity, oxygen, nitrate, phosphate, silicate — Data sourced from the CSIRO Atlas of Regional Seas (CARS) (<http://www.marine.csiro.au/~dunn/cars2009/>) (Ridgway et al., 2002; Dunn and Ridgway, 2002).
4. NASA Ocean colour (SeaWiFS and MODIS): chlorophyll, light attenuation, SST, surface PAR — satellite derived datasets were processed by IMOS (Edward King) over the period of 2003-2014, gridded at 0.01° (the Integrated Marine Observing System - IMOS is a national collaborative research infrastructure, supported by Australian Government) (IMOS, 2017; <https://imos.aodn.org.au>).
5. Derived variables: benthic irradiance, primary productivity, exported POC (Particulate Organic Carbon) — calculated from ocean colour variables using published algorithms.

6. Seabed current stress — Data sourced from the CSIRO RIBBON Model (<http://www.emg.cmar.csiro.au/www/en/emg/projects/-Ribbon--Model.html>).
7. Bottom stress, output from the GABRP Project 1.1: Bottom stress was averaged over a two year model simulation (2013-2014). The model was developed for Project 1.1.
8. Terrain morphology probabilities: ridge, channel, peak, depression, pass, plane — generated from bathymetric data by Vanessa Lucieer, University of Tasmania. (<http://www.imas.utas.edu.au/people/profiles/current-staff/l/Vanessa-Lucieer>)

See Table 3.1 for the complete list of the predictors and their derivation. All predictors were defined on a 0.01° spatial grid; maps are shown in Figure 3.1 to Figure 3.5, below.

Table 3.1 Descriptions of spatial environmental variables from web-servers, mapped and used in project analyses. Data source numbers refer to the above list of data sets.

Variable	Abbrev.	Description	Units	source
GA_BATHY	BATHY	Depth from bathymetry DEM	m	1
GA_SLOPE	SLOPE	Slope derived from bathymetry DEM	°	1
GA_ASPECT	ASPECT	Aspect of slope derived from bathymetry DEM	°	1
GA_CRBNT	CRBNT	Sediment carbonate (CaCO ₃) composition	%CaCO ₃	2
GA_GRAVEL	GRAVEL	Sediment gravel grainsize fraction, ($\phi > 2$ mm)	%	2
GA_SAND	SAND	Sediment sand grainsize fraction, ($63 \mu\text{m} < \phi < 2$ mm)	%	2
GA_MUD	MUD	Sediment mud grainsize fraction, ($\phi < 63 \mu\text{m}$)	%	2
GA_ROCK	ROCK	Rock exposure (%) at the sediment surface	%	2
GA_GRNSZ	GRNSZ	Sediment characteristic grainsize, log(mean) ϕ		2
GA_SORTG	SORTG	Sediment grainsize dispersion, ϕ standard deviation		2
CRS_NO3_AV	NO3	Nitrate bottom water annual average NO ₃	μM	3
CRS_NO3_SR	no3	Nitrate Seasonal Range	μM	3
CRS_PO4_AV	PO4	Phosphate bottom water annual average PO ₄	μM	3
CRS_PO4_SR	po4	Phosphate Seasonal Range	μM	3
CRS_O2_AV	O2	Oxygen bottom water annual average O ₂	mL L^{-1}	3
CRS_O2_SR	o2	Oxygen Seasonal Range	mL L^{-1}	3
CRS_S_AV	S	Salinity bottom water annual average S	‰	3
CRS_S_SR	s	Salinity Seasonal Range	‰	3
CRS_T_AV	T	Temperature bottom water annual average T	°C	3
CRS_T_SR	t	Temperature Seasonal Range	°C	3
CRS_SI_AV	SI	Silicate bottom water annual average SI	μM	3
CRS_SI_SR	si	Silicate Seasonal Range	μM	3
CHLA_AV	CHLA	Chlorophyll annual average from SeaWiFS	mg m^{-3}	4
CHLA_SR	chla	Chlorophyll Seasonal Range	mg m^{-3}	4
K490_AV	K490	Attenuation coefficient at wavelength 490nm annual average from SeaWiFS	m^{-1}	4
K490_SR	k490	Attenuation coefficient Seasonal Range	m^{-1}	4
SST_AV	SST	Sea Surface Temperature annual average from Modis	°C	4
SST_MAX	sst	Sea Surface Temperature maximum of monthly average	°C	4
NPP_AV	NPP	Net Primary Production annual average from SeaWiFS	$\text{mg C m}^{-2}\text{day}^{-1}$	4
NPP_SR	npp	Net Primary Production seasonal range	$\text{mg C m}^{-2}\text{day}^{-1}$	4

Variable	Abbrev.	Description	Units	source
PAR_AV	PAR	Photosynthetically Active Radiation (PAR) from MODIS	E $\text{m}^{-2}\text{day}^{-1}$	4
PAR_SR	par	Photosynthetically Active Radiation seasonal range	E $\text{m}^{-2}\text{day}^{-1}$	4
EPOC_AV	EPOC	Export Particulate Organic Carbon flux annual average from SeaWiFs	mg C $\text{m}^{-2}\text{day}^{-1}$	5
EPOC_SR	epoc	Export Particulate Organic Carbon seasonal range	mg C $\text{m}^{-2}\text{day}^{-1}$	5
BIR_AV	BIR	Benthic Irradiance annual average, $\text{BIR} = \text{PAR} \times e^{-(K_{490} \times \text{Depth})}$	E $\text{m}^{-2}\text{day}^{-1}$	5
BIR_SR	bir	Benthic Irradiance Seasonal Range	E $\text{m}^{-2}\text{day}^{-1}$	5
BSTRESS	BSTRESS	Seabed tidal current stress from CSIRO Ribbon model, RMS mean	Nm^{-2}	6
BSTR_AV	BSTR_AV	Average bottom stress derived from BENTHIS model (mean over 2 year model simulation)	Nm^{-2}	7
BSTR_MAX	BSTR_MAX	Maximum of bottom stress derived from BENTHIS model (max of 2 year model simulation)	Nm^{-2}	7
BSTR_SD	BSTR_SD	Standard deviation of bottom stress derived from BENTHIS model (stdev)		7
TERAN_CHAN	CHAN	Terrain channel, probability of membership of topographic shape "channel"		8
TERAN_PASS	PASS	Terrain pass, probability of membership of topographic shape "pass"		8
TERAN_PEAK	PEAK	Terrain peak, probability of membership of topographic shape "peak"		8
TERAN_PIT	PIT	Terrain pit, probability of membership of topographic shape "pit"		8
TERAN_PLAN	PLAN	Terrain plane, probability of membership of topographic shape "plane"		8
TERAN_RIDG	RIDG	Terrain ridge, probability of membership of topographic shape "ridge"		8

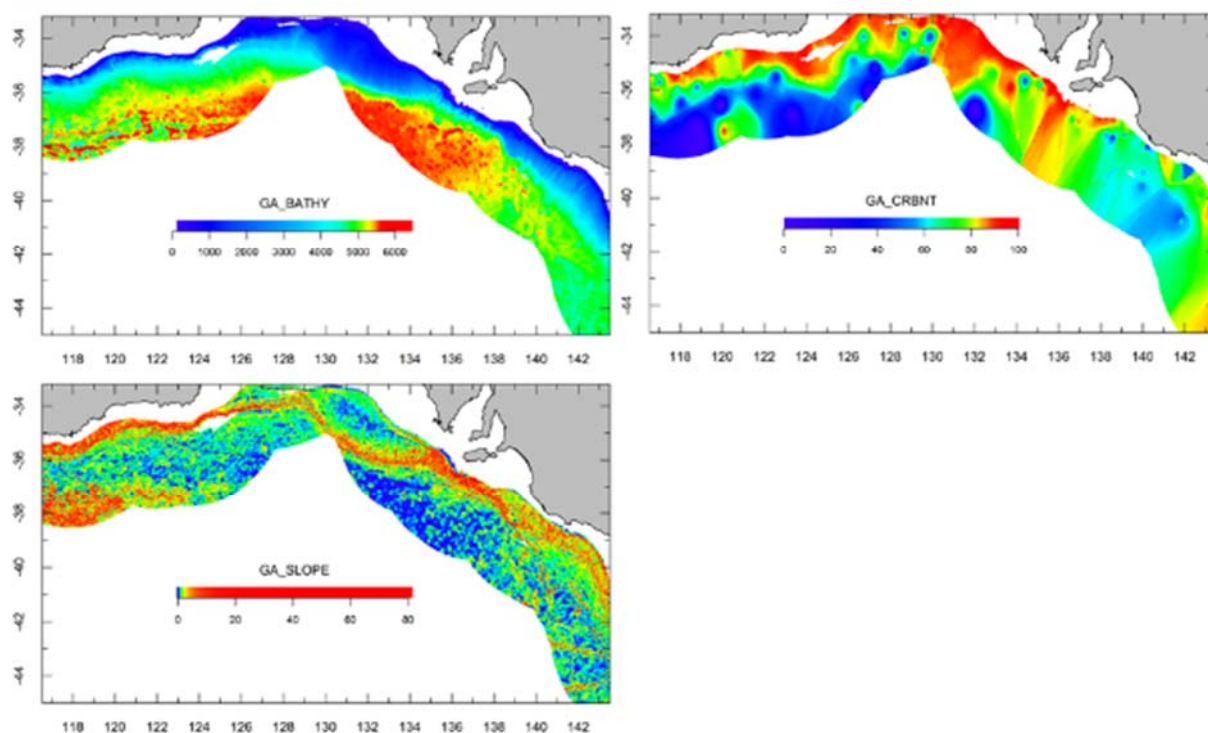


Figure 3.1 Bathymetry variables defined on a 0.01° spatial grid; for definition of the abbreviations and units see Table 3.1 – source 1.

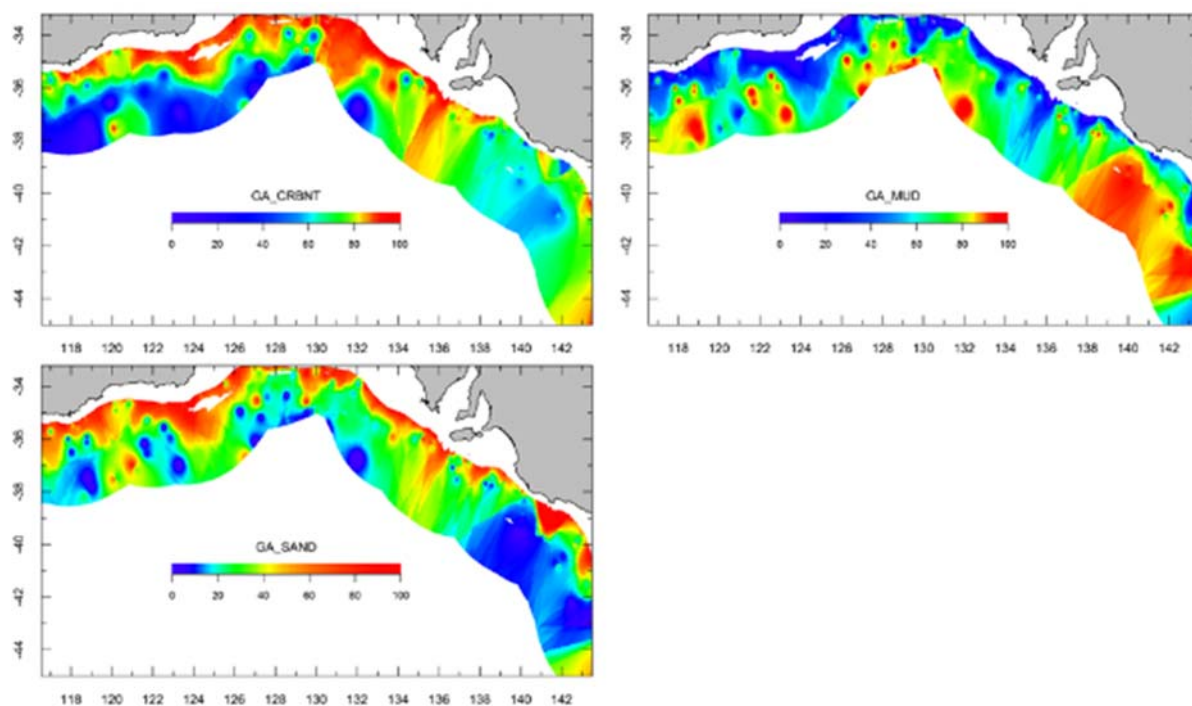


Figure 3.2 Sediment variables defined on a 0.01° spatial grid; for definition of the abbreviations and units see Table 3.1 – source 2.

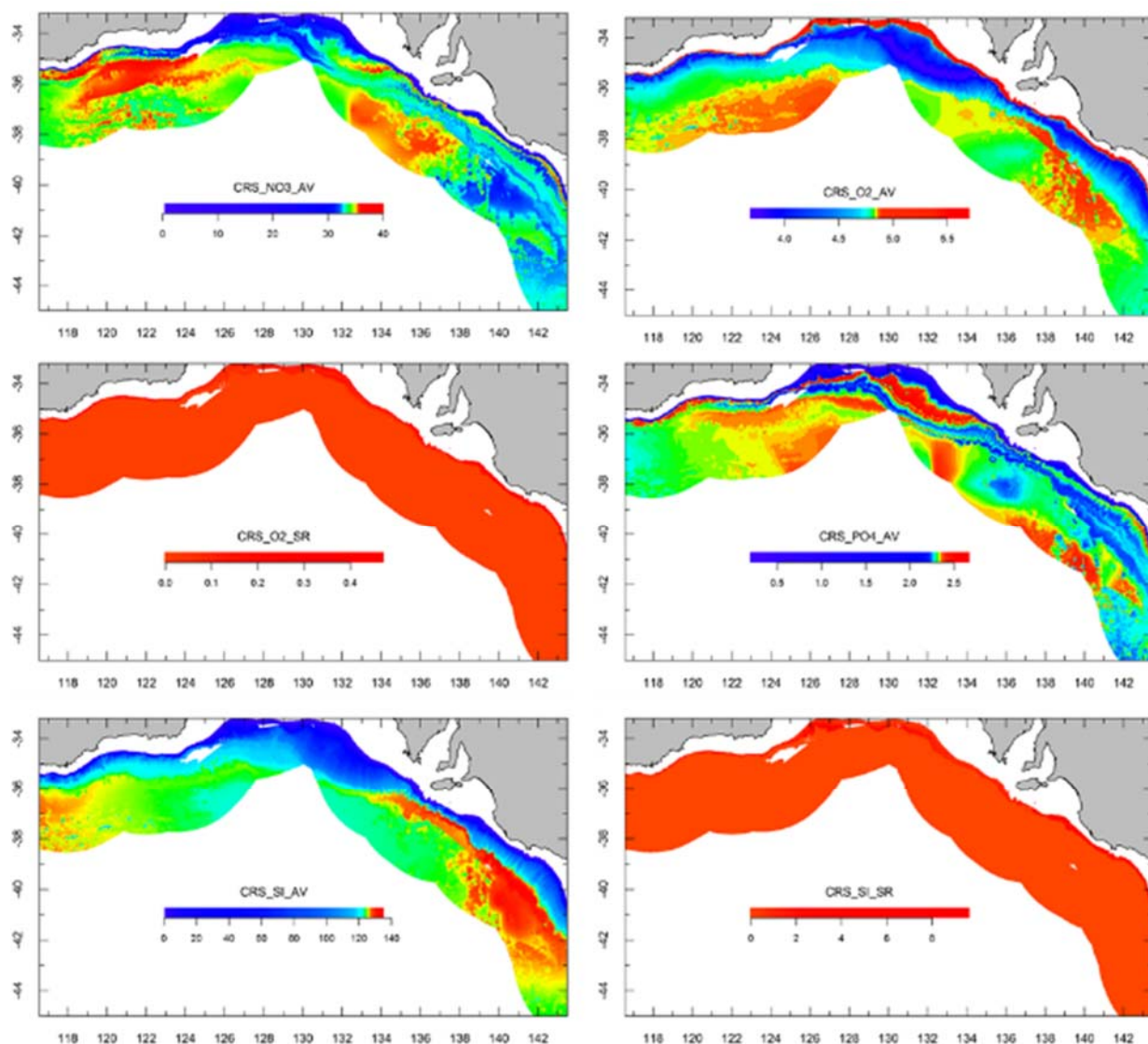


Figure 3.3 Bottom water-column variables defined on a 0.01° spatial grid; for definition of the abbreviations and units see Table 3.1 – source 3.

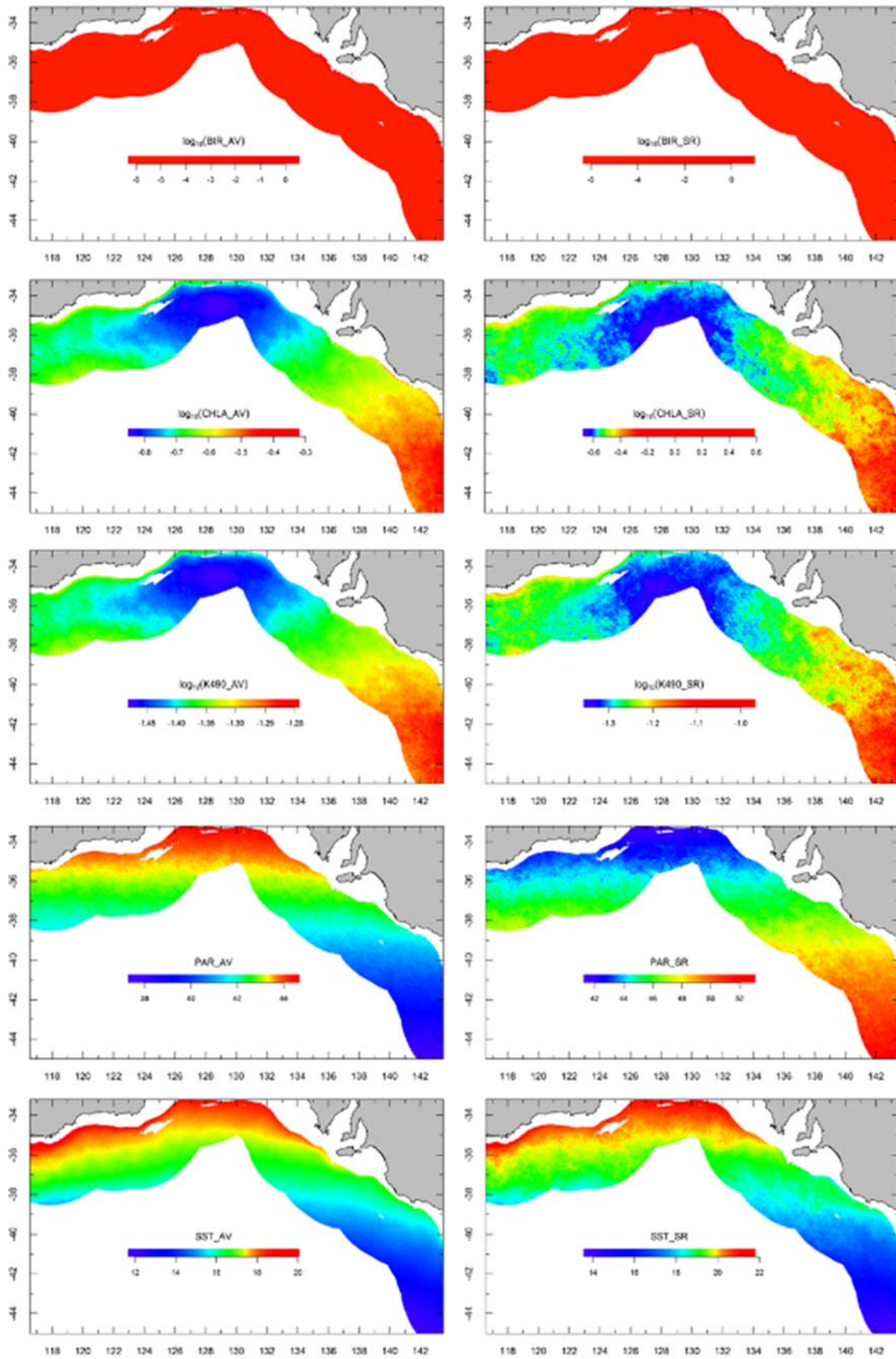


Figure 3.4 Remotely sensed variables defined on a 0.01° spatial grid; for definition of the abbreviations and units see Table 3.1 - source 4 and 5.

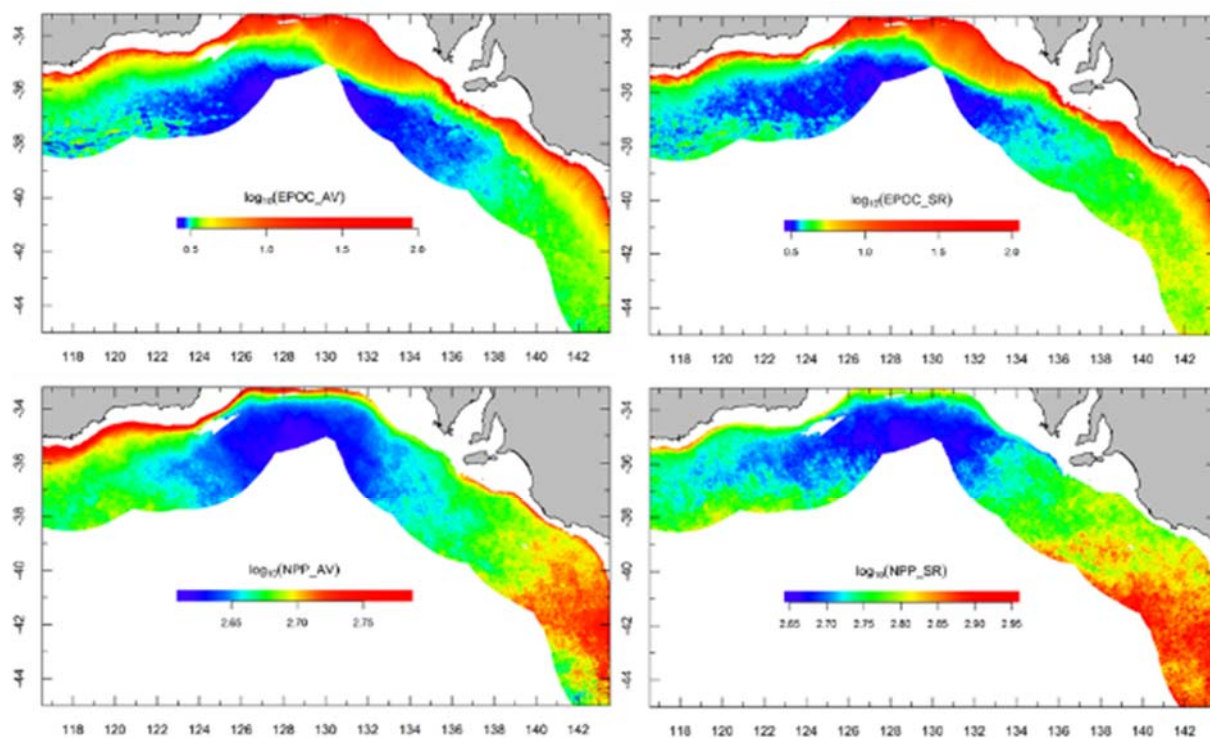


Figure 3.5 Productivity variables defined on a 0.01° spatial grid; for definition of the abbreviations and units see Table 3.1 – source 4.

4 Collation of historical data for Australian temperate deep-sea epibenthos

Shirley J. Sorokin¹, Franziska Althaus², Alan Williams², Jason E. Tanner¹ (SARDI¹ and CSIRO² project team)

4.1 Introduction

4.1.1 Background

As part of the Great Australian Bight (GAB) benthic biodiversity characterisation research program, existing information on the deep-sea (>200 m depth) epibenthos and demersal fish present in both the GAB region and other temperate Australian deepwater biomes needs to be collated to help develop our understanding of what assemblages are present in the GAB, and how they relate to those present in similar adjacent environments.

4.1.2 Objectives

Our aim was to document museum holdings of specimens, as well as historical survey catch-data holdings from the region. Initially this was only to include deep-sea (200 m depth and greater) GAB specimens held by the South Australian Museum (SAMA). This was expanded to include SAMA holdings from the whole of the temperate Australian slope, and database extracts of specimen holdings from all other Australian Museums for depths >200 m from Perth to Sydney where available. The objectives of documenting this data collection were to:

- highlight gaps in our knowledge of benthic groups living on the GAB slope.
- contribute to providing a ‘baseline’, albeit mostly presence only data, to compare with new collections.
- enable biogeographic comparisons to be made between the GAB and adjacent deepwater biomes.
- identify the taxonomic expertise currently available in Australia

4.2 Methods

4.2.1 Collation of Museum holdings

South Australian Museum (SAMA)

SAMA has recently introduced Emu, an Electronic Museum database management tool, but at the start of this study almost no data from the marine invertebrate collection had been entered into this system. To document deep-sea benthos, a time-consuming systematic search of museum shelves

was necessary. Data were entered into Excel and then transferred into the EMu system with the assistance of SAMA staff. SAMA collections of fish specimens were not fully curated or databased, and therefore were not systematically examined.

Data from other Australian museums

Database extracts were requested from museums throughout Australia for all specimen lots with collection depth >200 m from temperate Australia (collection location between 32°S and 44°S) (Figure 4.1). The received data were collated into a single table and mapped (where valid coordinates were available). An identification level flag (species, genus, etc.) was added to the data for summaries.

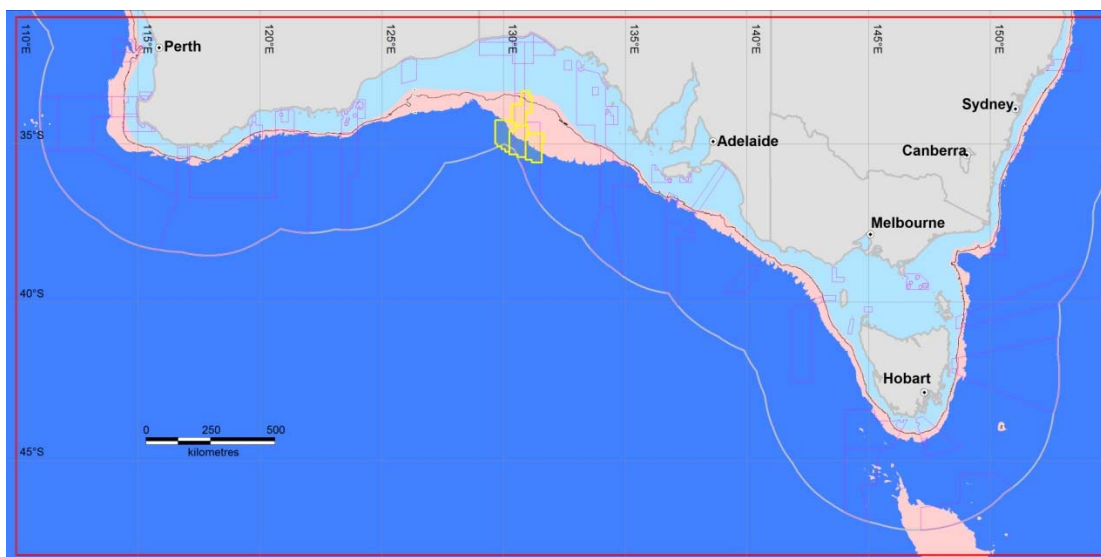


Figure 4.1 Area of study (red box) showing the Australian EEZ (grey outline), the Commonwealth Marine Reserve network (pink outlines) and the BP exploration leases (yellow); The 200 m to 2000 m depth range is highlighted (red) and the 700 m contour shown (black line).

4.2.2 Historical survey catch data

Catch composition data from scientific surveys have the advantage over museum collections of being truly quantitative. The CSIRO Data Trawler, a public data portal of survey data held at the CSIRO data centre (<http://www.cmar.csiro.au/trawler/>), was queried for all biological catch data from research surveys located in our target area (31° to 48°S and 110° to 155°E). In addition, we extracted survey data from published SARDI reports. Selected specimens and potentially whole collections from some of these surveys would have been lodged with various Australian museums, resulting in some overlap of these data with the museum holdings data. However, it may be expected that the majority of the catches from these research surveys were discarded after being identified and documented in a catch composition record.

4.2.3 Taxa of interest

We have concentrated our efforts on seven ‘taxa of interest’: six epibenthic invertebrate taxa and demersal fishes. A short synopsis of the taxa of interest is given below. Identifications used in this analysis are the best available at the time of writing; the process of upgrading taxonomic identifications is an ongoing process and some groups such as sponges are being actively worked on during and beyond the project.

Most of these taxa have been the focus of detailed taxonomic work for biodiversity surveys on Australia’s continental slope off Western Australia and Tasmania, led by CSIRO (see Williams et al., 2005; 2007a; 2007b; McEnnulty et al., 2011; Alderslade et al., 2014). They were chosen based on the availability of taxonomic experts for those groups, and recent and ongoing work on the Australian fauna. The distribution of these taxa in the GAB will fill in a gap in these data. Additional taxa were chosen due to their potential for informing biogeographic patterns in the GAB (Bryozoa), or because of their potential to act as indicator species (Sipuncula) (Weisberg et al., 2008). Other invertebrates (Annelida, Tunicates and minor phyla) were not examined — any specimens from these phyla included in the data are incidental and have been entered for completeness of data entry if they are part of a collection e.g. ‘Benthic Protection Zone’ (BPZ) collection (Currie and Sorokin, 2011b).

Porifera

Porifera (sponges) commonly have the greatest biomass in temperate epibenthic communities (e.g. Currie et al., 2008). Collections off the WA coast (including in the western GAB) have been identified to species or operational taxonomic units (Fromont et al., 2011), and described in ‘mud maps’ by Jane Fromont and Oliver Gomez (see McEnnulty et al., 2011). Shirley Sorokin has reported on the sponge collections from the GAB shelf (Sorokin et al., 2005; 2007). Including sponges as a taxon of interest enables us to build on this previous work.

Cnidaria: Alcyonacea and Scleractinia (corals) and Actiniaria (anemones)

Coldwater corals are important habitat formers in the deep-sea that are often used as indicators for vulnerable marine environments (VME) (e.g. Munoz et al., 2009). Phil Alderslade is actively identifying deepwater (>80 m depth) octocoral collections from Australia (e.g. Alderslade et al., 2014). This work identified a data gap for this taxon in the GAB. In addition, reef-forming stony corals (Scleractinia), such as *Solenosmilia variabilis*, have been collected from seamounts in the western GAB and south of Tasmania (Koslow et al., 2001; Williams et al., 2010a). It was expected that this species will be found in suitable habitats in the central GAB, as well. Actiniaria may be colonisers in disturbed deep-sea environments (CSIRO unpublished data).

Mollusca

Molluscs are a well-studied group of benthic epifauna. Rogers et al. (2013) point out that there are historical collections of molluscs from the GAB shelf, however, their distribution has not been well studied in the region. No-one is currently examining deepwater specimens.

Echinodermata

Echinodermata, and in particular Ophiuroidea (brittle stars), are identified as being a taxon of interest due to previous deepwater biogeographical work by Tim O'Hara (O'Hara, 2008) through the National Environmental Research Program (NERP) Marine Biodiversity Hub (e.g. O'Hara et al., 2014). Holothurians (O'Loughlin and Maric, 2008; O'Loughlin et al., 2007), and Asteroids (O'Loughlin, 2009), are the focus of current research by Mark O'Loughlin (NMV). Australian crinoids have been the subject of phylogenetic work by Greg Rouse (Rouse et al., 2013).

Arthropoda: Decapoda (crabs, lobsters, prawns) and Pycnogonida (sea spiders)

Decapod crustaceans are well studied in Australian waters (Poore, 2004, Poore et al., 2008). Taxonomists including Gary Poore, Anna McCallum (NMV) and Shane Ahyong, Australian Museum (AM), are involved in current research projects identifying and analysing the distribution of various groups within the decapod crustaceans, for example through the NERP Marine Biodiversity Hub (e.g. McCallum et al., 2013a; 2013b). New species of Pycnogonids (Sea spiders) in Australia have been described by David Staples (NMV) (Staples, 2002; 2007). Specimens from recent CSIRO biodiversity surveys have been identified by Claudio Arango and their distribution noted (e.g. McEnulty et al., 2011).

Bryozoa (lace 'corals')

Bryozoa form an important part of the GAB shelf epifauna and contribute a high proportion of the biofragments in the GAB sediments (James et al., 2001). This taxon is not the subject of active research in Australia, and many samples remain unprocessed in museums (Phil Bock (NMV) pers. comm.); however, the existing distribution data may be informative.

Sipuncula

The sipunculans were included as a potential indicator group for hydrocarbon seeps (Weisberg et al., 2008). Very little is known about their distribution in Australia.

Chordata: Pisces (fishes)

Demersal fishes are relatively well studied in deepwater temperate Australia, and have been used for bioregionalisation of the Australian shelf and slope waters (Last et al., 2005). A recent text (Gomon et al., 2008) documents the species occurring in the GAB and information on distributions

and ecology. Whilst this book is fairly up-to-date on deep-sea fishes, there are few records from depths below the mid-slope (~1500 m). Local taxonomists include Ralph Foster at the SAMA.

4.3 Results

4.3.1 South Australian Museum Data

A total of 1795 specimen lots were registered and entered into the SAMA database; of these, 1774 specimen lots belonged to the seven targeted phyla (Table 4.1).

Table 4.1 Summary of SA Museum specimen lots for the seven targeted phyla.

Phylum	Total registered	ID to Species	ID only	ID only	ID only	ID only to Class	ID only to Phylum
			to Genus	to Family	to Order		
Arthropoda	445	244 (58%)	43	99	41	17	1
Bryozoa	101	33 (32%)	38	21	1	2	7
Cnidaria	430	208 (48%)	98	23	63	22	16
Echinodermata	451	198 (44%)	57	40	0	156	0
Mollusca	230	145 (63%)	28	52	0	5	0
Porifera	120	18 (15%)	24	11	4	39	24
Sipuncula	7	1 (14%)	0	1	0	0	5
TOTAL	1774	848 (48%)	289	247	109	233	49

Notes:

- Phylum Arthropoda: the arthropods are a vast phylum, occupying several ecosystems in the ocean. For the purposes of this study only the order Decapoda and the class Pycnogonida were documented at the SAMA. Parasites, infauna and plankton were excluded from this documentation. However, these are included in other Australian museum data (below).
- Most of the material (86%) had been collected by Wolfgang Zeidler and Karen Gowlett-Holmes from commercial fishing vessels (by-catch) (58%) and surveys on the CSIRO research vessels RV *Soela* and RV *Franklin*, and more recently by David Currie on the National Facility vessel RV *Southern Surveyor* (28%) (Table 4.2). There are also some old collections from Joseph Verco, however, few of these from depths greater than 200 m have explicit geolocation data; they were entered into the database for completeness.
- 48% of the specimens in the database are identified to species level; 86% are identified to family level. Specimens of the class Ophiuroidea have been examined by Tim O'Hara when he identified the survey collection described above; updates on identifications for these specimens are now available.

- There are many occurrences of multiple specimen lots for one species, so specimen lots not identified does do not necessarily reflect the number of species to be identified.
- Ralph Foster at the SA Museum has provided a spreadsheet of 164 ‘deep-sea’ fishes from the GAB kept at the SAMA, however no depths were given.

Table 4.2 Summary of vessels used for collection of deepwater samples that are lodged at the South Australian Museum.

Vessels	Years	Sample lots	Main collectors
<u>Research vessels</u>			
RV <i>Franklin</i>	1994-5	165	CSIRO/Zeidler, Gowlett-Holmes et al.
RV <i>Soela</i>	1981,84,87,89,92	289	CSIRO/Zeidler
RV <i>Southern Surveyor</i>	2010	62	Currie
FIS <i>Endeavor</i>	1909-10	2	Verco
<u>Fishing vessels</u>			
FV <i>Adelaide Pearl</i>	1988	113	Gowlett-Holmes et al.,
FV <i>Akebono Maru III</i>	1989	8	Baron
FV <i>Belinda</i>	1992	106	Gowlett-Holmes
FV <i>Comet</i>	1989	212	Gowlett-Holmes, Zeidler
FV <i>Corvina</i>	1992	16	Gowlett-Holmes
FV <i>John Longva</i>	1989-90	15	Smenes/Davey
FV <i>Labrador</i>	1990	92	Gowlett-Holmes
FV <i>Longva III</i>	1989-90	347	Gowlett-Holmes
FV <i>Merindah Pearl</i>	1988	2	Jubb
FV <i>Ocean Raider</i>	1988	15	K. Golgan
FV <i>Orion</i>	1990	4	Turner
RV <i>Rosalind Star</i>	1980	1	-
FV <i>Saxon Progress</i>	1989	64	Wheenan; Lowe; Jubb
FV <i>Silent Victory</i>	1987-88	53	Gowlett-Holmes et al.,
FV <i>TeenaB</i>	1992	1	CSIRO/Lewis
<u>Naval vessel</u>			
HMAS <i>Diamantina</i>	1972	1	Unknown
Unknown (no vessel on label)		231	Various

4.3.2 Data from other Australian museums

Database extracts were received from the Australian Museum, Museum Victoria, Queensland Museum (QM), Western Australian Museum (WAM) and the Northern Territory Museum of Arts and Sciences (NTM) (Table 4.3 and Figure 4.2). Data from Tasmanian museums were not received; large deepwater collections, particularly from waters east of Tasmania, are held but their data entry system makes it impossible to sort specimens on geolocation data. The AMS and NMV have the largest holdings of Australian marine invertebrates (Table 4.3). The geographic distribution of samples in Australian museums (Figure 4.2), shows that the bulk of specimen lots from the GAB *sensu stricto* are at SAMA, while the NMV collections range across temperate Australia. AMS collections are predominantly from Australia’s east coast. Table 4.4 shows an approximate estimate of the number of specimen lots that are held by museums, but not yet databased.

Table 4.3 Data for holdings of deepwater temperate invertebrates (6 phyla) and for fishes at Australian museums.

Phylum	AMS	NMV	NTM	QM	SAMA	WAM	Total
Arthropoda	3486	3862	20	1	445	80	7894
Bryozoa	120	13	0	1	101	0	235
Cnidaria	349	126	40	20	430	4	969
Echinodermata	1696	1347	0	0	451	46	3540
Mollusca	5916	1239	17	0	230	232	7634
Porifera	64	6	3	165	120	17	365
Sipuncula	33	4	0	0	7	0	44
Total invertebrates	11664	6597	80	187	1774	379	20681
Fishes	4703	6315		52		4703	

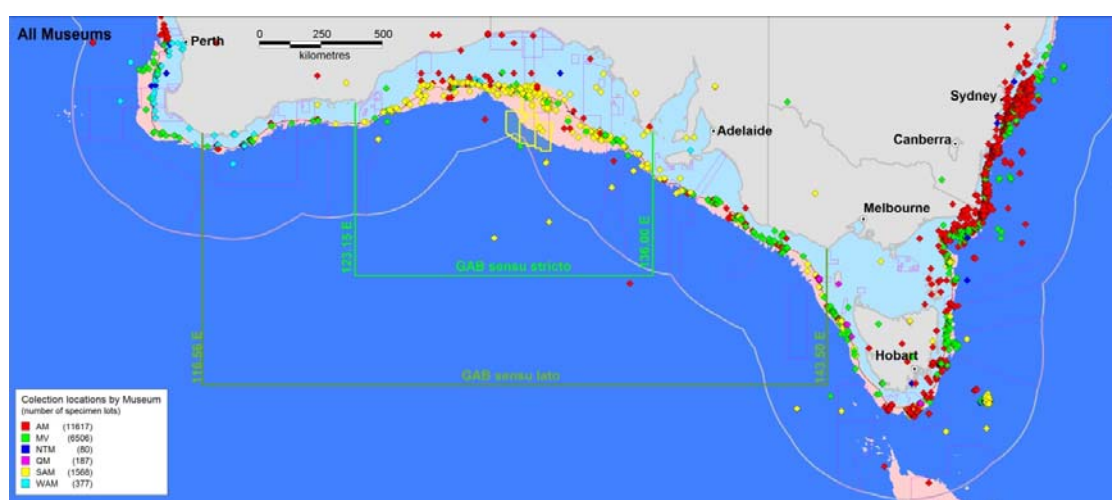


Figure 4.2 Mapping of all marine invertebrate specimen lots that have a valid geographical reference – coloured by institution (includes all phyla).

Table 4.4 Missing data: approximate percentage of deepwater temperate marine invertebrate lots still to be databased for each museum.

Phylum	AMS %	NMV%	NTM%	QM%	SAMA%	WAM%	TMAG%
Arthropoda	10 (400 lots)	n.p.	0	0	?10-20 ¹	10-15%	100
Bryozoa	25 (30 lots)	n.p.	0	0	0	n.p.	100
Cnidaria	15 (50 lots)	n.p.	0	0	0	n.p.	100
Echinodermata	6 (100 lots)	n.p.	0	0	0	n.p.	100
Mollusca	~60 (? Lots)	n.p.	0	0	0	n.p.	100
Porifera	30 (20 lots)	n.p.	0	0	0	n.p.	100
Sipuncula	30 (10 lots)	n.p.	0	0	0	n.p.	100

1. Only decapods and pycnogonids were databased. No parasites or plankton included in database. n.p = not provided.

4.3.3 Historical survey catch data

The CSIRO data trawler (CSIRO, 2017) query yielded 108 surveys between 1965 and 2007, with a total of 9934 sampling stations and 171 200 catch records (Figure 4.3).

Of the surveys, 37 were field program dive surveys in shallow waters (a total of 468 sampling stations). The remaining 71 surveys were research voyages; a total of 6980 sampling stations from these voyages were on the shelf (<200 m depth), and the remaining 2486 were on the slope (>200 m). Sixteen surveys sampled only shelf stations, while 55 surveys sampled in water beyond 200 m depth (Figure 4.4).

SARDI reports and publications identified location data for repeat surveys in 2002 and 2006 in the central GAB and toward Port Lincoln (Currie et al., 2007 - infauna; Currie et al., 2008 - epifauna) and a 2008 survey in two canyons south of Adelaide (Currie and Sorokin 2011a); 3 deep samples in the central GAB were also taken on a transit survey (Currie and Sorokin 2011b) (Figure 4.3, below). A total of 234 sampling locations are covered, but most samples (121 – especially from the 2002/2006 surveys) were taken on the shelf, and only 93 were from depths >200 m.

Benthic invertebrate data from the slope are of particular interest. The SARDI surveys list comprehensive catch compositions of all epibenthic and infaunal invertebrates sampled.

The CSIRO data trawler data-set included (Figure 4.4):

1. 43 surveys between 1965 and 2001 where only fish were reported
2. 11 surveys between 1978 and 1994 where fish and molluscs were reported
3. 12 surveys between 1979 and 1993 where fish, molluscs and some crustacea were reported

4. 8 surveys between 1994 and 2007 where all epibenthic invertebrates and fish (if caught) were reported.

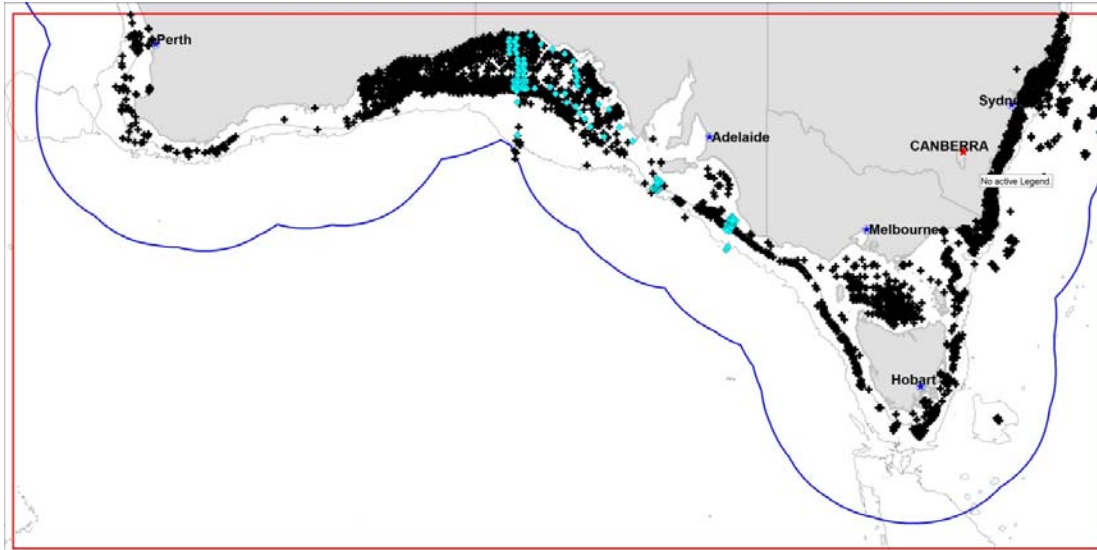


Figure 4.3 Location of sampling stations with catch data published in the CSIRO data trawler (black +) and from SARDI (blue diamond) (Currie et al., 2008; Currie and Sorokin 2011a and b).

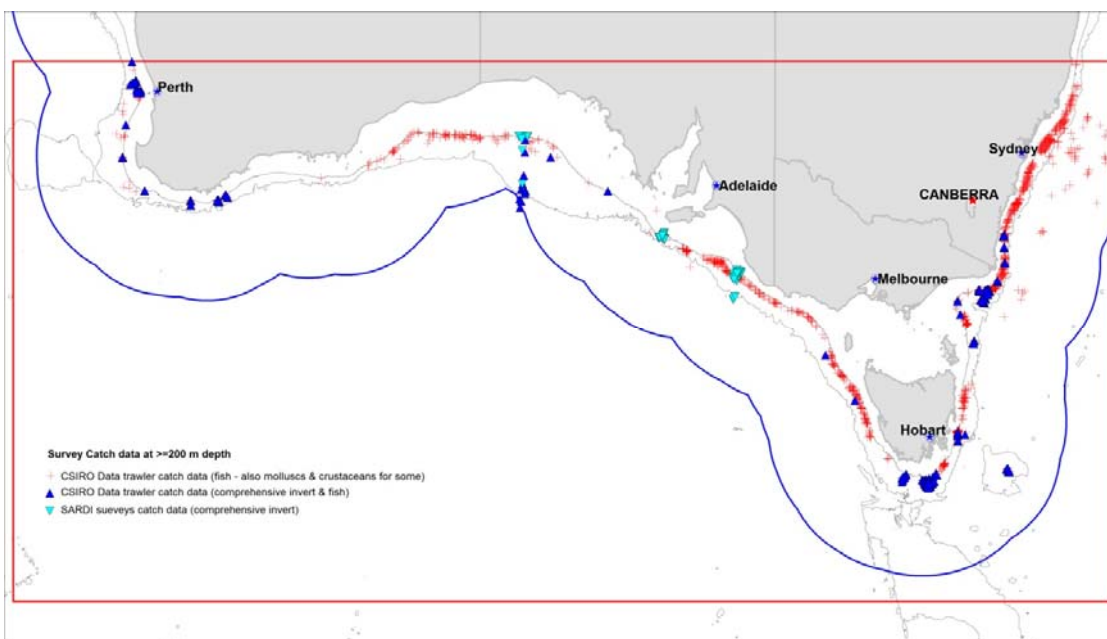


Figure 4.4 Sampling stations on the continental slope (>200 m depth) from the CSIRO trawler and SARDI, segregating the data sets where benthic invertebrates were included in the data from basic fish catch data.

4.3.4 New taxonomic work on potentially informative taxa

Ophiuroids from the SA Museum's historical collection, and three 2013 GAB beam trawls, were identified for this project by Tim O'Hara. This work has resulted in the recent publication of a new

species and new records of ophiuroid species in South Australian waters in the Memoires of Museum Victoria (O'Hara and Harding, 2014).

Galatheidae (squat lobsters) from the SA Museum holdings had been identified previously by Shane Ahyong. In addition, Anna McCallum has been identifying selected galatheids held at SAMA, including specimens collected by the 2013 GAB survey (SS2013_C02).

Porifera (sponges) holdings of the SAMA, were preliminarily examined by Shirley Sorokin (SARDI). There are 120 sponges databased from SAMA, plus 20 from the SS2013_C02 beam trawls. On first inspection, some appear to be the same types as the WAM specimens (as per McEnnulty et al., 2011). Most Calcarea 'lots' are a mixture of calcareous sponges and need to be separated before putting to Operational Taxonomic Units (OTUs) – this means an increase in the number of lots from the raw data presented here. Species identification 'mud maps', similar to those produced for sponges from WA by Fromont and Gomez (in McEnnulty et al., 2011), species mapping and biogeographical data (from ABRS data) are presented in a separate GABRP report (Sorokin et al 2017).

Preliminary examination of fish holdings at the SAMA by Alan Williams revealed a relatively small collection, which is being actively upgraded and recorded in an electronic database. As such, the SAMA collection will make a small but valuable addition to existing presence-only records of deep benthic GAB fishes. There is no existing quality-assured dataset of distributions of individual fish species in the GAB region. Data in the Atlas of Living Australia (ALA) provide useful checklists and distribution maps for fishes in deep GAB waters, but these are generated from species-distributional records defined predominantly by range end-points. Database extracts of species point distributional records (presence-background data) could be made from some individual museum databases (e.g. held at CSIRO and NMV), but many of the deep water species identifications are at low taxonomic resolution and/or have low reliability. The considerable effort required to upgrade these data is outside the scope of this project.

As part of an ongoing CSIRO project (MarLIN record 14446; <http://www.cmar.csiro.au/marlin/>), Phil Alderslade has examined and consistently identified all museum octocoral holdings (239 lots) from the GAB region (data include are from AMS - 117, SAMA - 89, NMV - 5, NTM -28). These records have been integrated into a database of Australian octocorals described by Alderslade et al., (2014). The museum records from the GAB region have added 64 octocoral species to the database, three of which are new to science (CSIRO unpublished data).

4.4 Discussion

4.4.1 Utility of the data

Survey data and specimen collections hold information about species distributions and the composition of communities at a regional scale. In order to assess the risks that human activities pose to the local ecosystem, and to develop ecological monitoring strategies, it is important to have a baseline of the communities and species present prior to commencement of any activities.

Our data compilation provides an important supplement to the new survey data collected during the project, to help establish baseline conditions (faunal composition and abundance at contrasting locations) prior to the commencement of current exploration activities. This is in contrast to preparedness in other locations, including for example the Gulf of Mexico, where no pre-spill macrofauna sampling was available from the vicinity of the Deepwater Horizon spill site. In order to assess the magnitude of the spill's impact in that location, Wei et al. (2012) used historical survey and collection data from the general region to model the pre-spill benthic biomass.

Our data are also valuable in helping focus the collection of new survey data, including to identify the taxonomic expertise required to tackle informative faunal groups, and to fill knowledge gaps. The identification and collation of existing museum records for the GAB region facilitates our engagement with taxonomic experts tasked with identifying new collections - such as those generated by our 2013 and 2015 surveys.

Our work has made the GAB faunal data much more 'discoverable', and will accelerate the process of examining and comparing collections from the GAB region – including by using new taxonomic techniques (e.g. O'Hara and Harding, 2014). Thus, our work not only benefits the current project, but also contributes to a broader scientific understanding of the temperate Australian region by increasing the knowledge of species distributions, populations and evolutionary processes.

A key advance for the project has been to understand the form of the historical data, and to evaluate suitable methods for its analysis. The GAB historical data are not suited to analysis of community structure and predicted distributions using well-established methods because these rely on having records of 'presence-abundance' - counts or biomass for all species. In contrast, the historical GAB data are predominantly 'presence-only' data, in which there are typically records of only the species present, most often without records of their abundance, in restricted locations and not spanning environmental gradients.

In Section 10, we use these historical data in combination with our own data for species distribution modelling, to develop predictive models to establish the potential distribution of benthic fauna across the broader GAB including in regions that lack samples. Our compilation of data across

southern Australia (i.e. beyond the central GAB) will facilitate making biogeographic comparisons with adjacent deepwater biomes, helping us to determine whether the deepwater GAB fauna are unique, or if the deepwater GAB is part of a broader southern Australian biogeographic province.

5 Invertebrate diversity in the deep Great Australian Bight (300-4500 m)

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5.1 Introduction

It is often repeated how vast and unexplored the deep sea is, but it is a rare opportunity to explore a completely unknown region – especially right offshore a country like Australia, famed for its unique diversity. This is the case with the Great Australian Bight (GAB), an area encompassing most of southern Australia's coastline that has been virtually unsampled below shelf depths around 200 m (Currie and Sorokin, 2011). The recent issuing of deep-sea oil and gas leases in the region has highlighted this lack of baseline environmental data, and affirmed the need to characterise the composition, abundance and distributions of benthic fauna within the deep GAB.

From 2013-2015, four surveys targeted the benthic diversity of the deep GAB (Section 2), resulting in a substantial and high-quality collection of epifauna (animals dwelling at or slightly above the surface of the seabed) and infauna (animals dwelling within sediment).

Post survey, the material was distributed to participating institutions for analysis by specialist taxonomists, with contracting and project management overseen by Museum Victoria. Upgrading of the fauna included identification to the species level, as well as adding notable taxonomic and occurrence data including whether species were new to science or previously recorded from Australia. The analysis phase examined 38 major invertebrate groups.

Here we summarise and discuss the upgraded taxonomic dataset from these GAB surveys, with results placed into a taxonomic and biogeographical context. As a result of the post-processing and analysis, we have a high quality biological dataset encompassing some of the deepest environments in Australian waters. All specimens are now stored in Australian museums and other research institutes where they are accessible to researchers conducting taxonomic revisions, describing new species, and other studies, ensuring this benthic data set will continue to contribute to knowledge and understanding of the deep-sea fauna in local, regional and global contexts.

5.2 Biological sampling

Benthic invertebrates were collected on three offshore surveys: the RV *Southern Surveyor* voyage SS2013_C02 (2013) and RV *Investigator* surveys IN2015_C01 and IN2015_C02 (2015) (MNF 2013; 2015a, 2015b). Infauna samples were supplemented with opportunistic collections of macrofauna samples from a BP funded geological survey conducted in 2013 by Fugro (FU201301) on the industry vessel *Southern Supporter*. Biological sampling totalled 155 operations (Table 1), using seven gear

types at 50 sites (Figure 1). This mix of sampling gear ensured a wide range of habitat types and their associated fauna were able to be sampled.

Beam trawls were primarily employed for sampling epifauna, recovering over 67,000 specimens of invertebrates in 52 operations. The beam trawl operations largely sampled animals larger than 10 mm in size, and living on or just below the sediment surface. Rock dredges and benthic sleds were used to sample harder substrates, such as seamounts and rocky outcroppings.

In addition to the epifauna collections, 72 operations were conducted to collect soft sediment macro-infauna, using corers and grabs; sediment samples were processed on board to retrieve any microscopic specimens, with more detailed sorting and analysis post-survey. The infaunal invertebrates are included with the epifauna as part of the total abundance and diversity.

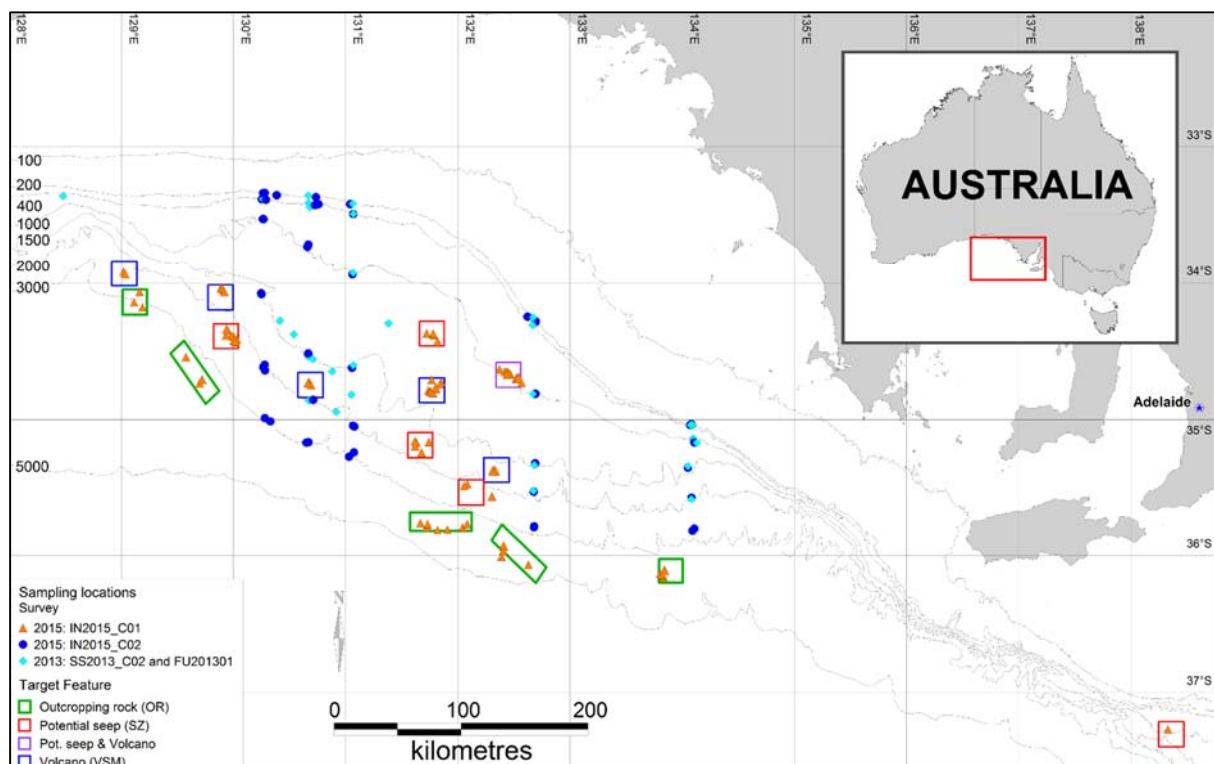


Figure 5 Map of the central and eastern GAB regions showing the sampling stations from each of the three GAB deep water surveys: SS2013_C02 and FU201301 (cyan diamonds), IN2015_C01 (orange triangles) and IN2015_C02 (blue circles).

Table 5.1 Summary of operations where invertebrate fauna was collected, with total specimens and species collected by each gear type.

Gear type	Total operations	Total specimens	Total species
Beam Trawl	52	67703*	933
Rock Dredge	21	979	133
Benthic Sled	10	230	73
Instrumented Corer	46	1368	235
Multicorer	8	51	32
Piston Corer	8	90	25
Smith-Macintyre Grab	10	109	50

*Totals include specimens not included in further totals and analyses, due to damage or lack of taxonomic expertise (e.g. Nematoda)

5.3 Invertebrate diversity

5.3.1 Overview

The combined biological sampling operations collected a total of 63,340 benthic invertebrate specimens, with 2,795 separate 'lots'. After taxonomic analysis, the material comprised 1,073 species, 602 genera and 357 families, from eleven phyla. Of the total species, 275 (26%) were new to science. The major taxa recovered are summarised in Table 2.1, with a more detailed listing contained in Section 20.1. More detailed analysis of each major group follows.

Table 5.2 Summary of abundance of invertebrate fauna by major taxonomic group showing numbers of undescribed genera and species.

Phylum	Major group	Total specimens	Families	Genera	Species	Undescr. species	Undescribed genera
Porifera	Demospongiae	10770 (84 Kg)	34	56	137	1	
	Calcarea	106 (1.4 Kg)	11	15	34	7	
	Hexactinellida	84 (3 Kg)	4	4	28	0	
Cnidaria	Hydroida	55 (.5 Kg)	-	-	-	-	
	Siphonophorae	120	1	1	1	0	
	Antipatharia	29 (0.1 Kg)	-	-	-	-	
	Octocorallia	606 (5.3 Kg)	17	32	46	17	3
	Actiniaria	801	6	14	38	4	
	Corallimorpharia	43	1	2	2	0	
	Zoantharia	177	-	-	-	-	
	Scleractinia	1734 (37 Kg)	5	8	12	0	
Brachiopoda	-	373	4	4	5	0	
Bryozoa	-	2	4	4	6		
Nemertea	-	13	-	-	-	-	
Nematoda	-	382	-	-	-	-	
Annelida	Sipuncula	662	-	-	7	-	
	Echiura	4	1	1	1	-	
	Polychaeta	1117	39	88	159	80	
	Oligochaeta	34	2	2	2	-	
Mollusca	Aplacophora	23	2	1	4	1	
	Polyplocophora	3	3	1	1	0	
	Bivalvia	1705	17	27	36	0	
	Scaphopoda	200	4	5	9	3	
	Cephalopoda	78	13	15	21	4	
	Gastropoda	1291	39	67	95	47	2
Echinodermata	Crinoidea	5	1	1	1	0	
	Asteroidea	1397	15	31	64	4	
	Ophiuroidea	34616	22	33	55	12	
	Echinoidea	875	11	14	17	1	
	Holothuroidea	1667	12	20	27	11	
Arthropoda	Cirripedia	532	5	16	25	1	
	Cumacea	15	-	-	-	-	
	Tanaidacea	75	-	-	13	-	
	Isopoda	516	20	36	56	45	4
	Amphipoda	99	23	25	47	13	
	Lophogastrida	12	1	1	2	0	
	Decapoda	2522	35	70	108	19	
	Stomatopoda	15	1	1	1	0	
	Pycnogonida	134	4	7	13	5	
Chordata	Asciacea	448	-	-	-	-	
Total		63340	357	602	1073	275	

5.3.2 Porifera (Sponges)

Shirley Sorokin¹, Lisa Goudie²

1. SARDI Aquatic Sciences, West Beach, Adelaide, South Australia; 2. Lisa Goudie consultancy, Sandringham, Victoria

There are over 8,500 valid sponge species worldwide; of these approximately 83% are in the class Demospongiae, with the remainder distributed amongst the classes Calcarea (8%), Hexactinellida (8%) and Homoscleromorpha (1%) (van Soest et al., 2012). Hexactinellida in particular have predominantly bathyal and abyssal distributions (van Soest et al., 2012), although the other three classes are also found in deep water (Van Soest, 2009; Rapp et al., 2011; Domingos et al., 2016). In Australia, the most up-to-date Porifera species list is found at the online register of Codes of Australian Aquatic Biota (CAAB) (Rees et al., 1999 onwards). This lists 1710 named sponge species in Australia, approximately 20% of the worldwide count.

In the combined GAB surveys, 199 taxa were identified. The sponge fauna is poorly described, thus identification of the majority of the sponges could not be determined to species level, instead they were assigned alpha-numeric codes, each of which has a detailed sponge 'mudmap' description (following Hooper et al., 2013) for future reference. In the sponge literature it is also common to cite the number of species per the 'order' level to compare similar collections. The four most speciose orders in this collection were Haplosclerida (37), Axinellida (28), Dictyoceratida (25) and Suberitida (22). However, molecular systematics have recently instigated major changes in the classification of Demospongiae (Morrow and Cárdenas, 2015), making comparisons with previous collections difficult.

Demospongiae (137 taxa) were the most common class, followed by Calcarea (34) and Hexactinellida (28). Two species dominated the sponge biomass. The haplosclerid fan sponge *Callyspongia* (*Callyspongia*) sp. made up 27% of the total sponge biomass and dominated the shelf edge (~200 m), and the tetractinellid *Thenaea* sp. made up an incredible 42% of the total sponge biomass. This species dominated the slope and was the most widespread species, being found at all depths between 400 and 3000 m, with the highest concentration at 1000 m. Overall, there was little overlap of species between depth strata, with 93% of species only occurring at one depth. The genus *Thenaea* has been found in aggregations in other deep-sea sites around the world e.g. off Norway and Greenland (Witte et al., 1997), their long spicules well-adapted for living on deep-sea mud (Schönberg, 2016).

Sponges from the Class Calcarea were only collected at the 200 m depth stratum and apparently absent at the deeper sites. Calcarea have been thought to be depth-limited by the oceans' calcium compensation depth, but previous work has shown that this occurs deeper than 1000 m in the GAB (James et al., 2005) and so the apparent depth limitation of Calcarea may be due to factors other than spicule solubility. Identification of sponges in the Class Calcarea was facilitated by a specialised

taxonomic workshop; nevertheless electron microscopy will be needed to confirm some of these species identifications. Hexactinellid or glass sponges were the dominant class of sponges collected from the deeper sites. With a total of 28 taxa from at least 4 families, only one glass sponge was identified to species level, *Walteria flemmingi*, which has previously been recorded from the Western Pacific region at depths between 350 and 5000 m (van Soest, 2008). No sponges of the class Homoscleromorpha were collected.

Of the total 199 sponge taxa, only eight were identified to known species, all of which have previously been recorded from Australia. Seven of the Calcarea were recognised as species new to science. Two Demospongiae warrant further investigation as being possibly new genera. It is likely that there are several new species of Demospongiae, although further taxonomic work is needed to confirm this. In a deep water collection in waters of Western Australia (100-1100 m) almost a third (28% of 372) of the species were new to science (McEnnulty et al., 2011).

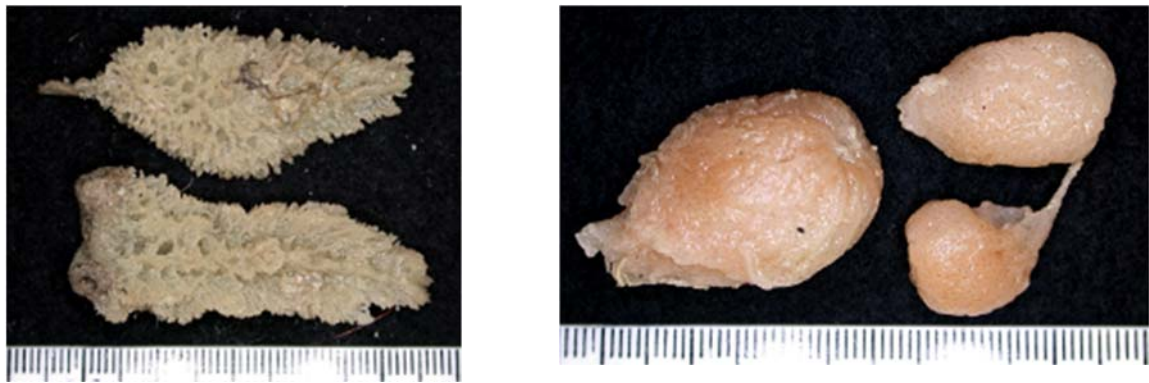


Figure 5.6 Sponges from IN2015_C02. L: *Raspailia* (*Clathriodendron*) sp. 1; R: *Ascoleucetta* n. sp. 4

5.3.3 Siphonophorae

Hugh MacIntosh¹

1. Museum Victoria, Melbourne VIC

Analysis of siphonophores, particularly deep-sea varieties, is not normally a priority in biodiversity surveys due to the relative scarcity of both specimens and taxonomic expertise.

Benthic sampling at seven stations collected numerous small, rubbery, mushroom-shaped objects which were recognised as the rarely-seen *Dendrogramma enigmatica*, an unusual invertebrate which had not been placed in any known animal phylum. Originally collected off southeast Australia in the 1980s, the species had not been found since, and the original formalin preservation of specimens prevented genetic analysis.

The collection of fresh material allowed for detailed phylogenetic analysis of the species. Results show that *Dendrogramma* is a benthic siphonophore in the family Rhodaliidae, a poorly-understood group of benthic siphonophores related to Portuguese Man-o-Wars. The mushroom shaped ‘creatures’ are in fact structures called bracts which are protective outgrowths from a siphonophore colony. A small gas float and main colony were also collected and matched by DNA to *Dendrogramma*, but the appearance of the colonies and bracts in life remains unknown. These results were published recently in the journal Current Biology (O’Hara et al., 2016).



Figure 5.7 *Dendrogramma enigmatica* Just et al. 2014. Left and center: *D. enigmatica* bracts. Right: *Pneumatophore*.

5.3.4 Octocorallia (Octocorals)

Phil Alderslade¹, Franziska Althaus¹

1. CSIRO Oceans and Atmosphere, Hobart TAS

Deep water octocorals are primarily represented by the orders Alcyonacea and Pennatulacea. The Alcyonacea comprise the bulk of the octocorals, which, depending on colony form, are generally referred to as soft corals and gorgonians (sea fans and sea whips), while members of the Pennatulacea are referred to as sea pens or rock pens. These two orders are cosmopolitan in distribution, occurring from pole to pole and from the intertidal to abyssal depths. They are well represented in Australian waters and jointly referred to below as “octocorals”.

Octocorals were collected in most of the net samples (50 beam trawls, 19 rock dredges and 12 benthic sleds) with a distinctive drop in abundance of octocoral catches at the 400 m depth horizon. Catches of octocorals were generally small (mostly <100 g, with by far the largest containing 3 kg of *Dendronephthya* cf. *waite*), and the diversity within a catch was usually low. Collectively, however, the Alcyonacea were represented by 11 families, 25 genera and 24 species and the Pennatulacea by six families, seven genera and 12 species.

Many taxa were assigned an alpha-numeric code that CSIRO has been consistently applying to deepwater octocoral collections in Australian waters (Alderslade et al., 2014; MarLIN, 2014). This is

because the octocoral fauna is poorly described in the literature, and many identifications at species level could not be resolved to named species without extensive generic revision (Alderslade et al., 2014). Nevertheless, it was possible to distinguish three new genera and 14 new species of alcyonaceans, two new species of pennatulaceans, and an additional 17 new records for Australian waters including 12 new to the Great Australian Bight. In all probability this reflects a paucity of collecting activities, not only in the Bight but in deep waters around the Australian continent as well.



Figure 5.8 Octocorals from IN2015_C02: L: *Callogorgia* n. sp. B; R: *Pennatula* (cf.) *inflata*

5.3.5 Actinaria (Sea Anemones)

Andrea Crowther¹ and Michela Mitchell²

1. South Australian Museum, Adelaide SA; 2. Museum Victoria, Melbourne VIC

Knowledge of the Australian deep-sea Actinaria fauna is still in its infancy and the taxonomic literature is small. Current records show that three families of Actinaria dominate the deep-sea environment: Hormathiidae, Actinostolidae, and Actinoscyphiidae. The combined surveys collected 801 Actinaria specimens, with 38 species from six families. Due to the complexity of anemone taxonomy and damage to some specimens, 8 OTUs were identified only to genus level, and 12 to family level. Nine OTUs were unable to be identified below the level of order Actinaria.

The collections were dominated by the family Hormathiidae (18 OTUs, 707 specimens); representatives of this family of sea anemones are common in the deep sea. The remaining lots were identified as belonging to five other families (excepting the nine lots not identifiable beyond Order). The most abundant OTUs were all hormathiids: *Monactis* cf. *vestita* (334 specimens), Hormathiidae sp. 1 (130 specimens) and *Paracalliactis* cf. *rosea* (95 specimens). *Monactis* cf. *vestita* was the most abundant species but all 295 specimens were collected from only three stations, all at a depth of 1500 m; these sea anemones are relatively small, and often found in groups, possibly clonal, attached to the same hard substrate. Another abundant hormathiid, *Paracalliactis* cf. *rosea*, has a depth range of 1000–3000 m and a mutualistic association with hermit crabs, where the sea anemone attaches to and extends the crab's shell by the production of a proteinaceous secretion.

The genus *Actinauge* has been recorded from Australia and the Great Australian Bight and are represented in museum collections but further work is needed to accurately determine if the specimens collected here represent unique species.

Other species represented notable range extensions or additions to the Australian fauna. A single specimen of *Isactinernus quadrilobatus* is the first known record for this genus outside of the tropical West Pacific. The Amphianthidae genera *Amphianthus* and *Stephanauge*, found on coral columns and scaphopod shells, have never been recorded from Australia. *Pacmanactis* sp. 1, likely to be a new species, was represented by three lots (six specimens) collected from a depth of 400 m. The only other described species in this genus is found on hydrothermal vents off Papua New Guinea. This is a new record for Australia.



Figure 5.9 Actinaria from IN2015_C02. L: *Pacmanactis* sp. 1. R: *Hormathiidae* sp. 1.

5.3.6 Annelida (Segmented worms)

Robin Wilson¹, Elena Kuprianova², Hugh MacIntosh¹, Anna Murray², Hannelore Paxton²

1. Museum Victoria, Melbourne VIC; 2. Australian Museum, Sydney NSW

The Annelida, or segmented worms, includes many of the groups important in marine, terrestrial and freshwater habitats: polychaetes, earthworms and leeches. In addition, recent discoveries based on molecular genetics (e.g. Andrade et al., 2015) have established that the small former phyla Echiura, Sipuncula and Pogonophora must also be subsumed within the Annelida. One outcome of these recent advances is that the taxon Polychaeta is now synonymous with Annelida. Despite this consensus from recent publications, Polychaeta continues to be widely used in the literature, but will slowly be replaced by Annelida, as we do here. (When comparing this report with previous

studies, our use of “Annelida” is for practical purposes almost equivalent with the “Polychaeta” of earlier authors.)

In the marine environment, particularly soft sediments, annelids are typically dominant, representing 40% or more of all individuals and species collected in typical benthic surveys (e.g. Hilbig and Blake, 2006; Shields and Blanco-Perez, 2013). However, most annelids are small and live on or below the sediment surface and are thus counted among the infauna in this study, although a few larger annelids are either found living on the sea floor and large enough to be retained in a beam trawl or similar gear, or are associated with corals, sponges and similar larger host invertebrates – these are considered epifaunal.

The annelid fauna from the combined surveys comprised 42 families represented by 169 unique species, of which about half (80) are likely to be undescribed. Among these, the dominant epifaunal annelid families are exactly those that would be expected from these depths anywhere in the world’s oceans: Ampharetidae, Amphinomidae, Aphroditidae, Eunicidae, Onuphidae, Polynoidae and Serpulidae (Paterson et al., 2009). Serpulidae (worms whose calcareous tubes encrust corals, mollusc shells and other hard substrates) were especially diverse, with 9 genera present. Other diverse epifaunal annelid families include Onuphidae (6 species) and Polynoidae (12 species). Sabellariidae were also present in epifaunal samples, represented by a species of a deepwater genus not previously recorded from Australian waters (*Gesaia*). Annelids are vastly more numerous in infaunal samples where they are by far the dominant major taxon. Infaunal samples are a more representative sampling of the annelid fauna and included families typical of deep-sea habitats in other parts of the world. Among these the most species-rich were Cirratulidae (6 species), Paraonidae (5 species), Sabellidae (9 species), Spionidae (18 species) and Syllidae (14 species). Other typical deep-sea annelid families such as Ampharetidae, Amphinomidae, Fauveliopsidae, Goniadidae and Siboglinidae have never before been collected in Australian waters at these depths.

Since this is the first systematic study of Annelida from depths to 4500 m in Australian waters, it is entirely to be expected that many apparently new species and new records have resulted. Further taxonomic studies by specialist taxonomists are expected to confirm these results and result in formal description of many new species in coming years.

The annelid fauna discovered in the deep Great Australian Bight is, at the family level, broadly representative of annelid faunas at similar depths elsewhere in the world. It is at the species level, however, that informative regional, bathymetric and other ecological distribution patterns are expected to emerge with further study.

5.3.7 Bivalvia (Clams, Mussels and Scallops)

Hugh MacIntosh¹

1. Museum Victoria, Melbourne VIC

Well known in shallow areas, bivalves also occur in the very deepest reaches of the oceans (Allen, 2008; Kamenev, 2015; Knudsen, 1970). They have adapted to the unique conditions of the deep sea and can constitute an important part of the benthos (Allen, 2008). These adaptations have included chemosymbiosis to survive in vent or seep environments and multiple evolutions of carnivory, making up for the lack of phytoplankton (Poutiers and Bernard, 1995; Barroso et al., 2016). As with other molluscan groups, shallow water bivalves are reasonably well studied in Australia, but the deep water fauna is poorly understood (Lamprell and Whitehead, 1992; Beesley et al., 1998).

The 2013-2015 surveys collected a large sample of bivalves of 1705 total specimens representing 17 families and 36 species. These covered a wide range of bivalve groups including protobranchs (*Nucula*, *Tindaria*), scallops (*Propeamussium*, *Hyalopecten*), more typical 'clams' (*Abra*, *Pratulum*) and a variety of carnivorous 'septibranchs' (*Poromya*, *Cuspidaria*, *Spinosipella*). The overall diversity and abundance of bivalves were typical of similar deep water areas (Allen, 2008; McEnulty et al., 2011), with the only notable differences being comparatively low numbers of protobranchs and no chemosynthetic species (e.g. *Thyasiridae*). Some notable finds include the families *Tindariidae* and *Vesicomyidae*, which have not been previously recorded in Australia. Additional specimens from southeast Australia have since been found in museum collections but have not previously made it into the published record. Another unusual find was a large aggregation of *Limopsis* 'sp. 3', with over 1000 individuals collected in a single trawl. These bivalves are specialist filter feeders in the deep sea (Oliver and Allen, 1980), suggesting the local environment has a high suspended bacterial or sediment load.

Despite the lack of undescribed species, only nine species were previously recorded from Australian waters, most likely due to the lack of deeper water (>2000 m) sampling in Australia. Several species found in the survey have been previously recorded in New Zealand, the central/eastern Pacific or even have cosmopolitan distributions (*Abra profundorum*). No species could be confidently determined as undescribed, but many merit further investigation.



Figure 5.10 Bivalvia from IN2015_C02. L.: *Limopsis* sp. 3. R.: *Hyalopecten* sp.

5.3.8 Scaphopoda (Tusk Shells)

Francesco Criscione¹

1. Australian Museum, Sydney NSW

Scaphopods are found at all latitudes and in depths from the littoral fringe to the abyssal (Davies, 1987; Scarabino and Scarabino, 2011), where they inhabit all types of sediments from soft mud and silts to coarse mud and gravels. They are primarily micro-carnivorous generalists in their diets (Shimek, 1990), feeding on foraminiferans, bivalve spat, ostracods, diatoms, small gastropods, marine mites and invertebrate eggs. Many species, including several Australian species, are found over a wide depth range (e.g. *Laevidentarium erectum* recorded from 11–2569 m). Compared to other molluscan classes, scaphopods generally exhibit rather conserved morphology and ecology and do not exhibit any particular adaptation to deep-sea environments. There are two major systematic groups in the Scaphopoda (the orders Dentaliida and Gadilida) with 11 families, of which eight are present in Australian deep waters (Beesley et al., 1998).

A total of 200 scaphopod specimens were collected, which were assigned to nine species in four families. The family with the largest number of species retrieved (five) was the Dentaliidae, of which three species were undescribed. One has been attributed to the genus *Fissidentarium*, another to the genus *Graptacme* and another is of uncertain generic placement. Two species of the Gadiliidae were collected, with two other families (Entalinidae and Laevidentariidae) each represented by one known species.

All scaphopods collected are members of families already reported for Australian waters.

Fissidentarium profundorum (E. A. Smith, 1894) and *Rhomboxiphus tricarinatus* (Boissevain, 1906)

are here reported for the first time for the GAB. The latter record fills the gap in the known distribution of this entalinid species between the eastern and western Australian coasts.



Figure 5.11 Scaphopoda from IN2015_C02. *Fissidentalium profundorum*.

5.3.9 Cephalopoda (Octopus, Cuttlefish and Squid)

Amanda Reid¹ and Julian Finn²

1. Australian Museum, Sydney NSW; 2. Museum Victoria, Melbourne VIC.

Cephalopods within the Australian Economic Zone are represented by approximately 230 species grouped into 10 orders. All are carnivorous, they occupy all depths from the surface to the sea floor, and feed at a range of trophic levels. Many species exhibit diel vertical migration and may occupy different habitats and depths at different stages in their life cycles. They are both key predators and prey species in marine ecosystems.

A total of 21 cephalopod species in 13 families were collected during the combined surveys. Four species are undescribed. While many are well known and also occur in other parts of Australia and elsewhere, a few species were new records for the GAB.

The cuttlefish Sepiidae (*Sepia cottoni* Adam, 1979, *S. cultrata* Hoyle, 1885 and *S. hedleyi* Berry, 1918), and the Sepiolidae (*Sepiolina* sp. nov. and *Austrorossia australis* Berry) are benthic Australian endemic taxa. All but *Sepia cottoni* Adam, 1949 were previously known to occur in the Great Australian Bight. Another sepiolid, *Heteroteuthis* sp. was collected. Unlike other sepiolids, this is a pelagic species, but evidence suggests they lay their eggs on the seafloor. Further study, including genetic comparison of tissue samples obtained from these specimens with those from other parts of the world, is currently underway to help clarify the determination of this species.

The octopod cephalopods included both incirrate and cirrate forms. Among the incirrate octopods '*Eledone' palari* (Eledonidae) was collected at depths between 200 and 300 m. Placement of this

species within *Eledone* has been questioned and material collected during this survey will aid in resolving the taxonomic assignment of this species. The specimens of *Benthoctopus* collected during this survey represent a new species; taxonomic study of existing museum material and specimens collected during this survey will allow formal description of this taxon. Specimens of the cirrate octopods, *Opisthoteuthis persephone* and *O. pluto* will also be valuable. These species have been previously collected throughout southern Australia but neither species is well-known as their gelatinous bodies are easily damaged during collection.

Among the squids, perhaps the most notable find was a specimen of *Joubiniteuthis portieri* (Joubiniteuthidae). This species is rarely collected and only a few dozen specimens worldwide are known in museum collections. This mesopelagic to bathypelagic squid has not previously been recorded from the Great Australian Bight. *Pyroteuthis margaritifera* (Pyroteuthidae) is generally thought to be a widely-distributed species, known to undertake diel vertical migration from about 250 m to shallower depths. Some morphological differences have been found among various populations of this species, which was originally described from the Mediterranean Sea. Whether all taxa that broadly conform to this species diagnosis are truly conspecific is yet to be determined. The specimens collected during this survey could not be distinguished morphologically from *P. margaritifera*. Preliminary molecular analyses comparing COI and 16S RNA genes with *P. margaritifera* from elsewhere also supports this identification.



Figure 5.12 Cephalopoda from IN2015_C02 . L: *Austrorossia australis*; R: An undescribed octopus, *Octopodidae* sp. 1.

5.3.10 Gastropoda (Snails)

Francesco Criscione¹

1. Australian Museum, Sydney NSW

The composition of bathyal gastropod assemblages is profoundly influenced by the lack of photosynthetic life, which determines the absence of true herbivorous gastropods. Given the food resource available, the deep-sea gastropod fauna is dominated by members of four major feeding guilds: scavengers, deposit-feeders, predators and parasites (Allen, 1983).

Scavengers are represented by a number of families in the subclass Vetigastropoda including the Osteopeltidae [whale and fish bones, (Marshall, 1987)], Lepetellidae [tubes of polychaete worms, empty egg-cases of sharks and rays (Powell, 1979)], and Pseudococculinidae [sunken plant remains (Hickman, 1983)]. In the subclass Caenogastropoda, some bathyal species of Buccinidae (e.g. *Enigmaticolus*, Fraussen, 2008) and Nassariidae (Dekker and Dekkers, 2009) are scavengers. Deep-sea scavengers in the subclass Cocculiniformia are limpets of the Cocculinidae (Haszprunar, 1987; Marshall, 1986 - herbivorous) and the Bathysciadiidae (Haszprunar, 1988 - feeding on sunken cephalopod beaks). Many of the deposit feeders are vetigastropods, such as species of the families Seguenziidae and Calliotropidae (Kano, 2008), but in this category there are also some caenogastropod families, such as the Rissoidae (Ponder, 1984). Deep-sea predators belong to a wide range of phylogenetically diverse caenogastropod groups, such as many conoidean families (e.g. Raphitomidae, Pseudomelatomidae, Drilliidae, and Borsonidae) (Bouchet et al., 2011), which paralyse their polychaete prey by injecting venom through modified arrow-like radular teeth. Other predators include the families Muricidae, Fascioliidae, Volutidae, Belomitridae, Naticidae, which bore a hole through the shell of their molluscan prey, using their radula and an acid secretion (Carriker, 1998) and the Cassidae, which also use a combination of radula rasping and acid secretion to access the flesh of echinoids (Beu et al., 2008). Among the parasites, the Eulimidae (Caenogastropoda) are always associated with echinoderm hosts, from which they extract the body fluids through a muscular proboscis (Bouchet, P., 1986). Other deep-sea ectoparasite species are present in the caenogastropod Epitoniidae (having cnidarian hosts) (Bouchet, P., 1986) and the heterobranch Pyramidellidae, with primarily polychaete hosts (Peñas and Rolán, 2010).

A total of 1291 gastropod specimens were collected, assigned to 95 species in 39 families. Forty-seven species are new to science. The family with the largest number of species retrieved was the Raphitomidae (1 described, 15 undescribed species), followed by the Muricidae (6, 2), the Fascioliidae (3, 2), the Epitoniidae (1, 4), the Arminidae (4 undescribed) the Velutinidae (3 undescribed), the Ranellidae (3 described). All remaining families included two species or less. All gastropods collected were members of families already recorded for Australia and (excluding the Belomitridae) for the GAB and all including species typical of deep-sea environments. Of the 48 described species, three (*Hadroconus diadematus* Marshall, 1988, *Enixotrophon veronicae* Pastorino,

1999 and *Spergo aithorris* Sysoev and Bouchet, 2001) represent the first record for Australian waters, while nine species have never previously been reported for the GAB.



Figure 5.13 Gastropoda from IN2015_C02. L: *Cadlina* sp. 1; R: *Columbrarium pagodoides*.

5.3.11 Asteroidea (Sea Stars)

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The diversity of shallow-water asteroids (also known popularly as starfish or sea stars) in the Australian region has historically been well-studied and is regarded as one of the richest in the world (Clark, 1921, 1938; Livingstone, 1932; Clark and Rowe, 1971; Rowe and Gates, 1995). In contrast, the asteroid deep-sea fauna in the Australian region is very poorly characterized. Deeper water faunas from the continental shelf are surveyed in part by H.L. Clark (1916) with early members reported by Sladen (1889). A far more extensive literature on the South Pacific deep-sea Asteroidea has been published on the New Zealand fauna (Clark and McKnight, 2001, 2000; McKnight, 2006), which includes many species also present in Australia and adjacent regions.

Asteroids are significant ecological members of shallow marine communities where they occupy significant ecological roles and can strongly affect community structure (Paine, 1969; 1966). Although the role of deep-sea asteroids is not as well understood as those in shallow-water, it seems likely that they occupy a similar role; some deep-sea species have been observed feeding on octocorals and have been recorded in abundance on abyssal plains.

The combined GAB surveys included 64 species from 31 genera in 15 families, with four species determined to be new to science. All families represented are known from lower bathyal to abyssal

depths and include several well-known deep-sea or cold-water members such as the Pterasteridae and the Zoroasteridae, amongst the most diverse of known deep-sea groups.

Apart from some shallower water species (*Luidia prionata*, *Pseudophidiaster rhysus* and *Smilasterias* spp.) the majority of taxa collected represent new occurrence records for Australia and the Great Australian Bight. Although many occurrence records had been recorded from nearby localities such as New Zealand, there were many which represented significant range extensions - the genus *Calyptaster* has previously only been known from the tropical Atlantic and southern Indian Ocean. Several species had not been recorded since the HMS Challenger surveyed nearby areas in the 19th Century.

Although poorly understood, some ecological information can be inferred from the taxa sampled. For example, members of the Astropectinidae, Pseudarchasteridae and especially the Porcellanasteridae occur on soft unconsolidated sediments (Mah and Blake, 2012). Many of the recovered species were members of groups which have been observed on unconsolidated sediment or soft-bottoms. Brisingids are suspension feeders, variably occurring on soft and hard substrates (Mah, 2016). Gut contents from species of *Calyptaster* and *Hymenaster* are new observations; these included gastropods and bivalves from muddy settings. Several asteroides including *Styracaster caroli*, *Dytaster* sp., *Plutonaster* spp., and *Pillsburiaster* spp. were observed with their disks gorged with mud. In addition to providing us with baseline information on echinoderm diversity for the region, observations such as these have provided valuable insights into substratum, habitat and ecology of the Asteroid fauna of the deep GAB.



Figure 5.14 Asteroidea from IN2015_C02. L: *Astropecten* sp. 1. R: *Hymenaster* cf *blegvadi*.

5.3.12 Ophiuroidea (Brittle Stars)

Tim O'Hara¹

1. Museum Victoria, Melbourne VIC

Brittle-stars are abundant in deepwater benthic habitats, where they feed on detritus, food falls or plankton. They are exclusively marine, but occur from the coast to the deepest oceanic trenches and from the equator to Polar Regions, inhabiting both rocky and soft-sediment substrata, and living epizoically on arborescent cnidarians and sponges (Stohr et al., 2012). Their ubiquitous distribution makes them a model group for the study of marine biogeography (O'Hara et al., 2011; Woolley et al., 2016). There are approximately 2100 described and several hundred undescribed morpho-species (Stohr et al., 2012). However, genetic studies indicate that traditional morphological species delimitation is problematic, and that many morpho-species are complexes of non-interbreeding cryptic species. The extant radiation of ophiuroids dates back to the Permian Period, 270 mya and there have been major radiations of ophiuroids in shallow water tropical habitats (e.g. Ophiotrichidae) and at upper bathyal depths (e.g. Ophiacanthidae, Ophiopyrgidae) (O'Hara et al., 2017).

The ophiuroid fauna of the GAB has been sampled previously as fisheries bycatch or incidentally from scientific expeditions, with most samples collected from less than 1000 m depths. The combined 2013-2015 surveys collected a large sample of larger ophiuroid species across a range of depths (200-4600 m) that comprised 53 species in 22 families and all six orders. Two species were very abundant, *Ophiomusa lymani* (1000-2800 m) and *Ophiocten australis* (here recognised as distinct from *Ophiocten hastatum*, 1500-4300 m). The most speciose genus was *Ophiomusa* (formerly confused with *Ophiomusium*), however, the GAB *Ophiomusa* species are not necessarily closely related as the genus is ancient (90 mya) and requires taxonomic revision.

There are numerous undescribed species in the collection. Although some of these species have been found elsewhere in temperate Australia (e.g. *Ophiomitrella* sp. MoV 2779), others appear to be new (e.g. *Ophiura* sp MoV 7067, *Ophioscolex* sp.). Many lower bathyal and abyssal species (2000-4600 m) have been found outside Australia. Whether these represent complexes of species is typically unknown, although for one abyssal species (*Amphiophiura bullata*) there is only shallow genetic divergence over vast geographical distances (GAB, Northern Pacific, Southern Atlantic).

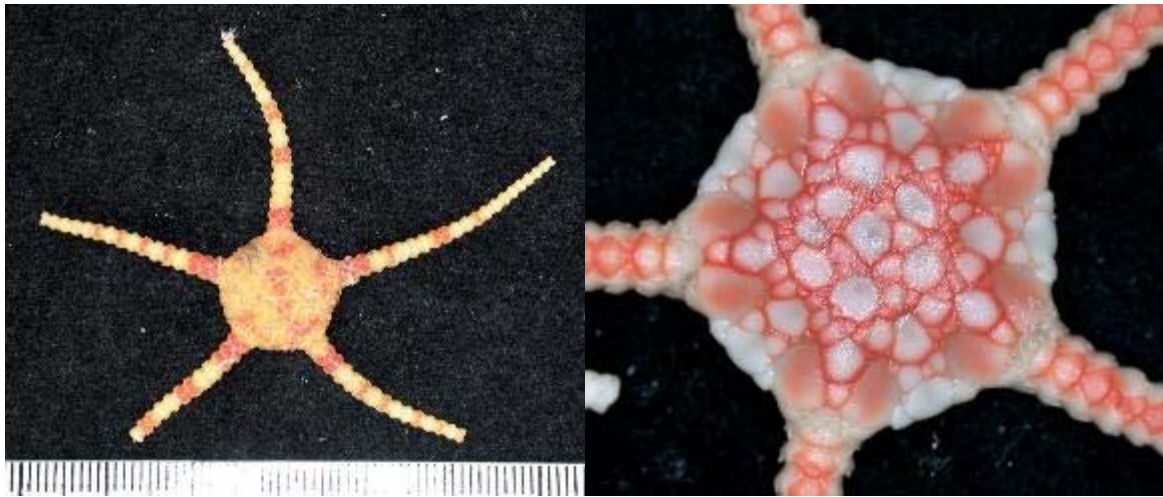


Figure 5.15 Ophiuroidea from IN2015_C02. L: *Ophiomusium scalare*; R: *Amphiophiura collecta*.

5.3.13 Echinoidea (Sea Urchins)

Ashley Miskelly¹

1. Australian Museum, Sydney NSW

Of the 300 or so echinoid species known to occur in Australia, many are widespread across the Indo-Pacific oceans, particularly those that live in sub-tropical and tropical areas. The southern Australian states show a greater number of endemic species, though these generally prefer shallower waters. Deepwater regular echinoid species are dominated by Echinothuriids and Phormosomatids, rather delicate urchins that “deflate” when they are brought to the surface, often losing spines and pedicellariae in the process, which can hinder identification to species level. Other minor families that are found in deep water include the Saleniidae, in particular *Salenocidaris hastigera*, (a small widespread species that also occurs north to the Indo-Malay Archipelago and New Zealand) and the Pedinidae, in which several deep water species are known from Australia and across to New Zealand. Irregular sea urchins such as sand dollars (Clypeasteroids) and heart urchins (Spatangoids) are poorly represented.

The combined GAB surveys collected 875 echinoid specimens, with 17 species from 11 families. Only a single species, the sand dollar *Clypeaster* sp. nov. 1 was determined to be undescribed. It was especially abundant at some sampling locations and is known from other specimens housed in Australian museum collections. Several ‘species’ could not be confidently identified due to being juvenile (*Caenopedina* sp), or damaged, particularly the unidentified heart urchin ‘*Spatangoida* sp.’. This species, if intact, would be likely an unrecorded species, as such thin walled heart urchins are rarely encountered.

Significant discoveries include the first Australian records for *Tromikosoma* and *Sperosoma*. Species showing range extensions include *Goniocidaris sibogae* (previously known only from New South

Wales, Victoria and Tasmania), *Lovenia camarota* (previously known from North Western Australia), *Aceste ovata* (known from only a few specimens in Australia) and *Pseudolovenia cf hirsuta*, which has only been recorded from Hawaii and Japan. A number of small sea urchins, probably belonging to the Echinothuriidae that were unable to be identified to species level due to their small size, could represent additional undescribed species.



Figure 5.16 Echinoidea from IN2015_C02 . L: *Pseudolovenia cf hirsuta*; R: *Clypeaster sp. nov.*

5.3.14 Holothuroidea (Sea Cucumbers)

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1. Museum Victoria, Melbourne VIC

Holothuroids (sea cucumbers) are amongst the dominant fauna at bathyal and abyssal depths, where they are predominantly soft sediment deposit feeders (Hansen, 1975). There are extensive collections of Holothuroidea from the eastern and western continental slopes of Australia (McEnnulty et al., 2011), but few have been recovered to date from the deep GAB.

The combined GAB surveys collected 1667 holothurian specimens, comprising 27 species in 20 genera from 12 families. Fourteen species were recognized and described, and of these 12 were known previously from Australia. There are 13 undescribed species.

This collection is remarkable both for the high proportion of what appear to be unknown species (about 40%), and for the absence of species known from the eastern and western Australian slopes (such as a number of *Laetmogone* and *Peniagone* species). In addition, many of the species collected were single specimens, and further sampling may be required to reach a more comprehensive representation of the taxa present. Over half the specimens collected were the small gelatinous swimming sea cucumber *Enypniastes eximia* Théel, 1882, known from abyssal environments worldwide.

Many of the holothuroid specimens were extensively damaged during collecting. External morphological form was frequently not evident, and identification was primarily through ossicle form and size. In many cases there was not adequate material for describing new taxa. For example, three new species of the order Molpadida are represented (in genera *Molpadia* and *Paracaudina*). Only one specimen represents each of these molpadid species, and in two cases the specimens are extensively damaged. One species of the order Synaptida (in genus *Protankyra*) is represented. Only one very damaged specimen represents this synaptid species.

Of the 14 described species, 12 have been recorded previously from the Australian slope: the deimatids *Deima validum* Théel, 1879 and *Oneirophanta mutabilis* Théel, 1879; the holothuriid *Holothuria* (*Panningothuria*) *austrinabassa* O'Loughlin, 2007 (in O'Loughlin et al., 2007); the laetmogonid *Laetmogone maculata* (Théel, 1879); the mesothuriids *Mesothuria regularia* Heding, 1940 and *Zygothuria lactea* (Théel, 1886); the myriotrochid *Protrochus roniae* O'Loughlin and Macintosh, 2015; the pelagothuriid *Enypniastes eximia* Théel, 1882; and the synallactids *Bathyplores natans* (Sars, 1868), *Molpadiodemas involutus* (Sluiter, 1901), *Pseudostichopus hyalegerus* (Sluiter, 1901) and *Pseudostichopus mollis* Théel, 1886.

The two known species not recorded previously for the Australian slope are the elpidiid *Peniagone azorica* von Marenzeller, 1893 and the psychropotid *Psychropotes longicauda* Théel, 1882. *Peniagone azorica* is thought to be cosmopolitan but numerous morphological variations are reported (Hansen, 1975). *Psychropotes longicauda* has also been thought to be cosmopolitan but recent genetic studies (Gubili et al., 2016) have revealed probable cryptic species diversity. We anticipate that genetic studies will reveal cryptic species diversity for a number of these supposedly cosmopolitan species.

Of the 13 undescribed new species, six belong to the typically bathyal order Elasipodida (in genera *Benthodytes*, *Ellipinion*, *Kolga*, *Peniagone* and *Psychropotes*). Four new species of the order Aspidochirotrida are represented (in genera *Mesothuria*, *Pseudostichopus* and *Synallactes*). Three new species of the order Molpadida are represented (in genera *Molpadia* and *Paracaudina*). There are eight lots of one species of *Mesothuria* that is widespread on the Australian slope but not yet described.

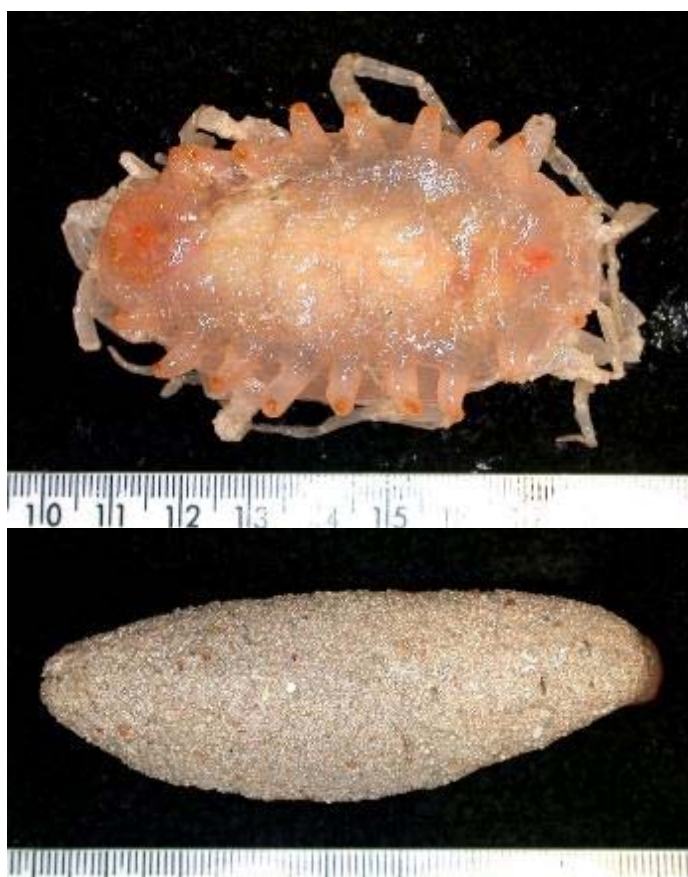


Figure 5.17 Holothuroidea from IN2015_C02 .Top: *Deima validum*; Bottom: *Molpadiodemus involutus*.

5.3.15 Cirripedia (Barnacles)

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Deep water barnacles have been relatively well documented in waters adjacent to Australia such as Antarctica (Newman and Ross, 1971), the Malay Archipelago (Hoek, 1883, 1907, 1913; Calman, 1919; Chan, 2009), New Caledonia (Buckeridge, 1997, 1994; Chan et al., 2014; Jones, 2000) and New Zealand (Foster 1978,1980, 1981). The deep water barnacle fauna of Australia has been summarised by Jones et al. (1990) and Jones (1991, 2012), but there are few recent taxonomic accounts that describe Australia's deep-sea barnacles (e.g. Zevina, 1981, 1988; Jones, 1992) and the results of many expeditions remain unpublished.

The present material reveals that the deep waters of the Great Australian Bight have a higher diversity than what was previously known and represents some of the deepest records of barnacles in Australian waters. In total 532 barnacle specimens were examined, resulting in the identification of 25 species in five families. As is expected in deep water, the stalked barnacle family Scalpellidae was the most diverse family, represented by 15 species. Five species were not conclusively assigned to a named species and four have been given tentative identifications (*Gibbosaverruca* cf *nitida*,

Metaverruca cf recta, *Neoscalpellum cf schizoplacinum*, *Trianguloscalpellum cf uniarticulatum*). The uncertainty of these identifications is a reflection of the paucity of knowledge on Australia's deep-sea barnacles. Members of the genera *Gymnoscalpellum*, *Meroscalpellum* and *Neoscalpellum* are particularly problematic as they are characterised by an extreme reduction of the capitular plates during ontogeny making identification of individual specimens very difficult. A compounding issue is that barnacles of these genera have often been described in isolation and from a single or a few specimens, giving little information on intraspecific variation.

The species collected show a high degree of novelty with one undescribed species, *Metaverruca* sp. nov. 1, and five, seven, and eight species recorded for the first time from the waters of Australia, temperate Australia and the Great Australian Bight, respectively. Of the species that are reported in Australia for the first time, *G. cf. nitida* and *Planoscalpellum distinctum* have been reported to be widely distributed in the tropical Indo-West Pacific (Foster and Buckeridge, 1994; Young, 2002) and *T. uniarticulatum* has only been recorded from Sino-Japanese waters (Liu and Ren, 2007). In contrast *Meroscalpellum bifurcatum* has been reported in the southern Atlantic and Indian Oceans (Foster and Buckeridge, 1995) and *Neoscalpellum cf schizoplacinum* is known from the Southeast Pacific Basin in the Southern Ocean (Newman and Ross, 1971).

Jones et al. (1990), in their catalogue of Australian barnacles, listed 19 species being present deeper than 200 m within the EEZ of the southern coast of Australia, of these only six were recollected during this survey (*Arcoscalpellum inum*, *Gibbosaverruca navicula*, *Glyptelasma hamatum*, *Metaverruca cf recta* and *Trianguloscalpellum regium* and *Verum candidum*). Thus, the number of known species has been increased to 38. Only *A. inum* is considered to be endemic to Australia, and is in fact only known from the Great Australian Bight. Overall, the barnacle fauna represented in this collection shows a mix of northern and southern species and are normally wide ranging. Two species *Amigdoscalpellum costellatum* and *Regioscalpellum regium* have been reported in all oceans. Other species, such as *Arcoscalpellum truncatum*, *Eutomolasma macLaughlinae* and *Verum australicum*, have previously been found in northern Australia and are typically found in deep tropical waters of the Indo-West Pacific.



Figure 5.18 Cirripedia from IN2015_C02. L: *Arcpscalpellum inum*; R: *Eutomolasma maclaughlinae*.

5.3.16 Isopoda (Sea lice, Slaters)

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1. Museum Victoria, Melbourne VIC

The Isopoda are an important component of shelf, slope and deep-sea ecosystems. One group, the Asellota, are the species-rich sub-order predominately found in these habitats (Brandt et al., 2004, 2007; Raupach et al., 2009), however our knowledge of this group in Australian waters remains limited (Poore et al., 1994).

The combined GAB surveys collected a rich and diverse sample of isopods, with 516 specimens consisting of 20 families, 36 genera and 56 species. The most frequently collected species was the serolid *Brucerolis victoriensis* Storey and Poore, 2009, which made up 77% of the overall specimens collected. All the isopod families collected were previously recorded from bathyal and abyssal depths.

The most diverse suborder was the Asellota, with 39 species from 10 families. This figure concurs with previous studies, showing that asellotes are the most dominant isopod group in the deep-sea (Brandt et al., 2004, 2007; Raupach et al., 2009). Overall, 80% of the isopod species collected are undescribed, and four species may also represent new genera. Such a high level of taxonomic novelty is not surprising, as previous Australian deep water surveys have invariably uncovered high levels of undescribed isopod taxa (Poore et al., 1994, 2004).

Of the described species, only two have been previously recorded from the GAB. Conversely, four families (Macrostylidae, Katianiridae, Nannoniscidae and Thambematidae) are new records for Australian waters and important additions to the deep water fauna of Australia.



Figure 5.19 Isopoda from IN2015_C02. L: *Antarcturus* sp.; R: *Aegiochus beri*.

5.3.17 Decapoda, Stomatopoda and Lophogastrida (Crabs, Shrimp and relatives)

Shane Ahyong¹, Caroline Farrelly² and Anna McCallum²

1. Australian Museum, Sydney NSW; 2. Museum Victoria, Melbourne VIC

Decapod and lophogastridan crustaceans are common in deep water, and stomatopods less common (Wilson and Ahyong, 2015). Most decapods and stomatopods are benthic or epibenthic, although some, like the lophogastridans, are pelagic or benthopelagic. Decapoda and Stomatopoda are most diverse in the shallow tropics, but are nevertheless common in temperate shelf and slope waters.

The combined surveys of decapods, stomatopods and lophogastridans collected 2549 specimens, dominated by decapods. The single species of the stomatopod collected (*Anchisquilla mcneilli*) is already known from southern Australia and the two lophogastridans are cosmopolitan at abyssal depths.

The decapods comprised 35 families, 70 genera and 108 species, spanning groups typical of the upper shelf to slope waters and deeper. Nineteen species (18%) are new to science and 32 (30%) represent new records for the GAB. The numerically dominant decapods at bathyal depths surveyed (>1000 m) were parapagurid hermit crabs. Other decapod families are more typical of the upper shelf such as the hermit crabs of the families Diogenidae and Paguridae, and brachyuran crabs of the families Dromiidae, Inachidae, Leucosiidae, and Majidae. Within the range of the shallower stations (~150–400 m), the dominant decapods are spider crabs (Epialtidae, Inachidae, Majidae). These general patterns are consistent with those observed for the deep water decapods off Western Australia (McEnulty et al., 2011; Poore et al., 2008). The several specimens of *Cymonomus delli* collected represent a significant rediscovery of the species, previously known only from the holotype collected off Sydney in 1972 (Ahyong and Ng, 2009).

All of the undescribed species belong to genera already recorded from Australian waters, although their nearest congeners may not be Australian as in the new species of squat lobsters, *Munida*, *Munidopsis* and *Gastroptychus*, whose nearest relatives occur farther afield in the Indo-West Pacific (Baba et al., 2008). The three new Australian records represent significant range extensions (*Heterogenys microphthalma* – cosmopolitan, nearest previous record from New Zealand; *Parapagurus furci* – previously known from tropical Indo-West Pacific including New Caledonia and the Lord Howe Rise; *Munidopsis arietina* – previously known from the Bay of Bengal and Taiwan).



Figure 5.20 Decapoda from IN2015_C02. L: *Lebbeus clarehannah*; R: *Munidopsis crenatirostris*.

5.3.18 Pycnogonida (Sea Spiders)

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Pycnogonids (sea spiders) are an exclusively marine group of arthropods found worldwide from the intertidal to the deep sea. Almost 1400 species are described, about 200 of which are from Australian waters. The combined GAB surveys collected 134 specimens, representing 13 species in 7 genera and 4 families. Five of the 13 species are new to science.

This collection is highly significant in that it is the most extensive collection of deep-sea pycnogonids collected to date from this poorly sampled and little understood region. The collection is dominated by specimens belonging to the deep-sea genus *Colossendeis*. This genus includes species that are the ‘giants’ of the pycnogonid fauna with leg spans commonly in the 125-500 mm range but where specimens with leg spans of up to about 700 mm have been recorded. These large specimens can only survive in the deep-sea and are well adapted to the stable environment which it provides. In common with other long-legged pycnogonids, specimens in this genus are reliant on slow-moving, deep-sea currents; not only in search of food but for the distribution of their gene pool. By treading water rapidly they can lift themselves into the water column and then be carried over vast distances with little further effort. The six species of *Colossendeis* identified here are widely distributed and probably cosmopolitan.

Included in this collection are forms that belong to the '*C. macerrima*' complex. Rarely has any group of pycnogonids been subjected to such rigorous taxonomic scrutiny and yet their status remains unresolved. The ongoing taxonomic confusion has largely extended from the incomplete description of the *C. macerrima* holotype, and based on specimens in this collection its status is clarified. The status of the other species herein referred to as *C. cf. minor* is not resolved. Molecular analyses suggest that more than one species is represented and further analysis based on morphological characters is required. Those specimens will form part of a detailed analysis of the species complex based on a wider range of southern Australian material.

This collection has several noteworthy taxonomic and biogeographic records. Four new species were found belonging to the genera *Callipallene*, *Parapallene*, *Meridionale* and *Chonothoa*. The genus *Chonothoa* was previously known from Japan and is a new record for Australian waters.

Bathypallenopsis antipoda represents a new record for Australia and this is only the second record of the species. *Colossendeis spicula* represents the second record of the species in Australian waters and is only known (outside Australia) from Oregon, USA. *Colossendeis cucurbita* is also a new record in Australian waters.

Lastly, the abundance of specimens belonging to the genus *Colossendeis* in this collection has enabled comparison with the original type material for the genus and the status of two species has been clarified. These species are perhaps the most commonly recorded representatives of the genus *Colossendeis* in deep-sea collections outside of polar regions.

5.4 Discussion and Conclusions

The combined surveys were highly successful, resulting in a diverse collection of benthic invertebrates. After taxonomic analysis, the collection was determined to contain 1073 species and over 63,000 specimens. A total of 38 major invertebrate groups were present from eleven phyla, with a total of 357 families and 602 genera.

The overall diversity and abundance of benthic invertebrates was typical of temperate deep-sea communities. The families and genera present were all known to occur in the deep sea and many species have been previously recorded in Australia and worldwide. Nonetheless, the material constitutes some of the deepest biological sampling in Australian waters and has provided an excellent opportunity to study Australia's abyssal fauna, particularly in the poorly-sampled southern coast. There are new records for Australia, several new genera and high-quality tissue samples for genetic analysis. These surveys will provide the means for further valuable ecological, biogeographical and systematic research.

The abundance of invertebrates was also typical of deep-sea habitats; species were patchily distributed and often rare. Of the total species, 335 (31%) were known from only single specimens, with 465 (43%) known from two or fewer specimens. This high degree of apparent rarity is likely to be due to relatively low sampling effort compared with well-studied regions elsewhere, and has also been seen in exploratory deep water sampling in Australia and overseas (Poore et al., 2014).

The number of undescribed species (275, 26% of total) was unsurprising, given the depths sampled and general lack of exploration in the region. The result closely matches the proportion of undescribed species by recent Australian deep water surveys (e.g. 36% on the WA shelf by Poore et al., 2014). Some taxonomic groups contained a high proportion of undescribed species e.g. (~80% Isopoda, 50% Polychaeta, 49% Gastropoda, 41% Holothuroidea) whereas for others the figure was comparatively low (~6% Asteroidea, 18% Decapoda). This is likely due to a combination of these latter groups being larger and more easily collected, occurring more widely in the deep sea and having more taxonomic attention paid to describing new species. It is indicative of the level of taxonomic novelty encountered by sampling for the first time at such depths, that in addition to new species, the material also included nine new genera.

Despite the number of undescribed species, a fair proportion (350 species, 33% of the total) were previously recorded from Australia, many having been encountered in other exploratory surveys of the west and south coasts of Australia (e.g. Poore et al., 1994; McEnnulty et al., 2011). Of these, only 186 were known previously from the GAB, highlighting the lack of sampling in the region. Wide distributions are common in deep-sea animals, but studies on regional and global scales are still too scarce to generalise, and this is an ongoing area of research with much effort directed to understanding the relationship between sampling effort, distribution patterns and diversity in deep-sea environments (Grassle and Maciolek, 1992; Gray et al., 1997; de Forges et al., 2000; Danovaro, 2009; Schüller and Ebbe, 2007 and references cited therein). Several species collected, including several of the most abundant (e.g. *Ophiomusa lymani*), have cosmopolitan distributions in the deep sea. New records include previously described species (e.g. *Enixotrophon veronicae*, *Munidopsis arietina*) and even families never reported from Australian waters (e.g. Vesicomysidae, Katianiridae).

In summary, analysis of the Great Australian Bight survey material has produced a high quality biological dataset encompassing some of the deepest environments in Australian waters. The specimens provide valuable morphological, genetic and ecological data that will serve as the basis for further analysis and provide new context for Australia's deep-sea diversity.

6 Macro-infauna from the GAB continental slope (200-3,000 m depths) and Sediment Analysis

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6.1 Introduction

The Great Australian Bight (GAB) is a dominant feature of the longest south facing east-west coastline in the world, and one of the largest temperate water carbonate factories. The continental shelf in this region is up to 260 km wide, before dropping off into the broad Ceduna Terrace on the continental slope. Sediments in this region are primarily biogenic in origin, as the adjacent land mass is arid and there is no riverine input. Slope sediments tend to be muddy foraminiferal, spicule and pteropod oozes, often containing skeletal remains of bryozoans, molluscs and echinoderms transported downslope for the adjacent shelf (James et al., 2001; James and Bone, 2011). On the outer shelf (150-200 m), summer upwelling is thought to promote the growth of bryozoan communities and other filter feeders due to increased phytoplankton production, except in the central GAB where year-round downwelling is thought to account for their absence (James et al., 2001; James and Bone, 2011).

The shelf waters of southern Australia are known for high levels of diversity and endemism (e.g. Wilson and Allen, 1987; Womersley, 1990), as a result of a lack of disturbance from glaciation (McGowran et al., 1997), and 80 million years of isolation from other land masses (Veevers, 1991; Phillips, 2001). There is a single study of infauna on the GAB shelf (Currie et al., 2007), which documented three infaunal assemblages correlated with depth. Sessile filter feeders dominated the inner shelf, while motile deposit feeders dominated the shelf break. Unlike other invertebrate groups, the infauna was not particularly diverse, with only 240 taxa found in 65 grab samples. However, the fauna of deeper waters in the GAB have not been subject to any previous systematic faunal sampling, despite the extent and uniqueness of this region, due to its remoteness and generally inaccessible nature. There has only been one previous study, which only collected samples at 2 sites (1000 and 2000 m) in the central GAB (Currie and Sorokin, 2011), with an additional study in the eastern GAB focusing on canyon infauna (Conlan et al., 2015).

The Benthic Biodiversity Theme of the Great Australian Bight Research Program (GABRP) aims to characterize the benthic assemblages in the central and eastern GAB, and in particular, those in the vicinity of oil and gas exploration leases. Infauna are of particular interest as it is relatively easy to collect replicate quantifiable samples, and different components of the assemblage have been

documented as good indicators of oil pollution elsewhere (e.g. Gray et al., 1990; Gesteira and Dauvin, 2000; Trannum et al., 2011; Washburn et al., 2016). Although generally inconspicuous, infauna can also play an important role in benthic-pelagic coupling, influencing nutrient cycling between the sediment and the overlying water column (e.g. Tahey et al., 1994; Caliman et al., 2011; Gammal et al., 2017).

This Section details the analysis of the infaunal assemblages sampled during the GABRP, as well as the physico-chemical properties of the sediments (excluding hydrocarbon analyses). The analysis includes incidental samples collected as part of geotechnical investigations for BP by Fugro, and as part of the GAB Deepwater Marine Program funded by Chevron.

6.2 Methods

The majority of samples analysed were collected on the RV *Southern Surveyor* survey SS2013_C02 in April 2013. Samples were collected at depths of 200, 400, 1000, 1500 and 2000 m along each of five north-south transect lines, for a total of 25 stations (Figure 6.1). One transect line was located through the middle of the benthic protection zone of the GAB Marine Park, with lines 10 nautical miles either side and outside the protection zone. Additional lines were located 80 and 150 miles east of the line through the GAB MP. At each of these 25 stations, an instrumented coring platform (ICP, Sherlock et al., 2015) was deployed to collect sediment samples, along with a range of ancillary data. The ICP was based around a KC6 multicorer (KC, Denmark), which collected a set of 6 100 mm diameter sediment cores from an area of $\sim 1 \text{ m}^2$. The top 150 mm of each core was extruded for analysis, with small subsamples retained for genetic analyses. This material was elutriated on a 300 μm sieve, and the material retained on the sieve preserved in 95% ethanol for later identification. Depending on the site, between 3 and 5 cores were available for biological sampling, with one additional core used to characterize sediment physico-chemical properties.

At station T2-200, a Smith-McIntyre grab was used to obtain an additional sample, and no suitable core samples could be obtained from stations T4-400, T5-200 and T5-400, so these were only sampled using the grab. Grab samples were subsampled to give samples that were as consistent as possible with those from the corer. An additional 8 samples were incidentally collected in April/May 2013 from the Fugro *Southern Supporter* as part of geotechnical investigations of potential drill sites for BP, again using a multicorer with 100 mm diameter core tubes.

Further samples were collected in late 2015 from the RV *Investigator* using the same equipment and protocols as used on the RV *Southern Surveyor*. IN2015_C01 sampled a range of sites between 950 and 2800 m depth, all within the boundaries of the region surveyed by the RV *Southern Surveyor*, but not on the transects. Rather, two topographic features: potential seep zones and volcanic

seamounts, were targeted due to their interest from a petroleum geochemistry perspective.

IN2015_C02 extended the 2013 transects to 2800 m depth, and resampled a small number of the 2013 sites to help determine if any differences between the 2800 m sites and those shallower might be related to time of sampling rather than depth. At a single 1000 m site, also sampled in 2013, 3 replicate casts were made to provide an indication of small-scale variability. In total, 200 samples were obtained from 68 separate casts.

All samples collected in 2013 were sorted at SARDI, with fine-scale taxonomy being undertaken by Museum Victoria, who did both for the 2015 samples. Samples for physico-chemical analysis were analysed for organic carbon, inorganic carbon, total nitrogen and CaCO_3 using a LECO Truespec and weight loss after HCl addition. Particle size analysis was undertaken on a Mastersizer. Samples for physico-chemical analysis were collected from all SS2013_C02 and IN2015_C02 sites, but only from a limited number of IN2015_C01 sites, and none from Fugro sites.

Patterns in the composition of the infaunal assemblage of the full data set were examined using Principal Co-ordinates Analysis using the PCO routine of the PERMANOVA+ add-on in Primer (Anderson et al., 2008; Clarke and Gorley, 2015) to perform a multivariate ordination. Data were fourth root transformed to reduce the influence of abundant taxa, and Bray-Curtis similarities were used in all analyses. Preliminary analyses suggested that a single core sample was not large enough to provide a sufficient representation of the infaunal assemblage to detect any patterns, and thus abundance was averaged over all available cores from a single cast (2-5 depending on other requirements for material). If only a single core was available from a cast, it was not included in the analysis. This resulted in 46 samples, and as a consequence, there was generally no replication to allow formal statistical analysis, and so all analyses are exploratory only. The influence of the sediment physico-chemical variables, latitude, longitude, depth and the variables described in Section 3 were examined using the DISTLM routine followed by distance-based redundancy analysis (Legendre and Anderson, 1999), with 499 permutation of the data, and using the adjusted R^2 criterion to select the best model of all possible models. Bathymetry and sediment characteristic variables from Section 3 were dropped, as they largely replicated variables that we had site specific data for, as were the TERAN variables, as they did not cover all sites. Bottom stress variables (mean, maximum and standard deviation) from GABRP Project 1.1 were used in favour of the seabed stress from the older CSIRO Ribbon Model. Nine of the twelve IN2015_C01 sites did not have sediment data, so were removed from the covariate analysis, as were three SS2013_C02 sites for which the organic carbon analysis failed. Covariates were initially examined using draftsmans plots, and BIR_SR, EPOC_SR, SST_SR, PAR_SR, CRSO2_SR and NPP_SR were eliminated from further consideration due to collinearity with the corresponding average values. Similarly, Benthic Stress

standard deviation was collinear with Benthic Stress Maximum, and K490_AV and K490_SR were collinear with Chla_AV and Chla_SR respectively, so were eliminated. Marginal tests were conducted for the remaining covariates to determine the proportion of the infaunal variance explained, and variables eliminated from the final analysis if they correlated with a better individual explanatory variable at $p \geq 0.9$.

Samples from SS2013_C02 and IN2015_C02 come from a structured survey design, and were more amenable to formal statistical analysis. As such, differences between Depths, Transects and Surveys were tested using Permutational Multivariate Analysis of Variance (Anderson, 2001), with post hoc pairwise tests when appropriate to determine where any differences lie. All 3 factors were treated as fixed, and 9999 permutations of residuals under a reduced model were used, again with Bray-Curtis similarities on fourth root transformed data. Analyses were undertaken for the full multivariate data set, as well as total infaunal abundance, without averaging across samples within a cast. As logistics prevented proper replication across surveys, no test was available for the Survey main effect, or the 3-way interaction.

To determine if particular taxa co-occurred, a non-metric multidimensional scaling (nMDS) analysis was performed on taxa at each taxonomic level. Species accumulation plots were also constructed, and the Chao2 estimator used to determine likely total number of taxa present.

Sediment analysis was undertaken using Principal Components Analysis (PCA), using only those samples for which all variables were available (grain size analysis, OC, IC and CaCO_3). Nitrogen was not used, as it was below the quantifiable limits in all samples. As all variables were measured as percentage composition, no transformation was undertaken.

6.3 Results

Overall, 1303 individuals were collected from the 200 samples. These represented at least 258 species, and with some taxa only identified to class or phylum, probably substantially more. Future references to species should be taken to mean these 258 taxa identified to the lowest taxonomic level possible. There were an average of 6.5 individuals per core, and 4.0 species (Table 6.1). A maximum of 41 individuals was found in a single core, and 19 species.

Each species found was represented by an average of only 5.1 individuals, and occurred on average in 3.1 cores (Table 6.2), with the maximum being 269 individuals and 93 cores (being for nematodes, which were not identified to a lower level). Excluding nematodes, these values were 165 and 68, respectively, being Hexanauplia (copepods). The most common and widespread organism identified to the species level was the cirratulid polychaete *Aphelochaeta* sp. MOV 6842, which was

represented by 27 individuals in 18 cores. 54% of all species were only represented by a single individual, and 62% only occurred in a single core.

At the species level, there were clear differences in the infaunal assemblage between 2013 and 2015, especially in the data from the transects (i.e. SS2013_C02 vs IN2015_C02) (Figure 6.2). These differences largely persisted at higher taxonomic levels, with the exception that samples from seeps and volcanic mounds in 2015 (IN2015-C01) were similar to those from the transects in 2013. They were largely absent at the class and phylum levels. At all taxonomic levels, sites that were sampled in 2013 and 2015 differed substantially between years, although the single site that was sampled 3 times in succession in 2015 grouped fairly closely. Interestingly, although the two RV *Investigator* surveys were back-to-back and sampled in the same area, there were distinct differences between them that persisted even at the phylum level. Depth patterns were less clear, and partially obscured by the shallowest sites only being sampled in 2013 and the deepest in 2015. In 2013, 200 and 400 m sites tended to be distinct from 1500 and 2000 m sites, with 1000 m sites being intermediate, particularly at lower taxonomic levels. In 2015, the 2800 m sites tended to separate out from the shallower sites on the same survey, although there was some overlap. The two stage nMDS showed that there were substantial differences in the patterns detected at each taxonomic level, with class and phylum level analyses being particularly distinct (Figure 6.3).

For the structured component of the data, there was a Depth by Transect interaction in the assemblage data, and a clear effect of Depth in the total abundance data (Table 6.3). The only differences picked up in the pairwise tests for assemblage structure were between the 400 m site and the 1500 and 2000 m sites on Transect 1 (westernmost transect). For total abundance, the 400 m sites differed from the 1000 m and deeper sites, the 200 m differed from the 2000 m, and the 2800 m sites differed from all others. Mean infaunal abundance peaked at 400 m ($1320 \text{ m}^{-2} \pm 175$ (SE)), and declined as depth increased to 268 ± 65 at 2800 m (Figure 6.4).

The year of sampling was consistently the most highly correlated variable with the infaunal assemblage composition, irrespective of taxonomic level (Table 6.4). Other important variables included depth, sediment grain size composition, chlorophyll_a (mean and seasonal range), nitrate seasonal range, and bottom temperature seasonal range. Most covariates explained an increasing proportion of assemblage composition as taxonomic level increased, with the exception of a decrease from class to phylum. The final DISTLM model explained a fairly constant proportion of the variation (75-81%), with the exception of a decrease to 69% at the phylum level. The number of covariates in the final model tended to decrease as taxonomic level increased, from 24 for species to 15 for phylum. Sample groupings in the distance-based redundancy analysis (Figure 6.5) reflected those in the principal co-ordinates analysis (Figure 6.2).

At the species level, there were no noticeable groups of taxa that occurred together (Figure 6.6), with most taxa forming a single tight grouping. At the genus and family levels, there were large numbers of taxa still grouping tightly, with other taxa spread around this group, with no obvious secondary groups. With much fewer taxa at the class and phylum levels, there were no large distinct groups, although at the class level Hexanauplia, Nematoda, Malacostraca and Polychaeta were all closely associated, as were Annelida, Nematoda and Arthropoda at the phylum level.

The species accumulation curve was still increasing in a straight line after 200 samples, indicating that a substantial number of species remain to be sampled, and the Chao2 estimator of total species richness reached a value of 628 (cf 258 observed), although it was also still increasing almost in a straight line (Figure 6.7). Both the sampled and estimated total genus richness were also still increasing, with the latter reaching 325 compared to 182 observed. While sampled family level richness was still increasing, the estimated total family richness reached an asymptote at 168 (cf 120 observed). A similar pattern occurred for classes, except the total maximum estimated number present was 29 (cf 20 observed). The 11 observed phyla was only 1 short of the total number predicted to occur.

Principal Components Analysis indicates a clear distinction between sediments from shallow and deep sites (Figure 6.5). 200 m sites are typified by fine to coarse sand, while 400 m sites have slightly finer sediments. Deeper sites are dominated by clay. Carbon composition did not appear to play an important role in structuring sediment samples in multivariate space. Sediment composition did not appear to vary between surveys

6.4 Discussion

There was a clear pattern of decreasing infaunal abundance from a peak at 400 m depth, with no variation in this pattern between transects. This pattern is consistent with what has been found elsewhere (e.g. Hyland et al., 1990; Tahey et al., 1994; Lourido et al., 2014; Conlan et al., 2015; Lubinevsky et al., 2017), although there are some localized exceptions such as trench environments where organic matter accumulates (Leduc et al., 2016). In the Arctic, depth accounted for 39% of the variation in infaunal abundance over a range of 68-4190 m, although not biomass (Clough et al., 1997), compared to 24% here. While no patterns in infaunal assemblage structure were found in the preliminary analysis of individual samples, the expected depth related patterns appeared when samples at each site were averaged, although they were not as clear as for abundance, and there was some variation in the depth effect with longitude. It is unlikely that depth per se is the main influence in this pattern, although organisms require specific adaptations to deal with the high pressure (Thistle, 2003), but rather that other environmental drivers correlated with depth are at work. Shallower waters tend to be closer to the continental shelf and land, where primary

productivity is higher and terrigenous inputs may contribute to food availability (Thistle, 2003). While terrigenous inputs are unlikely to be influential in the GAB, due to the lack of riverine inputs and the broad shelf, proximity to shelf water zones of high production could play a role. In addition, in deeper waters, any surface production has a greater chance of being intercepted before reaching the bottom than in shallower water. Temperature is another important factor that decreases with depth, and would be expected to have a strong influence on benthic production and biomass (Thistle, 2003; Cusson and Bourget, 2005). Sediment composition also varies with depth, as shown here, and can play an important role in structuring infaunal assemblages (Aller, 1997; Przeslawski et al., 2013; Lourido et al., 2014).

The eastern GAB (our T5), experiences summertime upwelling, while the central GAB (T1-3) experiences year-round downwelling (Middleton and Platov, 2003; McClatchie et al., 2006; Middleton et al., 2007). As a consequence of this, the sediment type and epibenthos at depths of 100-300 m have been shown to vary, with finer sediments and fewer epifauna in areas of year-round downwelling (James et al., 2001; James and Bone, 2011). We could not detect any effect of this in the infauna at our 200 m sites. Although they form two apparently distinct groups in the PCO plots (Figure 6.2), one group is composed of T2, T4 and T5, while the other is T1 and T3. At 400 m there is no grouping. Interestingly, however, carbon analysis on the T4 and T5 sediment samples from 200 m failed, likely as a result of most of the carbon being carbonate, and hence they are not in Figure 6.8. When a principal components analysis is done on grain size only, and including these samples, they separate out from T1-T3, and have coarser sediments (not shown), which is consistent with the model of James et al. (2001).

Infaunal densities in the GAB over a depth range from 200-2800 m sampled in our study (268-1320 ind m⁻²) are relatively low compared to what has been documented elsewhere. Infaunal densities sampled at 500-1000 m off northern Spain were ~1600 ind m⁻², while at 1000-1900 m they were ~1300 ind m⁻² (sorted on a 500 µm sieve). Off San Francisco at 2100-3150 m densities of ~5000 ind m⁻² were reported, based on samples sorted on a 300 µm sieve (Blake et al., 2009). Fischer and Brandt (2015) collated deepwater (2600 m +) infaunal densities in the Pacific, with values ranging from 64 to 3520, although values for depths of 550 -6080 m account for the lower part of this range, and those around 2800 m range from 176-1100. Most of these samples were collected using box corers, which have been shown to underestimate density by a factor of 2.9 compared to multicorers (Montagna et al., 2017), making the difference to the GAB samples even greater. The two studies examining infauna densities in the GAB reported considerably lower densities than we found: 50-450 ind m⁻² at 500-2000 m (Currie and Sorokin 2011); and at 1500 m (Conlan et al., 2015) report from

two nearby canyons a 10 fold lower density to our samples. Unfortunately, these studies only counted fauna retained on a 1 mm sieve, confounding these comparisons.

Whilst constraints on the sampling time available prevented replication, either between years or within a survey, at most sites, there was considerable variation between sample sets when they were replicated. One site had three casts in 2015, with two of these having almost identical assemblages, whilst the third was only slightly different. However, at the 4 sites sampled in both 2013 and 2015 (including the one with three 2015 casts), the variation between years was similar to that present between depths within a single year. This variation over time was consistent between sites and at all taxonomic levels, and occurred despite sampling (and subsequent processing) being undertaken with the same equipment using the same protocols and largely by the same people. This difference was particularly correlated with a high proportion of ostracods in 2015, and copepods in 2013. Nematodes were also virtually absent from the IN2015_CO2 samples, but abundant in the IN2015_CO1 samples (from just a few weeks before) and in 2013. However, removing these taxa from the analysis did not remove the temporal differences, which therefore also reflect subtler differences in a broader suite of taxa. Continental slopes are now known to be variable in both time and space (Levin and Sibuet, 2012; Qu et al., 2016), even without obvious disturbances. For example, Mamouridis et al. (2011) found seasonal variation in infaunal assemblages between 550 and 800 m depth, although at a site close to the coast and subject to seasonally variable riverine inputs. On the other hand, regular sampling over 10 years off San Francisco failed to show any temporal variation at reference sites (Blake et al., 2009). Infauna at 4000-5000 m depth off Nova Scotia vary in relation to flow regime, which can change sediment composition over time (Aller, 1997). Our 2013 samples were collected in autumn, when high summer phytoplankton production in overlying surface waters may augment food availability, while the 2015 samples were collected in late spring/early summer, when food availability may be just beginning to increase. Thus the temporal differences we document may be seasonal, although this will require sampling over future years to confirm.

Year also came out as the most important variable in the covariate analysis, and the only one capable of explaining >10% of the variation in the assemblage data. Depth was generally the next most important, with a long tail of significant variables that explained no more than 7% of the variation. Other consistently important variables included most of the sediment grain size variables, surface chlorophyll a values, bottom temperature, and seasonal range in bottom temperature and nitrate levels. Latitude, longitude, bottom currents, carbon content of sediments, slope, light related variables and phosphate all appeared to be unimportant. Despite low individual explanatory power, the suite of covariates examined explained 69-81% of the variation in the infaunal

assemblage. The low explanatory power of individual variables seems to be typical, not just for infauna (e.g. Przeslawski et al., 2013; Lourido et al., 2014; Fischer and Brandt, 2015), but also epifauna (e.g. Fromont et al., 2012; McCallum et al., 2013). In part, this may reflect the fact that most variables are measured on scales that are not relevant to the fauna being studied, and may average out relevant small-scale variation, especially if they are derived from remote sensing, predictive modelling or interpolation of sparse data, and are not directly measured when the sample was collected.

The patterns documented here were fairly consistent at the species, genus and family levels, but differed substantially at the class and phylum levels. There is a substantial literature on the subject of taxonomic sufficiency, in particular as it relates to the taxonomic level needed to assess changes in infaunal assemblages as a result of disturbance, that recommends that species level identification is unnecessary, with family generally being the recommended level of taxonomic identification when possible (e.g. James et al., 1995; Somerfield and Clarke, 1995; Dauvin et al., 2003; Terlizzi et al., 2003), and in some instances disturbance effects are even obvious at the phylum level (Gray et al., 1990; Warwick and Clarke, 1993). The majority of impact studies on deepwater infauna seem to take this approach, with identifications often at the family level (Montagna et al., 2013; Demopoulos et al., 2016; Washburn et al., 2016), saving considerable time and avoiding issues with a large proportion of species often being new to science.

The species accumulation curves suggest that only a small proportion of infaunal species present in the region were sampled. The Chao2 estimator of total species richness (628) was almost 2.5 times the observed (258), and still increasing strongly. The predicted number of genera appeared to just reach an asymptote (325 vs 182 observed), while the difference between observed and predicted decreased to 1 at the phylum level. Thus, any additional sampling is still likely to produce a high proportion of new species. Again, this is fairly typical for deepwater studies on infauna (e.g. Przeslawski et al., 2013; Conlan et al., 2015), although Lubinevsky et al. (2017) calculated that they had sampled 70% of species present with 150 samples.

Preliminary analysis of the 2013 data showed a high degree of variability between individual cores from a single multicorer cast, and no patterns with depth when analysed at the species level, suggesting that an individual core is too small to provide a representative sample of the assemblage, but that a group of 2-5 cores is sufficient. Any future studies on infauna in this region should take this into consideration, and preferably use either a single cast of a multicorer as one sample, or utilize a sampler that collects a larger sample. Experience indicates that a Smith-MacIntyre grab does not produce good samples at the deeper depths sampled, as much of the sample is lost on the return journey to the surface, and so this does not seem to be a viable option. Multiple casts also

require substantial time at a station. So for example with a deployment and retrieval speed of 60 m min⁻¹, it takes ~75-80 min to conduct a single cast to 2000 m, excluding deck handling time, which can add another 20-30 min. However, if analyses are conducted at higher taxonomic levels, such as family or class, it may still be possible to use individual cores as replicates, and much of the extraneous variability may be eliminated. In an analysis of sampling methods for deepwater infauna in the Gulf of Mexico, Montagna et al. (2017) found that individual cores from a multicorer provided good replicates for family level analyses, and recommended that it was better to increase the number of sites samples than to conduct multiple casts at a single site, as replicate casts only accounted for a small proportion of the variation in the assemblage. They also recommended that a multicorer be used in preference to a box corer, as the bow wave associated with the former reduced infaunal densities by a factor of 2.9, that a 300 µm sieve be used, and that only the top 10 cm of the core need be sorted. Indeed, Fischer and Brandt (2015) found 79% of macrofauna were in the top 2 cm of deepwater cores.

Overall, the patterns displayed by the infauna were fairly typical for these water depths. There was a clear peak in abundance at intermediate depth (400 m), with very low abundance in deep waters, although the GAB appears to be relatively depauperate from an abundance perspective compared to other areas in this depth range. Most species were represented in only a few samples, and there was a large proportion of species that are new to science. It is also apparent that we only sampled a small proportion of the species present, with estimated species richness being much higher than observed, and the estimate still increasing linearly with an increase in the number of samples. Assemblage level patterns were less distinct, although shallow sites (200 and 400 m) clearly differed from deeper sites (1000 – 2800 m). The most unexpected result was the clear difference in assemblage structure between surveys, which may in part relate to seasonal variation in food availability, and in part to differences in habitats sampled in the two 2015 surveys. No effects of differences in upwelling/downwelling regimes between the eastern- and western-most transects could be detected in the infauna, although they were present in the sediment physical characteristics, with shallow eastern sediments being coarser than their western counter-parts.

6.5 Tables

Table 6.1 Mean number of individuals and different taxonomic levels per core.

	Individual	Species	Genus	Family	Class	Phylum
Mean	6.5	4.0	4.0	3.9	2.6	2.2
Min	0	0	0	0	0	0
Max	41	19	19	18	9	6
SE	0.5	0.2	0.2	0.2	0.1	0.1
Total #	1303	258	182	120	20	11

Table 6.2 Details on average occurrence of taxa at varying taxonomic levels.

	Average # individuals per taxon	Average # cores per taxon	Average # individuals per taxon	Average # cores per taxon
Species			Genus	
mean	5.1	3.1	7.2	4.4
max	269	93	269	93
se	1.3	0.5	1.8	0.7
% singletons	54	62	43	50
Family			Class	
mean	10.9	6.5	65.2	26
max	269	93	359	140
se	2.8	1.2	26.5	9.8
% singletons	33	38	30	30
Phylum				
mean	118.5	40.2		
max	571	151		
se	60	17.7		
% singletons	18	18		

Table 6.3 Outcomes of PERMANOVA tests on the infaunal assemblage composition and total abundance for the structured component of the data (from SS2013_C02 and IN2015_C02). Note that there were no tests available for Survey or the 3-way interaction.

	Multivariate				Univariate		
	df	SS	Pseudo-F	P	SS	Pseudo-F	P
Depth	4	18624	2.24	<0.001	1.425	2.76	0.032
Transect	3	7442	1.19	0.17	0.438	1.13	0.34
Depth x Transect	18	43077	1.15	0.047	1.640	0.71	0.79
Depth x Survey	2	4226	1.02	0.43	0.130	0.50	0.60
Transect x Survey	2	4866	1.17	0.24	0.256	0.99	0.35
Residual	122	253320			15.754		

Table 6.4 Marginal proportional variation in infaunal composition at different taxonomic levels explained by environmental covariates and geographic variables according to DISTLM for averaged samples at varying taxonomic levels. Bold type indicates marginal fit is significant at $p=0.05$, grey background indicates variable was excluded from consideration as it was correlated with another variable at $\rho \geq 0.9$, green background indicates variable was included in the final model.

Covariate	Species	Genus	Family	Class	Phylum
Latitude	0.04	0.04	0.05	0.03	0.04
Longitude	0.04	0.04	0.04	0.05	0.02
Depth	0.07	0.07	0.09	0.13	0.10
Year	0.13	0.13	0.15	0.26	0.21
Benthic Stress Mean	0.04	0.04	0.04	0.01	0.02
Benthic Stress Max	0.04	0.05	0.05	0.03	0.04
Silt	0.04	0.04	0.03	0.03	0.02
Clay	0.06	0.06	0.07	0.11	0.07
Fine Sand	0.05	0.06	0.06	0.06	0.06
Medium Sand	0.06	0.06	0.06	0.09	0.07
Coarse Sand	0.05	0.06	0.07	0.07	0.05
Gravel	0.07	0.08	0.08	0.09	0.06
Inorganic Carbon (IC)	0.04	0.04	0.03	0.01	0.01
Organic Carbon (OC)	0.04	0.05	0.05	0.01	0.01
Total Carbon (TC)	0.06	0.05	0.05	0.06	0.05
Aspect	0.04	0.03	0.04	0.10	0.10
Slope	0.04	0.05	0.04	0.03	0.03
BIR_AV	0.04	0.05	0.04	0.01	0.01
CHLA_AV	0.05	0.06	0.07	0.09	0.07
CHLA_SR	0.05	0.05	0.06	0.08	0.05
SST_AV	0.05	0.05	0.06	0.06	0.07
PAR_AV	0.05	0.04	0.06	0.04	0.04
NPP_AV	0.06	0.07	0.08	0.10	0.09
EPOC_AV	0.06	0.06	0.06	0.06	0.06
CRS_NO3_AV	0.05	0.06	0.06	0.06	0.06
CRS_NO3_SR	0.06	0.07	0.07	0.09	0.10
CRS_O2_AV	0.05	0.07	0.07	0.07	0.07
CRS_PO4_AV	0.05	0.07	0.06	0.06	0.07
CRS_PO4_SR	0.06	0.07	0.06	0.08	0.10
CRS_S_AV	0.04	0.05	0.04	0.02	0.02
CRS_S_SR	0.06	0.07	0.07	0.09	0.10
CRS_SI_AV	0.07	0.07	0.08	0.11	0.10
CRS_SI_SR	0.04	0.04	0.04	0.05	0.05
CRS_T_AV	0.06	0.07	0.07	0.08	0.08
CRS_T_SR	0.05	0.06	0.07	0.08	0.08
Final model R ²	0.81	0.75	0.79	0.80	0.69

6.6 Figures

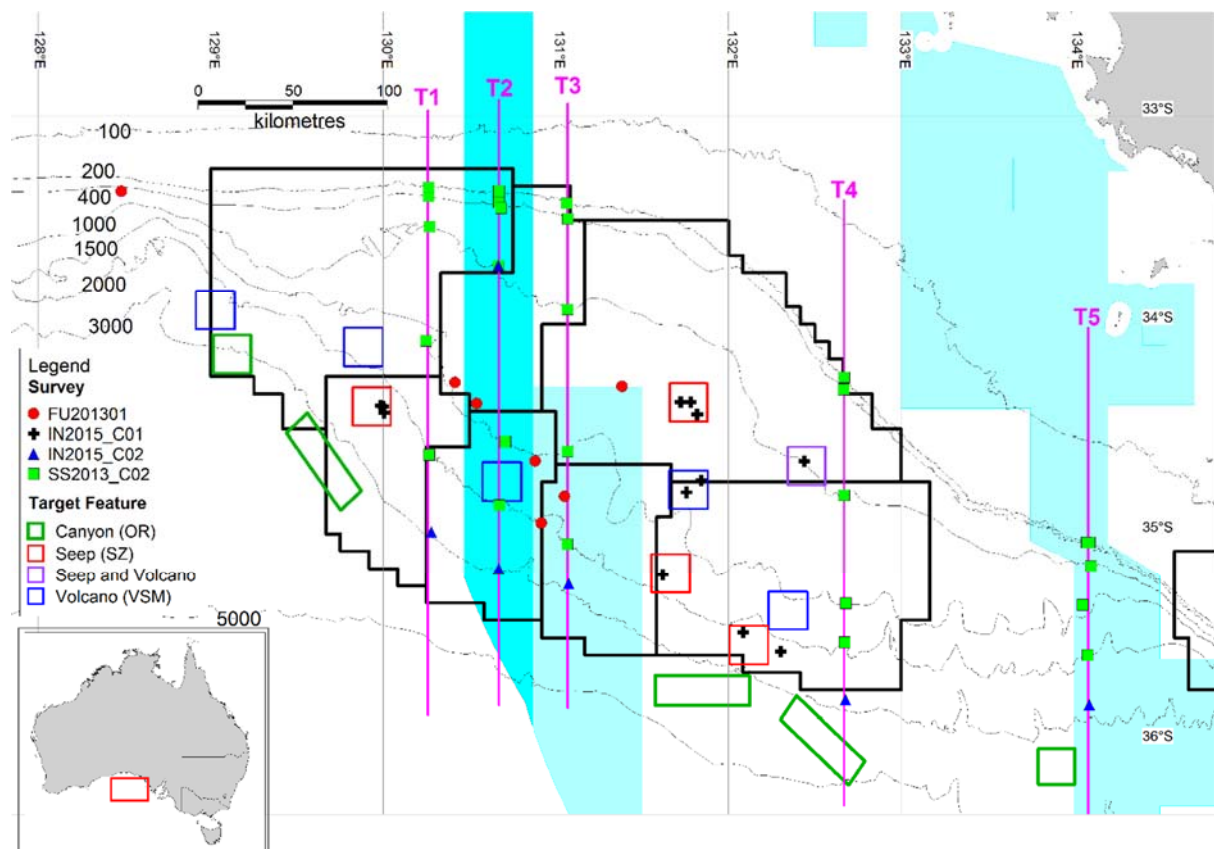


Figure 6.1 Map showing location of infaunal sample sites in the Great Australian Bight.

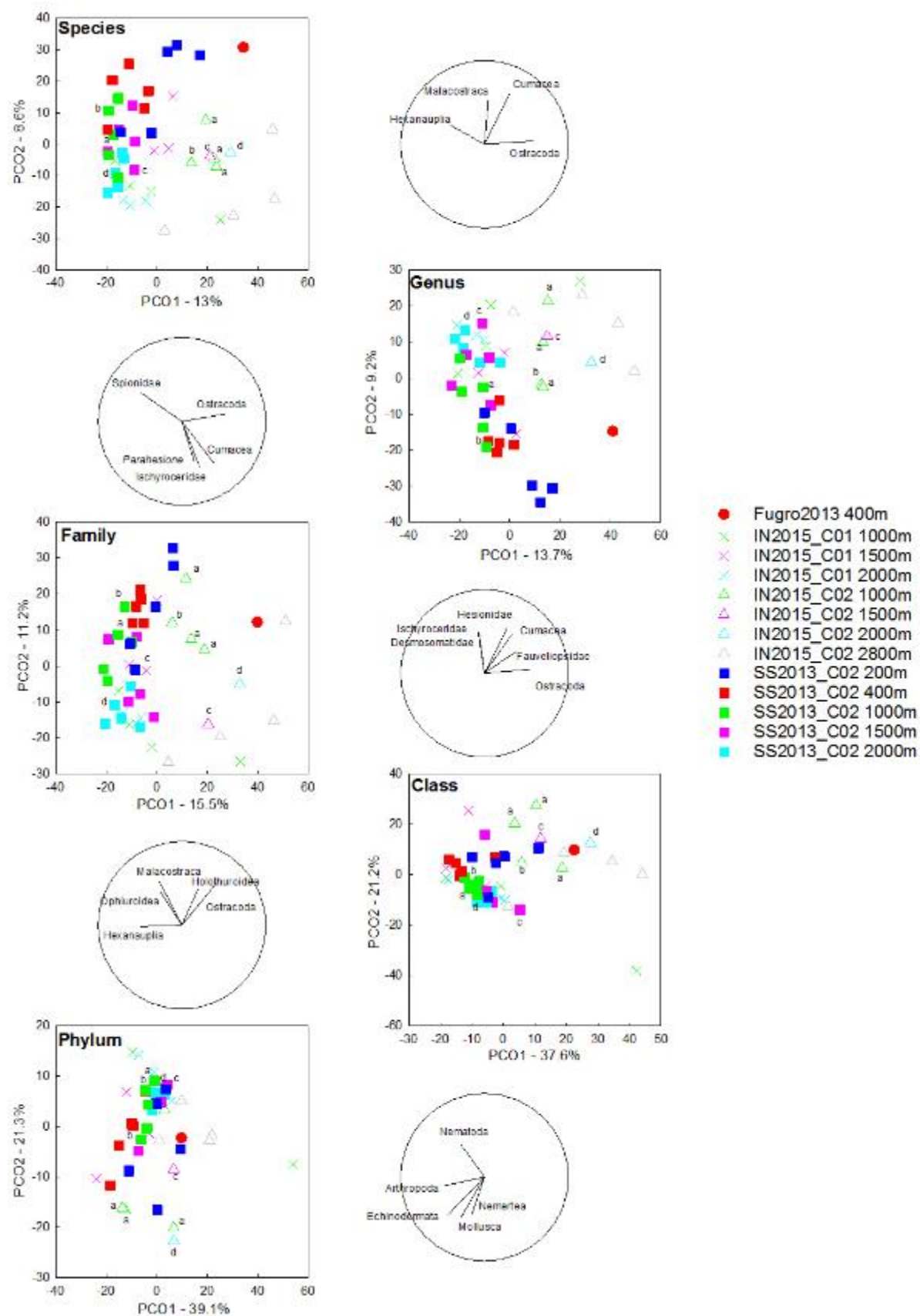


Figure 6.2 Principal co-ordinates analysis ordination of GAB infaunal data at varying taxonomic levels. Letters indicate repeat samples from a single site. The biplots show taxa with a correlation of >0.45.

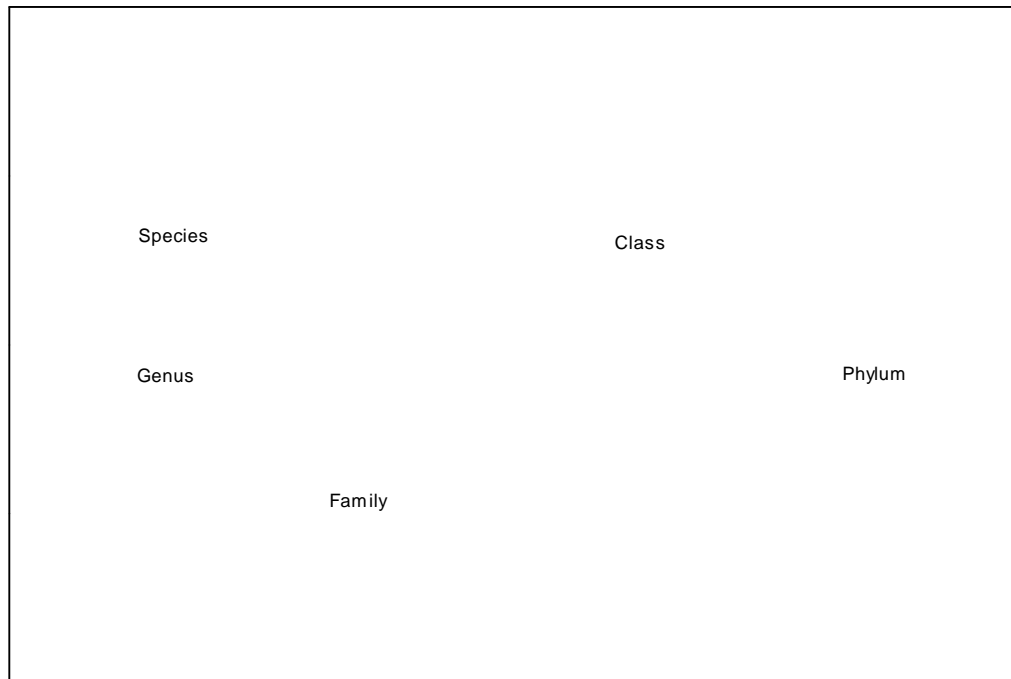


Figure 6.3 Results of the second stage nMDS showing degree of concordance in biogeographic patterns at different taxonomic levels. Points that are close together indicate that the analyses at the respective taxonomic levels (i.e. the plots in Figure 6.2) show very similar patterns, while those that are more distant do not show similar patterns.

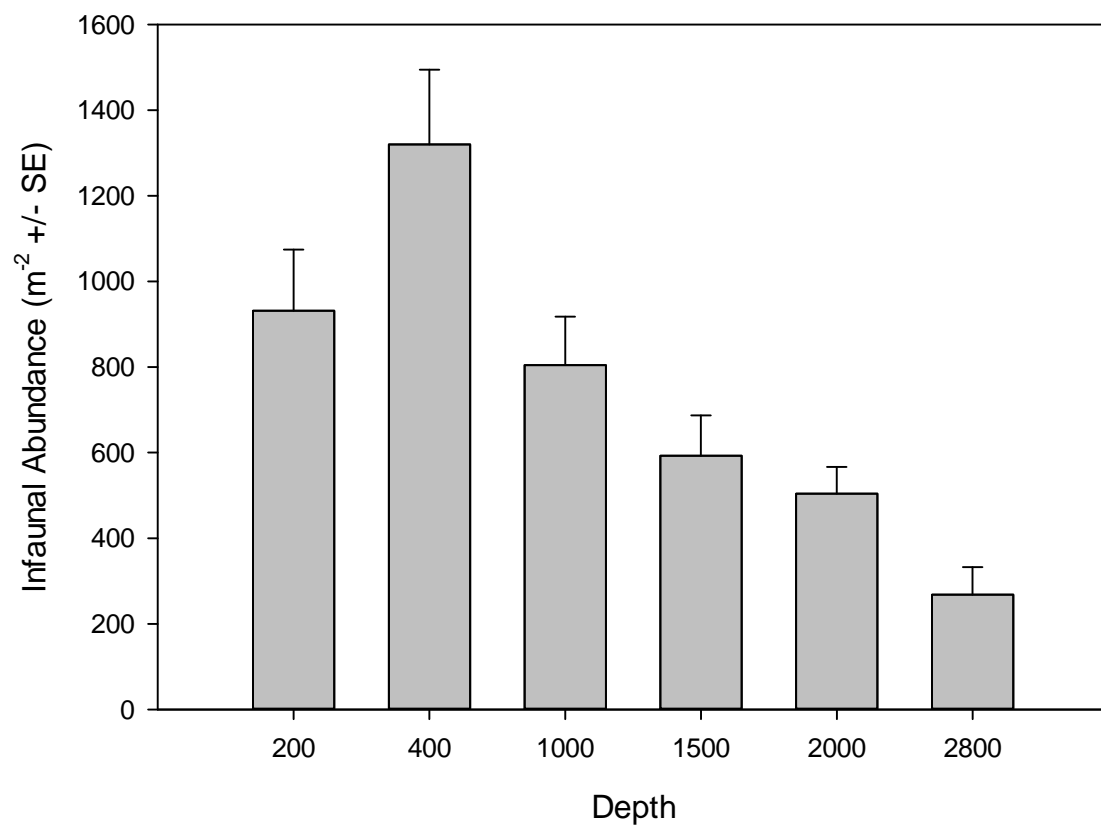


Figure 6.4 Depth trends in infaunal abundance from the structured survey data.

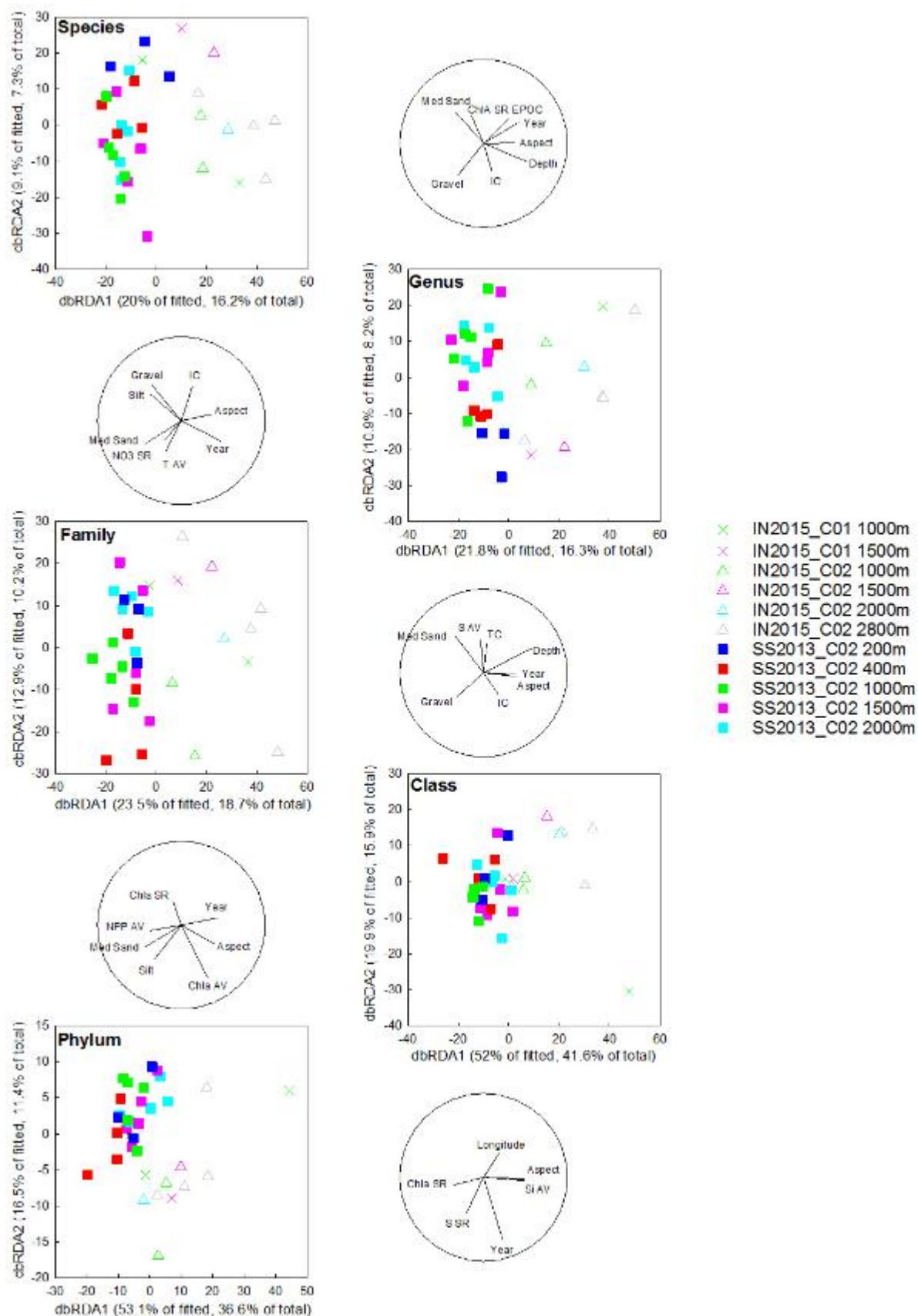


Figure 6.5 Distance Based Redundancy Analysis ordinations of GAB infaunal data at varying taxonomic levels showing the results of distance-based linear models. The biplots show covariates with a correlation of >0.3 with the plotted axes.

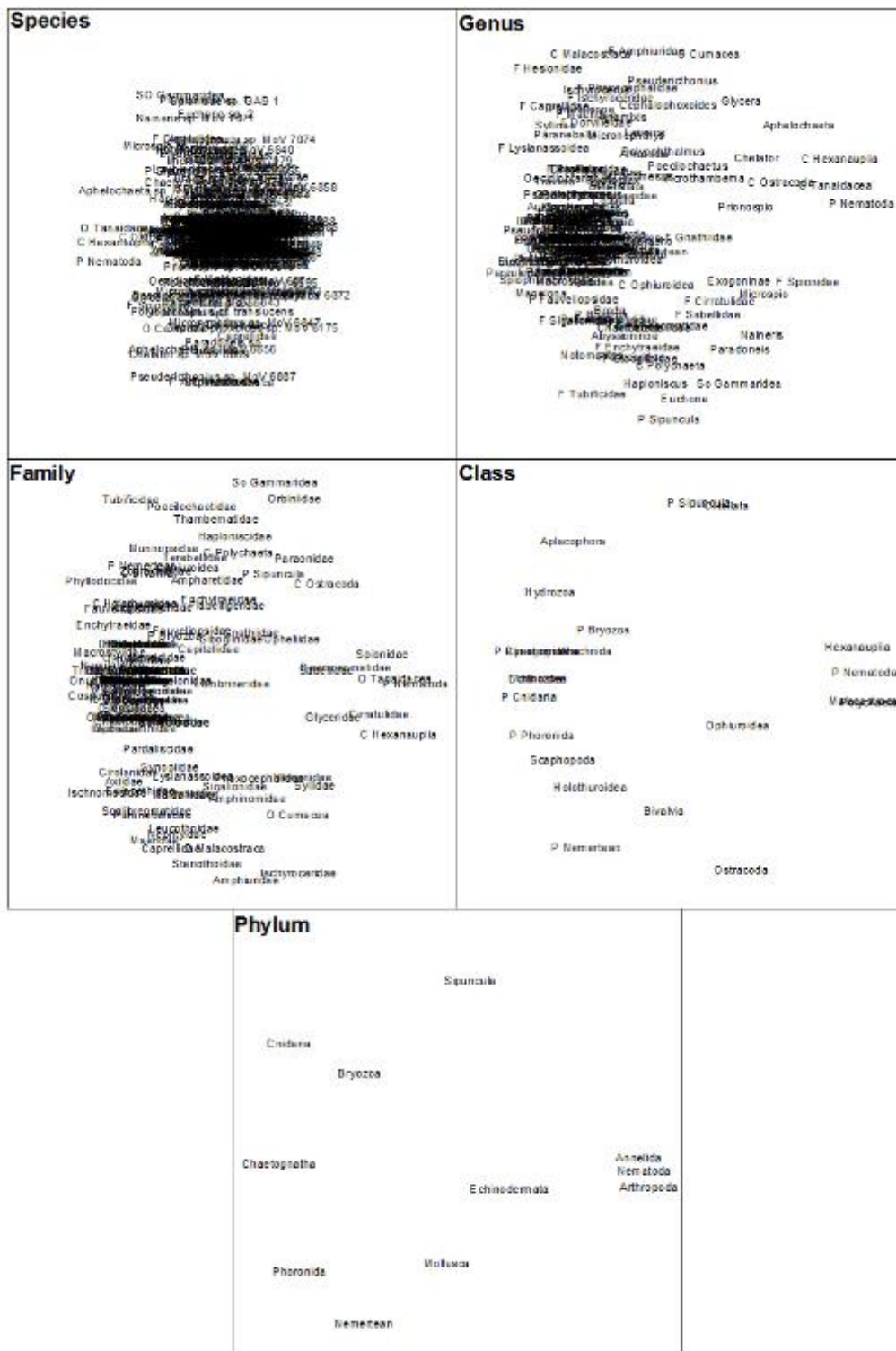


Figure 6.6 Ordination of taxa at varying taxonomic levels showing the extent of co-occurrence of different taxonomic groups.

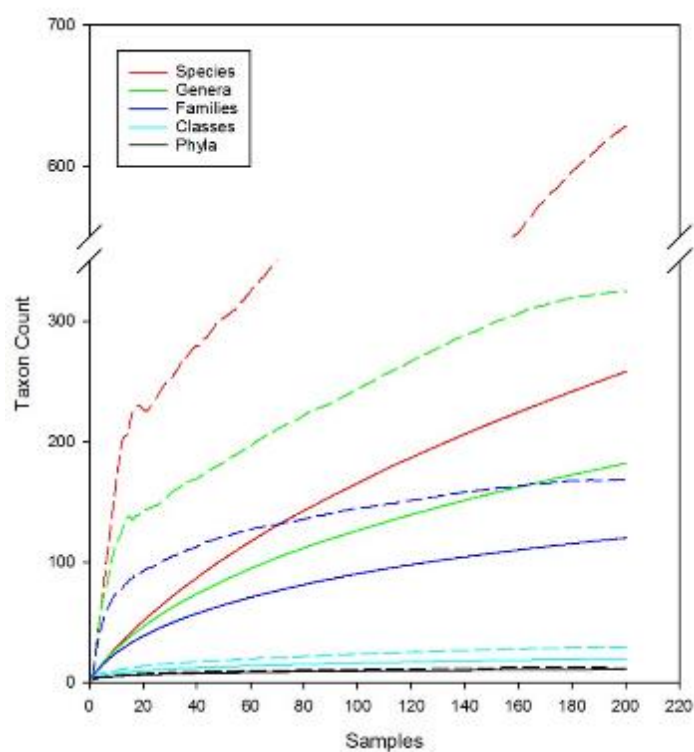


Figure 6.7 Taxon accumulation curves at varying taxonomic levels. Solid lines indicate observed accumulation, and dashed indicate predicted total number of taxa in the sampled region and habitat.

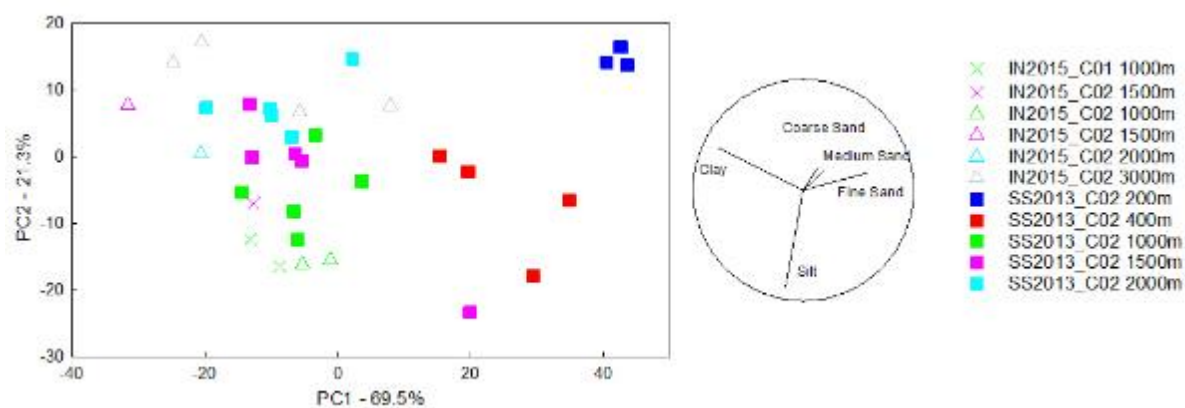


Figure 6.8 Principal Components Analysis of sediment composition.

7 Characterising the invertebrate megafaunal assemblages of a deep-sea (200-3000 m) frontier region for oil and gas exploration: the Great Australian Bight, Australia

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7.1 Introduction

The Great Australian Bight (GAB), which extends from Cape Pasley, Western Australia to Cape Catastrophe off southern Australia (Figure 7.1), is recognised as a unique marine bioregion on the basis of the high species richness and endemism of its near-shore invertebrate fauna (Ward, 2006). Its offshore area also has high conservation significance as evidenced by the proclamation of several large marine reserves (DEE, 2017). However, the conservation values generally attributed to shallow GAB waters are untested in the deep sea (Rogers et al., 2013). Continental slope and rise depths (200-3000 m) of the GAB are characterised by a paucity of data on benthic biodiversity to 1000 m, and near-absence of data beyond (Rogers et al., 2013). These deep sea areas make up the majority of the total 425,000 km² of seabed in the GAB: 20% is continental slope and rise (200-5000 m) and 45% abyssal depths (> 5000 m), with the remaining 35% being continental shelf in less than 200 m depth. Most of the GAB seabed is believed to be comprised of soft unconsolidated sediments (Rogers et al., 2013), although most areas are incompletely mapped or mapped at spatially coarse resolution.

Until recently, there had also been a paucity of data on epifaunal assemblages of the continental shelf (species composition and assemblage structure) and the environmental factors that drive patterns in their distribution and abundance (Ward et al., 2006). However, the shelf epifaunal assemblages of the eastern GAB are now better known following studies to assess the effectiveness of the Benthic Protection Zone of the GAB Marine Park, proclaimed in 1998. These studies found that the species composition of assemblages was significantly different among habitats: sediment grain size strongly correlated with epifauna distribution, biomass and species composition; specifically, biomass and species richness were negatively correlated with the percentage of mud (James et al., 2001; Ward et al., 2006). Muddy sediments supported lower biomasses and lower number of species than coarse sediments. In the single study in deeper water, Currie and Sorokin (2011), found that epifaunal species composition differed substantially between depths (upper-slope, mid-slope and lower-slope), although were only able to obtain a single sample at each depth.

The deep sea in the GAB may experience an increase in oil and gas exploration following release of oil and gas lease blocks. The need for information on the pre-exploitation status of the benthic environment is accentuated because oil and gas lease areas extend across areas of conservation significance (e.g. the GAB Commonwealth Marine Reserve, CMR, Figure 7.1). A major science program has been implemented to enhance ecological knowledge of the deep GAB: the GAB Research Program (GABRP, 2017). Benthic ecological work undertaken as part of the GABRP has included making a collection of invertebrates in 200 to 3000 m depths during a survey in 2015 (MNF, 2015). Analysis of the epibenthic invertebrate collection is reported here, with the following aims: (1) to document the composition, diversity and assemblage structure of deep-sea invertebrate megafauna in the central GAB, including from previously unsampled depths (1500 -3000 m); (2) to put the GAB invertebrate megafauna in biogeographic context; and (3) consider the characteristics of the fauna in regard to the needs for future ecological monitoring of the GAB benthic ecosystem given the increasing focus on the development of an offshore oil and gas industry.

7.2 Materials and methods

7.2.1 Survey design

Field sampling was completed during a survey that aimed to characterise regional ecological properties of the central GAB ahead of proposed exploration for oil and gas resources. The survey was designed to sample over two gradients along which ecosystem characteristics were expected to vary: depth and east-west (longitude). It was based on sampling at 6 depth strata (200, 400, 1000, 1500, 2000 and 3000 m) along 5 north-south transects (T1 to T5) at increasing meridians of longitude (Figure 7.1), i.e. a total of 30 sites. Nomenclature for the depth ranges sampled follow those proposed for depth-related patterns in fauna (bathomes) (Last et al., 2010): 200 m (shelf break); 400 m upper continental slope; 1000 and 1500 m (mid- continental slope); 2000 m (lower continental slope); and 3000 m (continental rise). To achieve relatively high sampling density in the region of the GAB Commonwealth Marine Reserve (GAB CMR) and active oil and gas leases, one transect (T2) was located in the centre of the GAB CMR, and one located at 10 n.m. either side of the GAB CMR (T1 and T3). Two others were located in the eastern GAB at 80 and 150 nm distance eastwards from the centre of the GAB CMR (T4 and T5 respectively) (Figure 7.1).

7.2.2 Data collection and dataset

Collections of invertebrate megafauna were made with a beam trawl adapted from an existing beam trawl design (Forest, 1981; Lewis, 2010). Its mouth is 4.0 m wide x 0.5 m high; the net has tickler chains on the foot rope and made of 25 mm stretch mesh. Tows followed a depth contour to avoid large variations in depth within a single sample unit; average towing depth was used to provide a single value for each sample. All tows were at a known speed (~2 kt), but tow duration varied, being

shortest (~20 minutes) at the shallowest sites (200 m) to regulate the catch volume (particularly sponges), and longest (~60 minutes) at the deepest sites (3000 m) to increase the volume of catch without reducing the quality of specimens. An ultra short baseline positioning system (USBL beacon) was used to confirm the location and bottom-contact distance in a GIS of each tow. Swept area (m^2) was estimated for each tow based on the net width (m) x tow distance (m). The swept area was used to standardise the sample from each tow into estimates of abundance: biomass (gm^{-2}) and density (individuals m^{-2} , shortened to ind.m^{-2}).

For the purpose of this study, invertebrate megafauna was defined as specimens exceeding approximately 10 mm in length and easily visible to the naked eye. Megafauna collected in the trawls were sorted and identified to an operational taxonomic unit (OTU) at sea. Once recorded, the specimen lots were preserved. Material that was dead (e.g. empty shells) and all pelagic taxa were excluded from the data set. The ship-board OTUs were equivalent to putative species for many groups. Each was given a unique identifier (name and number), counted, weighed and a representative sample was photographed. A library of the photographed ship-board OTUs was collated for each sample to ensure consistency of naming throughout the survey. Selected taxa were examined further by taxonomists who upgraded and/or confirmed the ship-board identifications. Full details of the taxonomic identification process, and the final list of species, is provided in Section 5. In cases where ship-board OTUs were upgraded, e.g. revised or lots split, the counts and weights of taxa recorded at sea were also updated. Records were excluded from analysis if the identification was ambiguous between OTUs due to damage from the sampling process; these amounted to 7.5 kg of biological material (~3% of the total) identified to 66 higher taxa, the largest fraction of this was 3.7 kg of undifferentiated sponge fragments. The final list of taxa with consistent identification to the lowest taxonomic level achieved are referred to as OTUs in diversity and assemblage analyses (Table 7.1). As there was no replicated sampling at sites, there was a total of 30 samples; these yielded 217 kg (44349 individuals) of 629 OTUs from 36 taxon groups in 11 phyla (Table 7.1).

As part of the taxonomic upgrading process, the prior known distributions of megafauna species were recorded, where possible. The categories identified were 'undescribed', 'known from the GAB', 'known from temperate Australia' (Perth to Sydney) and 'known from Australia'; where possible, notes on the wider distribution were added. These data were gathered from published literature and biodiversity databases including the Atlas of Living Australia (ALA, 2017), Australian Faunal Directory (AFD; ABRS, 2009), and Ocean Biogeographic Information System (OBIS, 2017). Broader distributions were further categorised into regions of southwest (Perth to Esperance) and southeast Australia (Victoria, Tasmania and New South Wales to Sydney) and the Indian and southern Pacific Ocean regions. As the goal was to test affinities with regions neighbouring the GAB, 'Indo Pacific' records in

the Indonesia-Papua-Philippine region were not assigned to either Indian or Pacific Ocean. Lastly, species were recorded as ‘cosmopolitan’ (i.e. known near-worldwide) where supported by literature and occurrence data. The compiled distribution data enabled results to be placed in a biogeographic context and provide further insights into the potential endemism of species in the deep GAB.

7.2.3 Physical covariate data

A set of environmental data were generated for each sampling station from data that were compiled and spatially assigned to a 0.01 degree grid for modelling in other projects from a variety of mostly web-based sources (Table 7.2) (Pitcher et al., 2016 and references therein):

1. Bathymetry: slope, aspect — based on model bathymetry combined from several sources. The data set uses the Geoscience Australia (GA) GA2009 250 m bathymetric product as a background (Whiteway, 2009). The Western Australian state official coastline (mean tide) was used to define 0 depth and islands. Commercial partners provided bathymetric data based upon LiDAR/LADS surveys and the Commonwealth Scientific and Industrial Research Organisation (CSIRO) and GA provided surveys based on acoustic systems. Australian Hydrographic Service (AHO) and the Western Australian Department of Primary Industries and Regional Development (WA DPIRD) provided historical soundings. These were integrated and processed in swath mapper processing software (CSIRO) into a 0.01 degree gridded product.
2. Sediment: gravel, sand, mud, carbonate — Data sourced from the Australian MARine Sediments Database (MARS), GA (Passlow et al., 2005).
3. Bottom water attributes (annual average and seasonal range): temperature, salinity, oxygen, nitrate, phosphate, silicate — Data sourced from the CSIRO Atlas of Regional Seas (CARS) (Dunn and Ridgway, 2002; Ridgeway et al., 2002).
4. NASA Ocean colour (SeaWiFS and MODIS): chlorophyll, SST, surface PAR — satellite derived datasets (2003-2014) were processed by the Integrated Marine Observing System (IMOS) (Edward King; IMOS, 2017).
5. Derived variables: benthic irradiance, primary productivity, exported POC (Particulate Organic Carbon) — calculated from ocean colour variables using published algorithms.
6. Bottom stress, output from the GABRP Theme 1 (Physical Oceanography): Bottom stress was averaged over a two year model simulation (2013-2014); maximum and standard deviation were also recorded. The model was developed by Middleton et al. (2017).

Each sampling station was assigned to a 0.01 degree spatial grid in GIS based on the mid- point between the gear touching bottom and being lifted off the seafloor, and the environmental data from this grid cell was used. A total of 36 environmental predictor variables (including the deployment depth, latitude and longitude) were available (Table 7.2).

7.2.4 Analysis methods

The swept area of each tow was used to calculate standardised estimates of abundance for each sample individually: biomass (g.m^{-2}) and density (number of individuals per square metre – ind.m^{-2}). These estimates were combined to calculate an average biomass and density for each OTU (and taxon group) for each depth stratum across transects and each transect across depths (Table 7.2).

Richness and taxon distributions were examined using summary statistics and randomly permuted species accumulation in PRIMER v7 (Clarke and Gorley, 2015). Average richness, biomass and density were compared between depth strata and transects using 2-way ANOVA without replication (assuming no interaction between the two factors). Bonferroni post hoc tests were used to identify any pairwise differences for significant main effects. Analyses were done using GraphPad Prism v5.02 software (<http://www.graphpad.com/>).

Differences in the OTU-level assemblage structure were examined using permutational multivariate analysis of variance (PERMANOVA; Anderson, 2001) and principal coordinate analysis (PCO) (Torgenson, 1958; Gower, 1966; Anderson et al., 2008) for both biomass and density. The PERMANOVA was used to examine differences between depths and transects; for significant results in the main test, a post-hoc pairwise test was used to determine where differences lie. Both factors (depth and transect number) were treated as fixed, and 9999 permutations of residuals under a reduced model were used. All analyses were performed on square-root transformed data, and the Bray-Curtis similarity measure was used. The multivariate correlation between density and biomass was examined using the RELATE procedure (Clarke and Gorley, 2015).

To examine the relationship between assemblage structure and environmental covariates, distance-based linear models (DISTLM) with distance-based redundancy analysis (dbRDA) was used (Legendre and Anderson, 1999; McArdle and Anderson, 2001; Anderson et al., 2008), with 999 permutations of the data, and using the adjusted R^2 criterion to select the best model of all possible models. The set of 36 environmental predictor variables was *a priori* reduced to 30 by removing measures of variability, seasonal range (SR), maximum (MAX), or standard deviation (SD), in an environmental factor, where these were highly correlated ($R > |0.9|$) with another measure of the same factor. Thus, BIR_SR, SST_MAX, NPP SR, PAR_SR, EPOC_SR and BSTR_SD were excluded. All multivariate analyses were performed in PRIMER v7 (Clarke and Gorley, 2015) and PERMANOVA+ for PRIMER (Anderson et al., 2008).

7.3 Results

7.3.1 Composition and diversity

The total of 629 invertebrate OTUs did not represent the full diversity of the deep GAB based on the trajectory of a rarefaction curve which showed no close approach to an asymptote (Figure 7.2).

Richness is also under-estimated because some of the 629 OTUs were not identified to species level, e.g. bryozoa and hydrozoa (Table 7.1), and are likely to represent many species.

Richness (number of OTUs per sample) varied by depth but not longitude. Depth accounted for 67.1% of the variance, contributing significantly to a difference in the richness per depth stratum (ANOVA: $F_{5,4}=10.27$, $P<0.0001$), whereas transect contributed a non-significant 6.7% of the variance ($F_{5,4}=1.28$, $P=0.31$). Richness was highest (~75 OTUs per sample) at the shelf edge and upper slope (200 and 400 m depths respectively), and relatively low (~35-40) between 1000 and 3000 m (Figure 7.3a). The Bonferroni test showed the significant between depths differences were between the 200 m stratum and all depths ≥ 1500 m, and between the 400 m stratum and the 1000, 1500 and 2000 m strata. There was no clear difference in the average number of taxa from west (T1) to east (T5) (Figure 7.3b).

Relatively few (185, 29%) OTUs were captured more than twice; 330 were singletons (52%) and 114 doubletons (18%). Only 3 species-level OTUs were collected in more than half of the 30 samples: *Parapagurus richeri* (hermit crab, 18 samples), *Ophiomusium lymani* (brittlestar, 17 samples), and *Nematocarcinus productus* (carid shrimp, 16 samples). The sub-class-level OTU 'undifferentiated hydroids' was also observed in 16 samples, however, this likely represents a number of species.

7.3.2 Abundance (biomass and density)

Megafaunal abundance (biomass and density) was relatively high in shallow depths (200-400 m) and consistently low in deep (>1500 m) strata, but there was some inconsistency in trend around 400 to 1000 m between the two measures of abundance (Figure 7.4a, b). Average biomass was highest at 200 m depth (2.2 gm^{-2}), followed by the 1000 m (1.3 gm^{-2}) and 400 m strata (1.0 gm^{-2}); biomass was less than 0.6 gm^{-2} in depths ≥ 1500 m (Figure 7.4a). However, high variability within depths meant that these differences were not significant (ANOVA: $F_{5,4}=2.54$, $P=0.062$), and neither was the transect effect ($F_{5,4}=0.89$, $P=0.49$). Average density was highest (0.5 ind.m^{-2}) at 400 m depth, relatively high at 200 m (0.3 ind.m^{-2}) and evenly low ($\sim 0.1 \text{ ind.m}^{-2}$) in deeper depths (Figure 7.4b). This density pattern with depth was significant (ANOVA: $F_{5,4}=4.10$, $P=0.01$), and explained 44.7% of the variation, but again there was no transect effect ($F_{5,4}=1.35$, $P=0.29$). The Bonferroni test showed the significant between depths differences were between the 400 m stratum, and the 1000 and 2000 m strata.

The assemblage composition (higher level taxa) of invertebrate megafauna changed markedly with depth, as measured by biomass and density of 10 dominant (top-ranked) groups – those making up 90% of total biomass and 89% of total density, respectively (Figure 7.5). Most striking was the overall dominance of sponges (Demospongiae) and brittlestars (Ophiuroidea) (biomass and density), and sea cucumbers (Holothuroidea) (biomass) (Figure 7.5). Sponges were highly ranked by biomass and density in the three shallowest strata, making up the majority (53%) of biomass in the shelf break depth stratum (200 m) and 41% in the 1000 m stratum – the depth strata where average biomass was greatest (Figure 7.4a). Sea cucumbers and brittlestars were top-10 ranked by biomass and density in all depth strata, although both groups made up small proportions (< 8%) in the shelf break stratum (200 m). Brittlestars had intermediate to high fractions of biomass (~15-59%) and density (> 41%, except for 12% at 1000 m) in all deeper strata, and exceptionally high density (> 80%) at 1500 and 2000 m. Sea cucumbers (relatively large in body size compared to brittlestars) made up small proportions of density in all strata, but were conspicuously dominant in biomass at 2000 m and 3000 m depth (>37%). Other noteworthy patterns amongst the top-ranked taxa (Figure 7.5) were the biomass (15%) and density (22%) of tunicates (Tunicata) at 200 m; biomass (25%) and density (13%) of stony corals (Scleractinia) at 400 m; density (21%) of calcareous sponges (Calcarea) at 200 m depth; and the top-10 ranking of crustaceans (Decapoda) in all strata but at consistently low (< 10%) proportions of biomass and density.

The assemblage composition (higher level taxa) across transects (longitude) was relatively consistent for both biomass and density compared to the differences between depth strata (Figure 7.6). The dominant taxa overall, sponges (Demospongiae) (biomass and density), Brittlestars (Ophiuroidea) (especially density), and sea cucumbers (Holothuroidea) (especially biomass), were conspicuous on all transects, and many other dominant taxa (Tunicata, Echinoidea, Scleractinia, Asteroidea, Decapoda, Gastropoda and Calcarea) were top-10 ranked on all transects. Some smaller-bodied (lighter) taxa (Calcarea, Bryozoa, Bivalvia) ranked only in density, and some larger-bodied taxa (Echinoidea, Octocorallia, Asteroidea) only in biomass (Figure 7.6). Despite the overall consistency in presence of dominant taxa across transects, there were some notable between transect (longitudinal) differences: brittlestar (Ophiuroidea) biomass was higher on transects T3 and T5 than on other transects, and relatively high biomasses of urchins (Echinoidea) and octocorals (Octocorallia) were observed on T4 (Figure 7.6a). The relatively higher densities of Bryozoa on T1 and of brittlestars (Ophiuroidea) on T4 were also noteworthy (Figure 7.6b).

7.3.3 Assemblage structure

Invertebrate assemblages were most strongly structured by depth (Figure 7.7), although there is little separation on the first two PCO-axes between the 200 and 400 m strata. The first two principal

coordinate axes explained 25.0% and 27.6% of the variation in the biomass and density data, respectively (Figure 7.7). The depth effect in the PERMANOVA is highly significant for both the biomass and density data (pseudo- $F_{5,4}=5.464$, $P=0.0001$ and pseudo- $F_{5,4}=5.963$, $P=0.0001$, respectively). The pair-wise tests showed there were only few instances with no differences ($P>0.01$). These were for biomass between the 1500 m stratum and its two adjacent strata, and between 200 m and 1000 m depths. There were no differences for density in the pair-wise comparison between all strata below 1000 m, and between the 1000 m and 1500 m strata. The PCO reflects these results with the samples in the 1500 m stratum being widely spread along the second axis. No consistent east-west pattern was discernible within the shallowest and deepest strata, however in the 1500 m stratum the density data shows a clear seriation from Transect 1 to 5 roughly aligned with the second PCO-axis (Figure 7.7). The transect effect was non-significant in the PERMANOVA (biomass: pseudo- $F_{5,4}=1.087$, $P=0.226$; density: pseudo- $F_{5,4}=1.072$, $P=0.2645$). Similarity patterns based on biomass and density data are highly correlated (RELATE analysis: $Rho=0.971$, $P=0.1\%$).

The marginal tests of the DISTLM analysis showed significant ($P = 0.001$) contribution by 25 of the 30 tested predictor variables, each accounting for between 11% or 13% (GA CRBNT) and 19% or 22% (CRS_O2_AV) of the variation in the assemblage data based on either biomass or density (Table 7.3). For sets of highly correlated ($R>|0.9|$) variables, only the one ranked highest in the marginal tests was retained in the final DISTLM analysis (Table 7.3).

The best solution (based on all possible combinations of predictor variables) for explaining the pattern in the invertebrate community structure was reached by using 17 (biomass) or 16 (density) of the 21 tested predictor variables (biomass: adjusted $R^2 = 0.50$; $R^2 = 0.79$; density: adjusted $R^2 = 0.50$; $R^2 = 0.78$) (Table 7.3). Average oxygen, salinity and temperature were the most influential variables accounting for 39% of the explained variation in the biomass model, while oxygen, silicate and salinity were the most influential in the density model (accounting for 40%). The first two axes of the associated dbRDAs explained 30.6% and 33.5% of the total variation, and 38.6% and 43.1% of the fitted model for biomass and density respectively (Figure 7.8). The variables with the highest correlations (>0.3) to the first two axes were: average silicate, proportion of sand, average temperature and seasonal range of nitrate in bottom waters for both biomass and density data; in addition, slope and average oxygen were also correlated to the first two axes of the biomass dbRDA (Figure 7.8). Silicate is highly correlated with depth and sand is correlated to mud; temperature and oxygen are both proxies for a range of chemical characteristics of bottom water (Table 7.3).

7.3.4 Biogeography

Of the 629 invertebrate OTUs, 376 identified to species-level (60%) possessed sufficient distribution data for analysis. Of these species, the majority (261 spp., 70%) had previously been recorded from Australia, with 146 (39%) previously recorded from the GAB. A quarter (n=92) of species were undescribed, although at least 15 of these had previously been collected from temperate Australia. This leaves 77 species (21%) that are not only undescribed, but are currently known only from the GAB (Table 7.4).

Only a small number of described species (n=37 spp., 10%) had not been previously collected in Australian waters and represent new occurrence records. A larger proportion (n=110 spp., 29%) were new records for the GAB region. Roughly a quarter of species (n=88) have been recorded as being endemic to Australia, but only two species (excluding undescribed species) could be confidently assessed as endemic to the GAB (Table 7.4).

In terms of broader distributions and biogeographic affinities, more species were associated with southeastern (n=183 spp., 49%) compared to southwestern Australian waters (n=104 spp., 28%). Extending further to adjacent ocean basins, over twice as many invertebrate species were recorded from the southern Pacific (n=149 spp., 40%), compared with the Indian Ocean (n=64 spp., 17%). A small proportion (n=22 spp., 6%) of species are known to have cosmopolitan distributions in the deep sea (Table 7.4).

7.4 Discussion

7.4.1 Diversity and assemblage structure of megabenthic invertebrates

The deep water survey represents a highly successful, systematic sampling of the deep GAB; more than 44,000 specimens of > 600 OTUs were collected. A good proportion of the species-level OTUs (92 of 376 species, 25%) were undescribed, and 77 of these were collected for the first time. The level of taxonomic novelty is consistent with other deep sea sampling in Australia (Williams et al., 2010a; Poore et al., 2015) and worldwide (Glover et al., 2002; Brandt et al., 2007; Ellingsen, 2007). In addition, the high level of apparent rarity (52% of species known from a single sample) is also consistent with previous reports from deep-sea surveys (Grassle and Maciolek, 1992; Ellingsen, 2007; Williams et al., 2010a; Poore et al., 2015).

The composition of the deep GAB invertebrate epifauna is broadly typical for temperate deep-sea regions. The families and genera present are all known to occur in the deep-sea and many species have been previously recorded in Australia and worldwide, e.g. Annelids (Alalykina, 2013; Shields and Blanco-Perez, 2013), Molluscs (Knudsen, 1970; Allen, 1983; Scarlato, 1981), Crustaceans (Brandt et al., 2007; Poore et al., 2008; Knox et al., 2012), Echinoderms (Hansen, 1975; Rodrigues et al.,

2011; Stohr et al., 2012). Consistent with previous deep water sampling in Australia (Williams et al., 2010a; 2011), the highest diversities (>80 OTUs) were recorded for within the Demospongiae, Decapoda, Gastropoda and the combined Echinodermata (Table 7.1). Cnidaria, particularly corals, were less diverse and abundant than in a similar survey in the Tasman Sea (Williams et al., 2011), perhaps because there was relatively less sampling of rocky habitats compared to the Tasman Sea survey. The beam trawl used for the collections appeared to be well suited to sampling on deep sediments targeted in the GAB; it sampled a wide range of mobile and sessile epibenthos and did not appear to have an obvious selection bias for particular taxa.

Sponges and echinoderms dominated the biomass and density, with the former being more prominent in shallower depths. Similar patterns were reported from canyon habitats in the GAB (Currie and Sorokin, 2014) and another deep-sea survey on the adjacent Australian west coast (Williams et al., 2010a). Tunicates feature strongly in the 200 m depth stratum shelf epifauna, which is consistent with Ward et al.'s (2006) description of the GAB shelf epifauna. The depth strata targeted in this study were based on generally reported bathymetric patterns in the deep sea: clearly defined shifts in community structure across the continental slope from the shelf edge ~200 m depth to the continental rise (~4000 m depth) (e.g. Schiaparelli et al., 2016), and mirroring the depth-related zonation observed in the Australian ichthyofauna (Last et al., 2011). Our analyses confirmed that the generalised pattern holds true for the epibenthic communities in the GAB, with clear changes in the assemblage structure between depth strata. Previous sampling in temperate Australia, including the GAB also showed clear depth stratification of the community structure (Williams et al., 2010a, Currie and Sorokin, 2011; Thresher et al., 2014).

Amongst co-varying environmental parameters, depth had relatively high explanatory power (>0.16) for the biological patterns. However, it was correlated with a variety of other factors, in particular the higher ranked average of silicate in bottom waters (explanatory power >0.18). In fact, most of the covariates (25 of 30 variables) had surprisingly high individual explanatory powers (>0.10), compared to those seen in other deep-sea epifauna studies – e.g. Fromont et al. (2012) or McCallum et al. (2013). The final 'best' models using 17 or 16 covariates, explained 78% and 79% of the variation in, respectively, the biomass and density data. In comparison, similar analyses of sponge or crustacea distributions along the Western Australian margin resulted in only 37% and 25% of the variation explained, respectively (Fromont et al., 2012; McCallum et al., 2013). Chemical and physical characteristics of the bottom waters were the most influential environmental predictors for the GAB megafauna, similar to the findings of McCallum et al. (2013). Other variables that were influential in McCallum et al.'s (2013) study such as bottom hardness were of less relevance in our data, as all samples were taken on sediments. Bottom stress from the hydrodynamic model developed under

the GABRP was expected to influence the distribution of filter feeding epifauna such as sponges and corals, but had no strong explanatory power in the model.

The GAB was identified as a single provincial-scale bioregion based on the distribution of brittlestars (O'Hara, 2008) and fishes (Last et al., 2005). The assemblage structure in our study is consistent with these findings, with no longitudinal pattern in assemblage, biomass or density distribution from the central and eastern GAB, despite summertime upwelling driving higher productivity in the latter (Rogers et al., 2013).

7.4.2 Biogeographic affinities of central GAB fauna

The recent surveys in the GAB have had the effect of filling in a large knowledge gap in Australia's deep-sea environment (Currie and Sorokin, 2011; Rogers et al., 2015). In addition to describing new diversity and categorizing ecosystem structure, it is important to place the fauna in a broader biogeographical context. The accumulated collections, combined with data from previous biodiversity surveys in western (McEnnulty et al., 2011) and south eastern Australia (Poore et al., 1994), now make it possible to examine the distribution and diversity of deep-sea species across southern Australia.

Approximately 70% of the invertebrate species (that could be assigned biogeographic data) have previously been recorded from Australia, with less than half (146 species, 39%) previously known from the GAB. Endemism was low however, with two species, the crab *Choniognathus granulatus* and barnacle *Arcoscalpellum inum* known only from the GAB; the remainder of species having been recorded elsewhere in Australia.

Whilst a further 77 invertebrate species (21%) were undescribed and known only from the GAB, it would be premature to assign them as having endemic status. These surveys sampled deeper than any previous survey in Australia so it is highly likely that many of these new species are a result of exploring new depth ranges, as opposed to geographic areas. The rarity of many species in the deep sea also makes it very difficult to assign endemism, as for many only one or two specimens have ever been collected. To ascertain whether the deep GAB has an endemic fauna, further sampling at similar depths (>2500 m) must be conducted elsewhere.

Results show an eastwards biogeographic affinity, suggesting that the deep GAB is not an equal mixing zone between western and eastern fauna. Within Australia, there was a noticeably stronger overlap in species distributions with southeast (n=183 species, 49%) than southwest waters (n=104 species, 28%). This pattern was also true for adjoining ocean basins, with over twice as many species previously recorded from the southern Pacific Ocean (n=149) than from the Indian Ocean (n=64). This pattern was more dramatic when considering species that occur in only one adjacent region,

with 90 species (24%) found in the southern Pacific but not the Indian Ocean, but only 6 species (<2%) from the Indian Ocean but unknown from the Pacific Ocean. The mechanism driving this trend is unknown and may be due to factors such as the higher availability of slope-depth habitats in the southern Pacific Ocean, combined with higher sampling effort (Richer de Forges et al., 2000; Williams et al., 2006).

A small proportion of species (6%) are recorded as having “cosmopolitan” distributions; occurring effectively worldwide in the deep sea. Several of these species, including the echinoderms *Enypniastes eximia* and *Ophiomusim lymani*, were amongst the most abundant species in the benthic sampling. Wide distributions have long been thought to be common in the deep sea (Gage and Tyler, 1991; Stuart et al., 2003), but further taxonomic revisions and genetic analyses may separate some of these cosmopolitan species into multiple cryptic species (Brandt et al. 2012).

7.4.3 Utility of the data for ecological monitoring

Scientific interest in indicators of status change in marine ecosystems has increased rapidly in response to national and international policy requirements for ecologically sustainable development, and societal demands for ecosystem-health reporting (Hayes et al., 2012). For the Australian government, these imperatives create a need to assess the status of marine ecosystems at a variety of spatial and temporal scales. These include local to regional-scale assessments associated with anthropogenic activities such as oil and gas extraction within individual or clusters of lease blocks; these inform national-scale state of the environment reporting that meets national and international obligations (Hayes et al., 2012). Ecological indicators are a key element of monitoring for assessing and reporting environmental changes, but deciding what variables and indicators should be measured is difficult (Hayes et al., 2015). Thus, whilst there are many candidate biological variables, there is little consensus on what to use because biological and ecological characteristics are complex, temporally and spatially variable in importance, and their interactions not well-understood (Fischer and Grimes, 2012).

The design of any monitoring program, and the basis for identifying suitable indicators and metrics, should be driven by the management questions that need to be addressed (e.g. Kropp, 2004; Peterson et al., 2001; Hammerstrom et al., 2012; Hayes et al., 2015). Further, in the context of oil and gas activities, environmental monitoring needs to be relevant to the phase of development (e.g. exploration, production, decommissioning) and the different potential effects resulting from them (Green, 2005; Cordes et al., 2016). However, whilst the international regulations for habitat protection during industry development typically include conservation objectives matched to requirements for environmental impact assessments (EIA), environmental approvals, and/ or ecological monitoring programs, there are many examples of jurisdictions where there are no

explicit objectives or prescribed methodology for completing assessments (Cordes et al., 2016; Table 7.5). Australia, including the GAB, is one such area. The objectives in the management plans of several Australian authorities that regulate industries (oil and gas, and fishing), and biodiversity conservation (to meet federal and international obligations) are only broadly specified and interdependent. All link to Australia's *Environmental Protection and Biodiversity Conservation Act (1999)* (EPBC), which does not specify details for monitoring, indicators or metrics. In addition, most experience in Australia is from relatively shallow (continental shelf) depths (e.g. Chevron, 2013) and this may provide little basis for direct inferences into deep-sea environments (Gage, 2001) – including because ecological processes in deep-sea environments operate and respond to anthropogenic pressures at a relatively slow tempo (Williams et al., 2010b; McClain and Schlacher, 2015). In summary, there are no clear pre-existing directions within the Australian jurisdiction to inform the selection of appropriate indicators and metrics for ecological monitoring of benthic ecosystems in the deep GAB.

Our survey of deep-sea invertebrate megafauna at baseline (unperturbed) sites provides the basis to evaluate indicators and metrics in future comparisons – a reference-site monitoring approach (Hayes et al., 2015; Cordes, 2016). We identified several opportunities to develop indicators and metrics by considering the data at both species- and assemblage-level (Table 7.5). Many of the opportunities are underpinned by establishing a robust (consistent species-level) taxonomic foundation for the collections taken during this and other studies (Section 5). This is essential to generate robust metrics for species and assemblage level indicators, and subsequently develop knowledge about community structural and functional changes (including recovery) in response to disturbance (Carney, 1997; Kropp, 2004). Monitoring the presence or abundance of individual species has potential to track the status of ecosystem engineers, endemics, and threatened/ endangered elements – all of which have significance for biodiversity conservation objectives. Monitoring sentinel species, those sensitive or tolerant to known stressors, may be possible but responses to either natural or human-induced stressors must be known to account for possible shifts in tolerance along natural environmental gradients and between biogeographic regions (Zettler et al., 2013). In the GAB, sentinel species include cold-water corals aggregated on seamounts that were not sampled in this study, but which are known from other surveys (Williams et al., 2016).

Data resolved to species-level enable a variety of assemblage-level (composite) metrics (e.g. richness, diversity, distinctness) to be derived, and this is possible across several major taxa collected from the GAB (Table 7.5). Species-level data also permit the effect of data aggregation on the ability to detect community changes (taxonomic sufficiency) to be examined. Data aggregated at higher levels may still be informative (Vanderklift et al., 1996; Olsford et al., 1997; Dauvin et al., 2003),

however, Gage (2001) suggested that this is premature for the deep sea, and that before any such approach is implemented, testing against baseline species-level data is necessary. Robust taxonomy identified a high proportion of rarely-seen species, a common observation in deep-sea fauna (e.g. Gage, 2001; Williams et al., 2010a; Poore et al., 2015). This implies a need for highly replicated sampling to generate representative assemblage-level metrics, but adequate representation of rare species in large numbers of samples will have little effect on analyses (Carney, 1997), especially when data are transformed to emphasise the ecological similarities of more abundant species (Olsgard et al., 1997).

Where reference sites should be established can only be determined once the exploration phase of industry development is further advanced because the spatial scales of potential impact are highly activity-specific (e.g. Cordes et al., 2016). However, our data show the high importance of depth to site selection. In our data, in common with other studies of megabenthos in Australian waters (Williams et al., 2010a) and more generally (Carney, 2005), assemblage composition (turnover), diversity, abundance and the proportion of endemic species are all highly correlated with depth. The GAB CMR has potential to provide reference sites, but it is overlain by active oil and gas lease blocks and has a history of bottom trawl fishing in depths to about 1200 m, including on seamounts. These factors need accounting for when reference sites are considered.

Comprehensive sampling of a large poorly known area such as the deep-sea in the GAB is not realistically feasible. Therefore, the use of physical surrogate data available at broad scales (remotely sensed oceanographic, hydrographic or acoustic data) is attractive for generating predictive maps of biodiversity and habitat distributions so that spatial extents and changes in them can be used as indicators. This has been done successfully for macrobenthos in the Gulf of Mexico where Wei et al. (2010) found zonal patterns of macrobenthos composition were correlated with depth and detrital particulate organic carbon (POC) export flux estimated from remotely-sensed phytoplankton pigment concentrations in the surface water. Similarly, in the North Atlantic, Johnson et al. (2007) found a relationship between the variance in benthic standing stock (biomass and abundance of deep-sea macrobenthos) and estimated particulate organic content (POC) flux at depth (derived from SeaWiFS satellite colour imagery). These analyses may be possible for the GAB, but the density, quality and relevance of physical covariate data available for the region is yet to be fully evaluated. Experience elsewhere (e.g. Anderson et al., 2016) shows that model validation is a key step for successfully using environmental surrogates to map deep-sea biological distributions.

7.5 Tables

Table 7.1 List of higher level taxa included in analyses showing the total number of OTUs and a summary of the taxonomic resolution achieved for each OTU within each taxon.

Taxon group	Number OTUs	Species	Number OTUs at respective taxonomic level						
			Genus	Family	Sub- order	Order	Sub- class	Class	Phylum
Phyl. Porifera									
Calcarea	30	27	3						
Demospongiae	118	108	9	1					
Hexactinellida	18	18							
Phyl. Cnidaria									
Actiniaria	34	33	1						
Corallimorpharia	2	2							
Hexacorallia	1					1			
Hydrozoa	2			1			1		
Octocorallia	24	22	2						
Scleractinia	9	9							
Siphonophorae	1	1							
Zoanthidea	1					1			
Phyl. Nemertea	1								1
Phyl. Priapulida	1								1
Phyl. Sipuncula	6	6							
Phyl. Brachiopoda	3	3							
Phyl. Bryozoa	1								1
Phyl. Annelida									
Hirudinea	1	1							
Polychaeta	27	16	11						
Phyl. Mollusca									
Aplacophora	3	3							
Bivalvia	22	22							
Cephalopoda	14	14							
Polyplacophora	1	1							
Scaphopoda	4	4							
Gastropoda	80	76	2	2					
Phyl. Echinodermata									
Asteroidea	43	41	1	1					
Crinoidea	1	1							
Echinoidea	11	8	3						
Holothuroidea	15	14	1						
Ophiuroidea	33	32	1						
Phyl. Arthropoda									
Cirripedia	14	14							
Decapoda	81	80			1				
Isopoda	12	11	1						
Lophogastrida	1	1							
Stomatopoda	1	1							
Pycnogonida	9	9							
S-Phyl. Tunicata	4			3				1	
Grand Total	629	578	35	8	1	2	1	1	3

Table 7.2 Environmental variables compiled for consideration as explanatory factors in community analyses. Numbers in the Source column refer to corresponding points in Section 7.2.3.

Variable	Description	Units	Source
DPTH_AV	Average of start and end depth of gear deployment	m	Survey data
LAT_MID	Latitude of midpoint of gear deployment	°	Survey data
LONG_MID	Longitude of midpoint of gear deployment	°	Survey data
GA_SLOPE	Slope derived from bathymetry DEM	°	1 Bathymetry DEM
GA_ASPECT	Aspect of slope derived from bathymetry DEM	°	1 Bathymetry DEM
GA_CRBNT	Sediment carbonate (CaCO ₃) composition	%CaCO ₃	2 MARS
GA_GRAVEL	Sediment gravel grainsize fraction, ($\phi > 2$ mm)	%	2 MARS
GA_SAND	Sediment sand grainsize fraction, ($63 \mu\text{m} < \phi < 2$ mm)	%	2 MARS
GA_MUD	Sediment mud grainsize fraction, ($\phi < 63 \mu\text{m}$)	%	2 MARS
CRS_NO3_AV	Nitrate bottom water annual average NO ₃	μM	3 CARS
CRS_NO3_SR	Nitrate Seasonal Range	μM	3 CARS
CRS_PO4_AV	Phosphate bottom water annual average PO ₄	μM	3 CARS
CRS_PO4_SR	Phosphate Seasonal Range	μM	3 CARS
CRS_O2_AV	Oxygen bottom water annual average O ₂	mL L^{-1}	3 CARS
CRS_O2_SR	Oxygen Seasonal Range	mL L^{-1}	3 CARS
CRS_S_AV	Salinity bottom water annual average S	‰	3 CARS
CRS_S_SR	Salinity Seasonal Range	‰	3 CARS
CRS_T_AV	Temperature bottom water annual average T	°C	3 CARS
CRS_T_SR	Temperature Seasonal Range	°C	3 CARS
CRS_SI_AV	Silicate bottom water annual average Si	μM	3 CARS
CRS_SI_SR	Silicate Seasonal Range	μM	3 CARS
CHLA_AV	Chlorophyll annual average from SeaWiFS	mg m^{-3}	4 NASA Ocean colour
CHLA_SR	Chlorophyll Seasonal Range	mg m^{-3}	4 NASA Ocean colour
NPP_AV	Net Primary Production annual average from SeaWiFS	$\text{mg C m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
NPP_SR	Net Primary Production seasonal range	$\text{mg C m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
PAR_AV	Photosynthetically Active Radiation (PAR) from MODIS	$\text{E m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
PAR_SR	Photosynthetically Active Radiation seasonal range	$\text{E m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
SST_AV	Sea Surface Temperature annual average from Modis	°C	4 NASA Ocean colour
SST_MAX	Sea Surface Temperature maximum monthly average	°C	4 NASA Ocean colour
BIR_AV	Benthic Irradiance annual average, $\text{BIR} = \text{PAR} \times e^{-\left(\frac{K490}{\text{Depth}}\right)}$	$\text{E m}^{-2} \text{day}^{-1}$	5 Derived variables
BIR_SR	Benthic Irradiance Seasonal Range	$\text{E m}^{-2} \text{day}^{-1}$	5 Derived variables
EPOC_AV	Export Particulate Organic Carbon flux annual average from SeaWiFS	$\text{mg C m}^{-2} \text{day}^{-1}$	5 Derived variables
EPOC_SR	Export Particulate Organic Carbon seasonal range	$\text{mg C m}^{-2} \text{day}^{-1}$	5 Derived variables
BSTR_AV	Bottom stress Average - mean over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)
BSTR_MAX	Bottom stress Maximum over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)
BSTR_SD	Bottom stress Standard Deviation of mean over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)

Table 7.3 The marginal test results from the DISTLM analysis showing the proportion of variation in the assemblage structure explained by environmental predictor variables tested for biomass and density data, respectively. Variables with correlation of $>|0.9|$ to a higher ranked variable were excluded from the DISTLM model run (grey cells). The selection of variables resulting in the 'best' result $\text{adj.}R^2 = 0.50$, $R^2 = 0.78$, $\text{adj.}R^2 = 0.50$, $R^2 = 0.79$ (biomass and density, respectively) are ranked by their relative influence on the models.

Variable	Biomass (g.m^{-2})			Density (ind.m^{-2})			Represented by (correlation $> 0.9 $)
	Prop	P	Selection (best)	Prop	P	Selection (best)	
CRS_O2_AV	0.192	0.001	1	0.215	0.001	1	
CRS_PO4_AV	0.187	0.001		0.212	0.001		CRS_O2_AV, CRS_T_AV
CRS_T_AV	0.187	0.001	6	0.209	0.001	3	
CRS_NO3_AV	0.184	0.001		0.209	0.001		CRS_O2_AV, CRS_T_AV
CRS_O2_SR	0.182	0.001	5	0.204	0.001	5	
EPOC_AV	0.181	0.001		0.203	0.001		CRS_T_AV, CRS_T_AV
CRS_S_SR	0.179	0.001		0.202	0.001		CRS_O2_AV, CRS_T_AV
CRS_SI_AV	0.180	0.001	2	0.197	0.001	6	
CRS_NO3_SR	0.172	0.001	4	0.193	0.001	4	
CRS_T_SR	0.171	0.001		0.192	0.001		CRS_O2_AV
CRS_PO4_SR	0.170	0.001		0.191	0.001		CRS_NO3_SR
NPP_AV	0.163	0.001	16	0.181	0.001		
CRS_S_AV	0.151	0.001	3	0.174	0.001	2	
Dpth (ave)	0.162	0.001		0.172	0.001		CRS_SI_AV, CRS_T_SR
CRS_SI_SR	0.149	0.001	12	0.168	0.001	16	
SST_AV	0.153	0.001	9	0.166	0.001	10	
GA_SAND	0.144	0.001	14	0.159	0.001	14	
GA_MUD	0.137	0.001		0.151	0.001		GA_SAND
BIR_AV	0.120	0.001	11	0.135	0.001	8	
PAR_AV	0.125	0.001		0.133	0.001		SST_AV, lat (mid)
CHLA_AV	0.119	0.001	17	0.133	0.001	12	
BSTR_Max	0.108	0.001		0.123	0.001		
BSTR_AV	0.104	0.001		0.116	0.001		
lat (mid)	0.106	0.001	8	0.113	0.001	9	
GA_CRBNT	0.106	0.001	10	0.111	0.001	13	
GA_SLOPE	0.057	0.027	13	0.048	0.098	11	
GA_GRAVEL	0.041	0.221	15	0.045	0.143	15	
CHLA_SR	0.043	0.193		0.041	0.238		
long (mid)	0.032	0.553	7	0.028	0.676	7	
GA_ASPECT	0.031	0.566		0.025	0.822		

Table 7.4 summary of the biogeographic information for 376 species-level OTUs where information was available. These represent 60% of the total 629 OTUs distinguished in the GAB collection; percentages are calculated in reference to 376 OTUs.

	No. OTUs	%
Total spp	632	
Spp with Biog data	376	59.5
Undescribed	92	24.5
Known from Australia	261	69.4
Known from GAB	146	38.8
Temperate Australia	247	65.7
SW Australia	104	27.7
SE Australia	183	48.7
Indian Ocean	64	17.0
S Pacific	149	39.6
Ind NOT Sth Pac	6	1.6
Sth Pac NOT Ind	90	23.9
Cosmopolitan	22	5.9
Australian endemic	88	23.4
New to Australia	37	9.8
Undescribed but prev collected	15	4.0
Undescribed and never found	77	20.5
GAB Endemic	2	0.5

* Percentage of total 632 OTUs

Table 7.5 Opportunities for survey collections of benthic invertebrate megafauna to inform ecological monitoring in the context of oil and gas development in the Great Australian Bight.

	Rationale	Indicators	Prospective taxa in GAB	Metrics	Considerations	Reference
Species						
<i>Sentinels</i>	Known or predicted response to impact/pressure	(1) Erect sessile fauna sensitive to smothering; (2) taxa responding to ambient hydrocarbon concentration	(1) Octocorals and sponges (2) Octocorals, decapods		Analyses based on traits (e.g. growth, reproduction) possible but inferential in GAB Responses likely have high spatial scale dependence	(1) Kropp (2004); Clark et al. (2015) (2) White et al. 2012; Fisher et al. 2014b; Fisher et al. 2014a; Felder et al. 2014
<i>Ecosystem engineers</i>	Support elevated diversity and/or abundance by increasing habitat complexity	Erect sessile fauna; reef/ thicket forming taxa	(1) Octocorals and sponges; (2) stony corals	Presence/ abundance (biomass and/or density)/ condition	(1) Known aggregations in GAB on volcanic seamounts	(1) Williams et al. (2016)
<i>Endemics</i>	Range limited species make dis-proportionately high contribution to biogeographic structure &	Potentially, species from any higher level taxon	(1) Invertebrate megafauna: the crab <i>Choniognathus granulatus</i> and barnacle <i>Arcoscalpellum inum</i> ; (2)		Endemicity is difficult to identify with confidence in deep sea areas with low sampling intensity	(1) this paper (2) Williams et al (this issue)
<i>Threatened, endangered</i>	High conservation value; subject to management recovery plans	Potentially, species from any higher level taxon	No invertebrate taxa presently listed	Presence/ abundance/ condition	N/A	N/A
Assemblage						
<i>Composition</i>	Assemblage characterised and baseline status described by simple composite metrics	Change in composite metrics	All higher level taxa for which species-level taxonomy is robust: Porifera, Actinaria, Octocorallia, Scleractinia, Mollusca, Echinodermata, Arthropoda	Richness Diversity Evenness Distinctness Indices	(1) High confidence in taxonomy; (2) high proportions of rarely seen species indicates many replicated samples needed; and (3) need for severe data transformation to identify signals; (4) Indices need calibration to specific locations	(1) MacIntosh et al. (this issue) (2) Gage 2001 (3) Carney 2001 (4) Dauvin et al. (2012)
<i>Structure</i>	Trajectory of assemblage change based on hypothesised mechanism	Trajectories of change indicated by composite metrics		Ecological similarity of multiple species in multidimensional space (e.g. MDS)		
<i>Predicted distributions</i>	Species distribution models or habitat suitability models indicate spatial extent of species and/or assemblages	Mapped extents		Change in spatial extent; areas or proportions inside protected areas or subject to impact	Data density is typically low in deep sea studies including the GAB; many environmental covariates, especially those with near sea-surface expression, have weak or unknown relevance in the deep sea; models need validation	(1) Anderson et al. (2016)

7.6 Figures

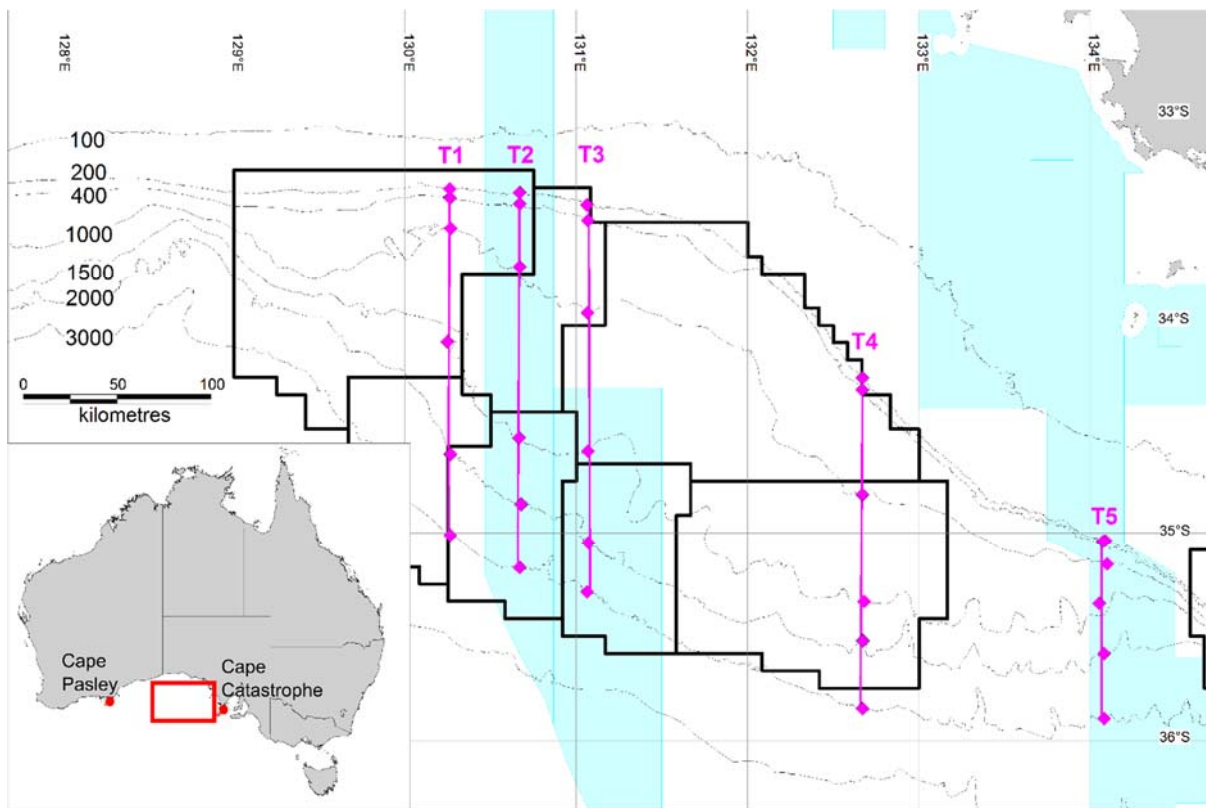


Figure 7.1 Map showing the study area in the central Great Australian Bight (GAB): sampling sites occur on transects T1 to T5, arranged from west to east, at six depth strata: 200, 400, 1000, 1500, 2000 and 3000 m. Also shown: relevant isobaths (labelled); proclaimed Commonwealth Marine Reserves (shaded light blue); active oil and gas lease blocks (black boundaries). Inset: Sampling location in relation to Australia.

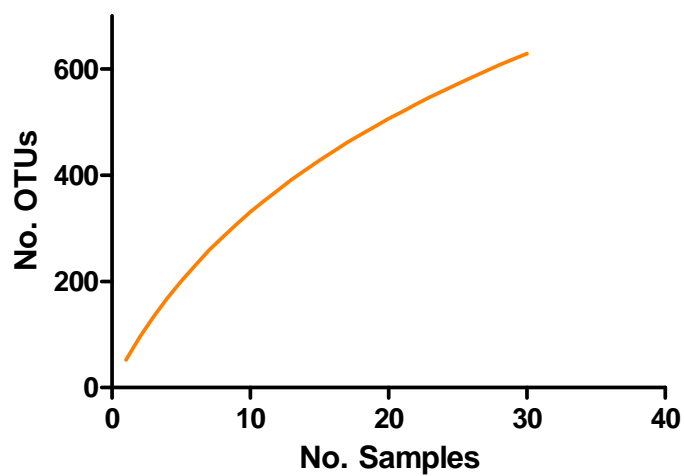


Figure 7.2 Rarefaction curve showing the accumulation of invertebrate OTUs over 30 samples (999 permutations).

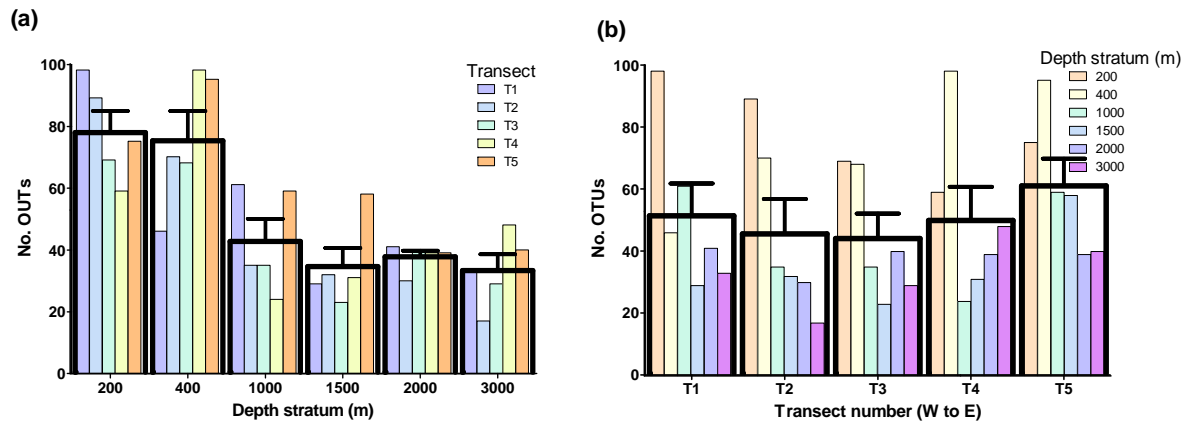


Figure 7.3 Richness of benthic invertebrates (measured as the average number of OTUs collected per sample) by (a) depth stratum (N=5) and (b) transect (T1-T5, west to east) (N=6); bar = SE.

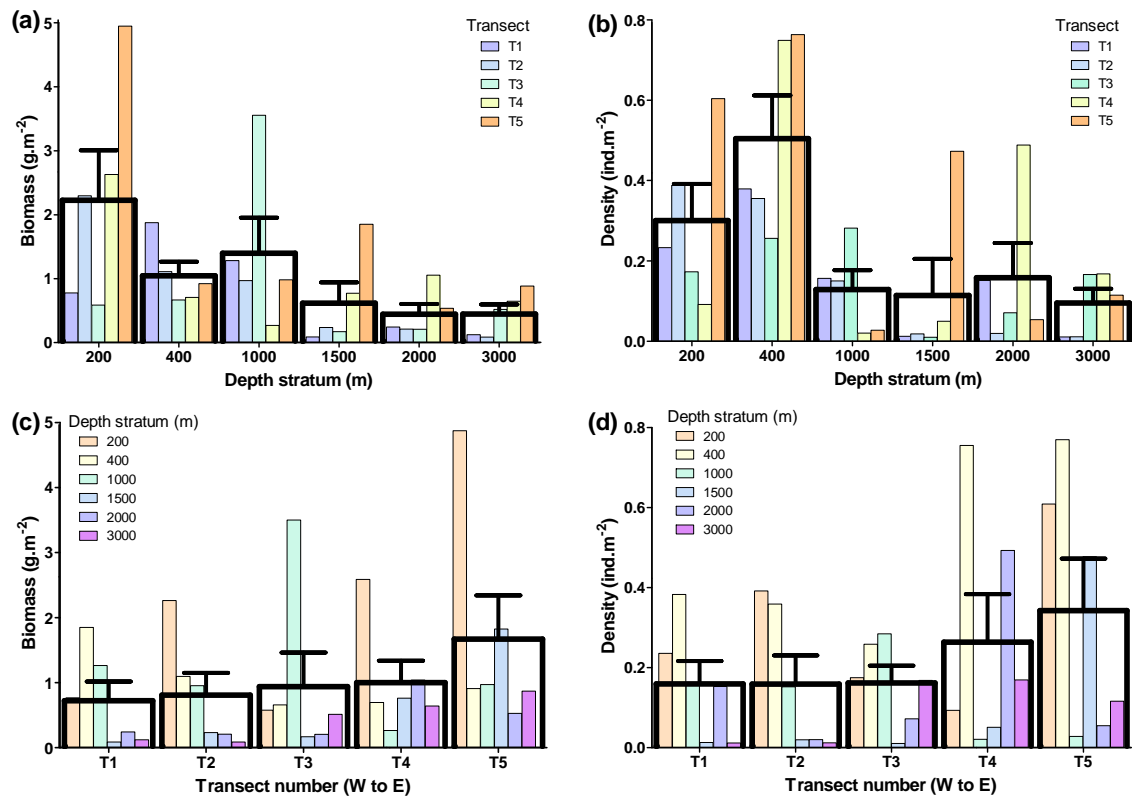


Figure 7.4 Abundance (biomass and density) of benthic megafaunal invertebrates in beam trawl samples by depth stratum and by transect (T1-T5, west to east): (a and d) average biomass per sample; (b and d) average density per sample. Number of samples per depth N=5, per transect N=6; bar = SE.

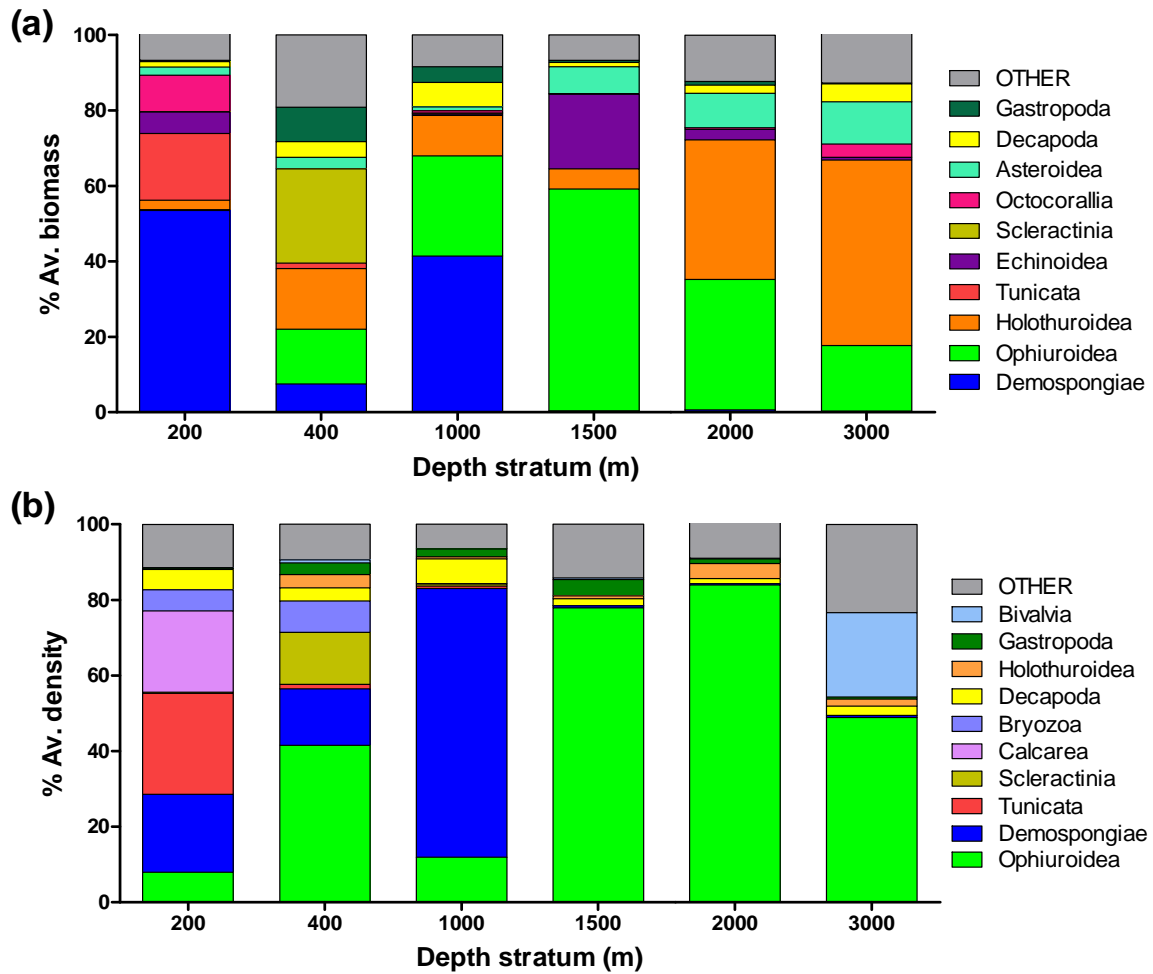


Figure 7.5 Assemblage composition by depth stratum based on percentage contribution of the 10 top ranked high level taxa (those making up >90% of the standardised biomass or >89% of the standardised density): (a) average biomass and (b) average density. The remaining taxa (~10% of totals) summed into 'other'.

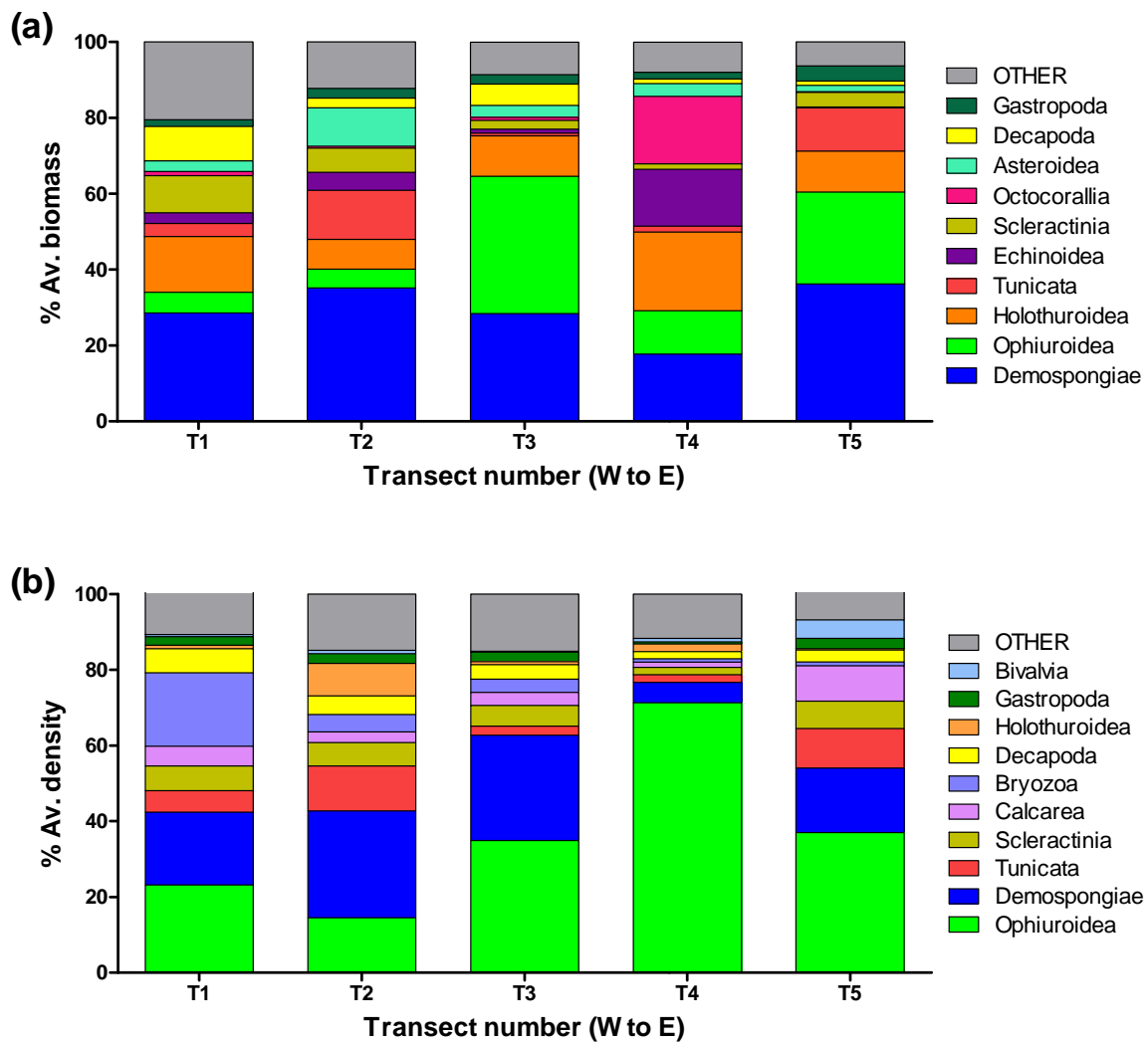


Figure 7.6 Assemblage composition by transect (T1-T5, west to east) based on percentage contribution of the 10 top ranked high level taxa (those making up >90% of the standardised biomass or >89% of the standardised density): (a) average biomass and (b) density. The remaining taxa (~10% of totals) summed into 'other'.

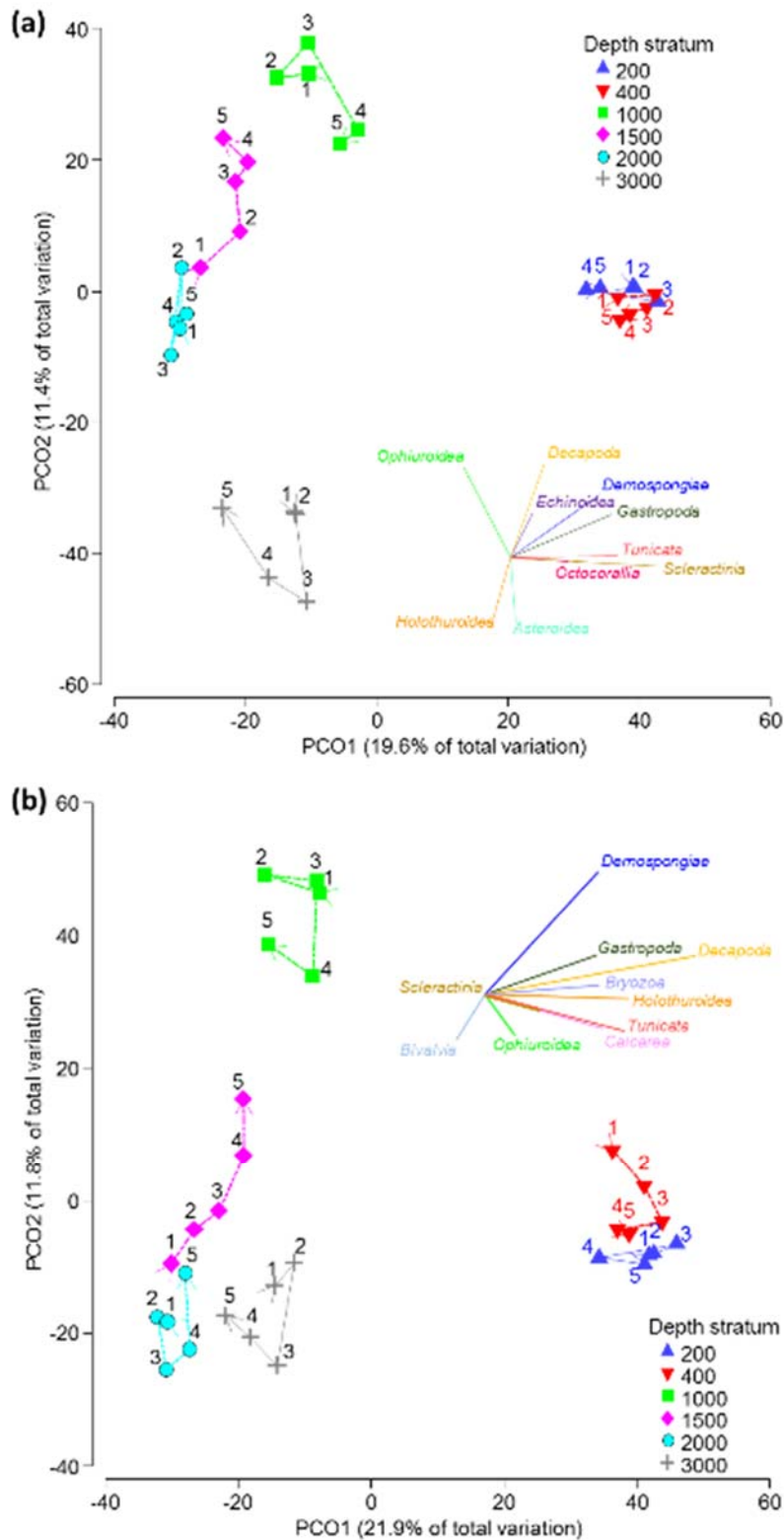


Figure 7.7 Relationships of sampling sites in multidimensional space using Principal Co-ordinate (PCO) analysis based on epibenthic invertebrate fauna coloured by depth strata: (a) biomass and (b) density. The sites are coloured by depth strata and labelled by transect number with trajectories from west to east (transects 1 to 5 as labelled) overlaid within each depth stratum. Vector correlations of the 10 most dominant taxon groups by biomass and density respectively are shown on the graphs (data transformation: square-root; similarity measure: Bray-Curtis).

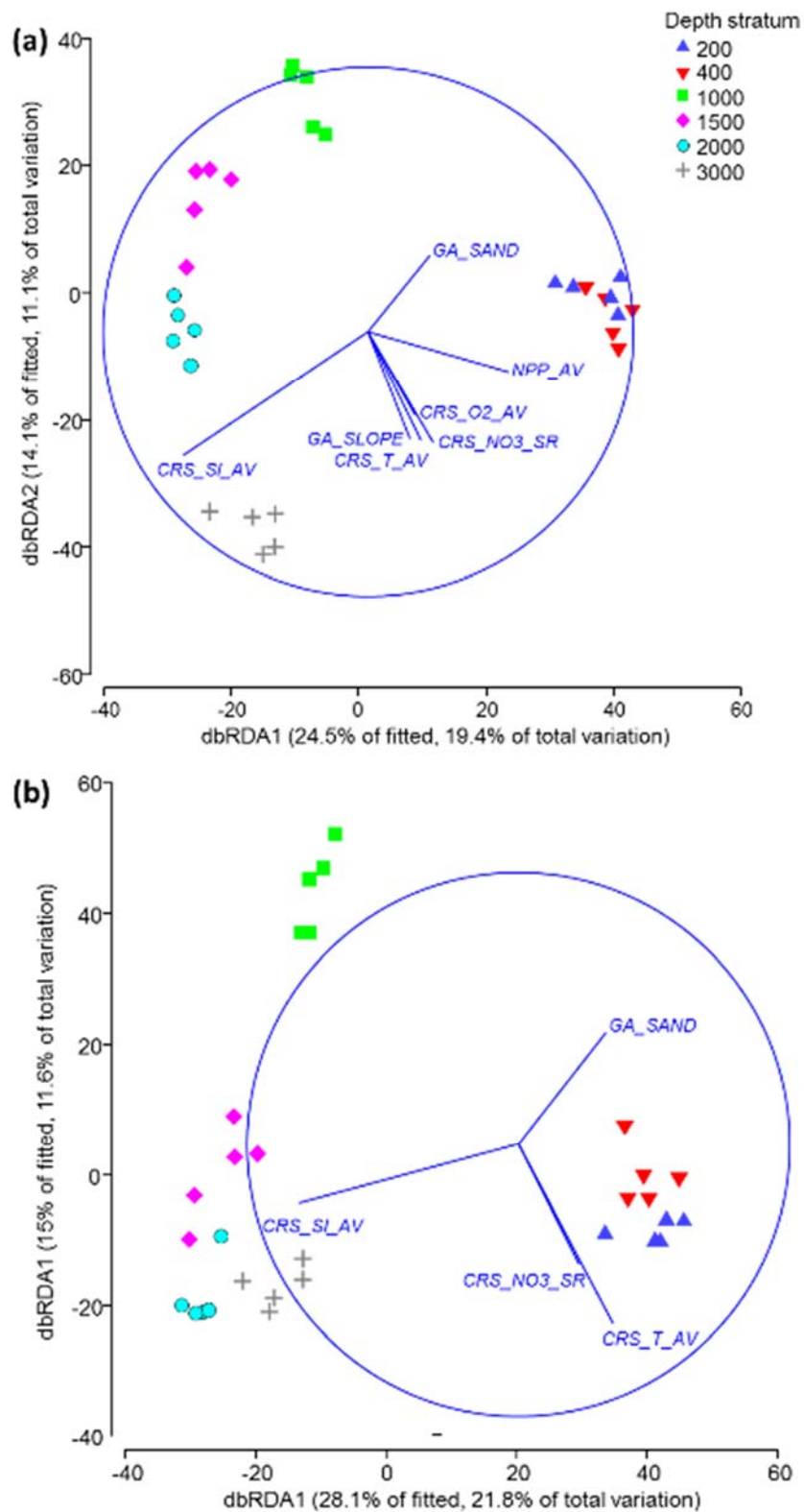


Figure 7.8 Distance based RDA based on the selected predictor variables from the DISTLM on (a) biomass and (b) density of epibenthic invertebrate fauna in the GAB. The overlay graph is limited to the variables that have a correlation to the RDA axes of >0.3 ; circle indicates correlation of 1.

8 Composition, diversity and biogeographic affinities of the deep-sea (200-3000 m) fish assemblage in the Great Australian Bight, Australia

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Key words: ichthyofauna, endemism, biomass, management, oil and gas, marine reserve

8.1 Introduction

The Australian continent is surrounded by geographically and bathymetrically extensive seas that support a highly complex fauna still being explored and discovered. Its marine fish fauna is characterised by high endemism resulting from the long isolation of the Australian plate and, in the tropics, a more recently derived high diversity following the collision of the Australian plate with Papua New Guinea (e.g. Hoese et al., 2006, Last et al., 2011; Puckridge et al., 2013; 2015). Historical fluctuations in climate resulted in changes to sea levels, temperatures and circulation patterns that, in turn, drove changes in biotic distributions, evolution and extinctions, ultimately culminating in Australia's continental waters now supporting a very rich species mix.

The number of Australian fishes being formally described (named) or newly recognised is yet to slow; the fauna presently comprises more than 5100 known species with at least 300 described or recognised in the past 12 years, including from Australia's offshore territories (Hoese et al., 2006; Rees et al., 2017). The trend is paralleled in the waters around neighbouring New Zealand with its extensive Economic Exclusive Zone (EEZ), where the recorded number of fish species has increased 21% from 1046 to 1260 in just 24 years (Roberts et al., 2016).

Challenges in understanding faunal compositions are especially great for waters beyond the continental shelf, with knowledge of fish communities decreasing rapidly with increasing depth because of the inherent difficulty and associated high costs of sampling the deep ocean. However, the last 50 years or more has seen increasingly sophisticated fishing fleets with vastly improved echo-sounders, sonar and geo-positioning technologies exploit commercial fish stocks to depths of 1500 m in many parts of the world. Concurrently, research vessels embraced these same technologies and extended their reach to enable effective sampling to abyssal depths. The advent of 'swathe mapping' by multibeam sonar in the last 25 years has given researchers a tool to closely

define seabed topography and map the distribution of hard (rocky) seabed types that previously presented a high risk to net-based sampling of benthic fishes in depths below 1000 m. The higher risk of sampling, together with fewer fishery surveys and bycatch collections in deep water, resulted in relatively low numbers of specimens from deep water in research collections compared to those from continental shelf depths (0-200 m). The resulting gap in taxonomic knowledge of Australia's deep-sea fauna was highlighted by a study of outer shelf and continental slope species by Last et al. (2005), who reported that of nearly 1500 species examined, 21% did not have accurate scientific names and many were new to science. Although there have been some recent opportunities to improve knowledge of Australia's deep-sea fish fauna by systematic surveys (Williams et al., 2001; Zintzen et al., 2011; Last et al., 2014), there are still considerable gaps in knowledge in the more remote parts of Australia's EEZ. One prominent example is the Great Australian Bight (GAB).

Although deep-sea sampling in Australia dates to the 1870s and HMS *Challenger* (Gunther, 1878), few early collecting efforts involved more than the odd trawl or dredge shot undertaken while traversing the region. This is especially the case for southern waters. Prior to the 2015 surveys reported here, knowledge of the deep-sea ichthyofauna of the GAB was amassed from early limited collecting trips and fishery surveys in the region (e.g. Newton and Klaer, 1991 and summarised by Maxwell, 1981), or from oddities sent to museums by curious fishers. Field guides treating fishes in the GAB, such as the series on fishes of South Australia starting with Waite (1923) and broader follow-up guides to fishes of Australia's southern coast (Gomon et al., 1994; 2008), relied mainly on specimens in museum collections. Species coverage was informally acknowledged at the time as being incomplete for the deep sea since no comprehensive sampling at depths >1500 m had been undertaken.

Against this backdrop, deep-sea areas of the central GAB have become a focus for oil and gas exploration, and since 2011, several exploration permits have been awarded to companies in the Ceduna sub-basin of the GAB. Most of the collective area contained within the lease blocks is 'deep-sea', being seaward of the continental shelf (>200 m depth), with offshore blocks extending to depths > 4000 m (Figure 8.1). A "Science Plan to Support [oil and gas] Exploration in the Great Australian Bight", which is endorsed by the permit holders, recognises that during oil and gas exploration in the GAB, and before production begins, there is a need to comprehensively assess the region's conservation values and enhance current understanding of its key ecological elements and processes. A review of existing knowledge (Rogers et al., 2013) identified that, "much remains unknown about the distribution, biodiversity and ecology of demersal fish assemblages inhabiting the GAB shelf and slope, while nothing is known from depths below about 1500 m. In particular, it is

not known how demersal fish assemblages change in response to oceanographic processes and environmental gradients.”

Two major science programs have been implemented to enhance ecological knowledge of the deep GAB: the GAB Research Program (GABRP, 2017), and the GAB Deepwater Marine Program (GABDMP, 2017). Benthic ecological work undertaken as part of these programs has included making a collection of fishes from 200 to 3000 m depths during two surveys in 2015. Analysis of the combined collection is reported here, with the following aims: (1) to document the diversity, abundance and assemblage structure of deep-sea benthic fishes in the Great Australian Bight (GAB), including from previously unsampled depths (1500 to 3000 m); (2) to describe this ichthyofauna in a biogeographic context; and (3) to consider the characteristics of the fauna in regard to future management needs of the GAB benthic ecosystem. Informing management processes is relevant to both the potential need for ongoing ecological monitoring if the offshore oil and gas industry develops further, and because management plans are being developed for recently proclaimed offshore marine reserves (DEE, 2017).

8.2 Materials and methods

8.2.1 2.1 Survey design

Field sampling was completed during two surveys in November-December 2015 aboard Australia’s Marine National Facility (MNF) vessel, RV *Investigator* (MNF, 2015 a and b); the surveys aimed to characterise regional ecological properties of the central GAB ahead of proposed exploration for oil and gas resources. Most samples (30 of 51) came from a transect-based survey (‘T’ in Table 8.1) – where sites were situated on large and unstructured sediment plains. These 30 ‘*transect*’ samples are a subset of samples used for analysis. The transect survey reflected the need for information over two gradients along which ecosystem characteristics were expected to vary: east-west (longitude) and depth. It was based on sampling at 6 depth horizons (200, 400, 1000, 1500, 2000 and 3000 m) along 5 north-south transects (T1 to T5) at increasing meridians of longitude (Figure 8.1). To achieve relatively high sampling density in the region of the Great Australian Bight Commonwealth Marine Reserve (GAB CMR) and active oil and gas leases, one transect (T2) was located in the centre of the GAB CMR, and one located at 10 nm either side of the GAB CMR (T1 and T3). Two others were located in the eastern GAB at 80 and 150 nm eastwards from the centre of the GAB CMR (T4 and T5, respectively) (Figure 8.1). Nomenclature for the depth ranges sampled follow those proposed for depth-related patterns in fauna (bathomes) (Last et al., 2010): 200 m (shelf break); 400 m upper continental slope; 1000 and 1500 m (mid-continental slope); 2000 m (lower continental slope); and 3000 m (continental rise). Additional samples (17) came from

a topography-based survey (Figure 8.1) – where sites were also on sediments but mostly within or adjacent to potential brine-seep zones (SZ) sites (9 samples), volcanic seamounts (VSM) sites (3 samples), and areas with outcropping rocky bottom (OR; 5 samples); or unstructured sediment (S) sites adjacent to the transect sites (4 samples) ('SZ', 'VSM', 'OR' and 'S' in Table 8.1). These topography-based sites were not uniformly distributed by depth or longitude: SZ and VSM sites were located between ~1500 and ~2500 m depth, while OR sites were below 3000 m (Table 8.1).

8.2.2 Data collection and dataset

Fishes were collected with a beam trawl (Forest, 1981; Lewis, 2010). Its mouth was 4.0 m wide x 0.5 m high; the net has tickler chains on the foot rope and made of 25 mm stretch mesh. Tows followed a depth contour to avoid large variations in depth within a single sample unit; average towing depth was used to provide a single value for each sample. All tows were at a known speed (~2 kt), but tow durations varied, being shortest (~20 minutes) at the shallowest sites (200 m) to regulate the large quantities of benthic invertebrates (mostly sponges) taken, and longest (~60 minutes) at the deepest sites (3000 m) to increase the volume of catch without reducing the quality of specimens. An ultra-short baseline (USBL) positioning beacon was used to confirm the location and bottom-contact distance in a GIS of each tow. Swept area (m²) was estimated for each tow based on the net width (m) x tow distance (m).

Fishes were caught in 47 of the 51 sampling operations; no fish were caught in 4 operations at 3 of the OR sites (all >4000 m depth - OR02, OR07 and OR10). In total 187 kg of benthic fishes (2004 individuals) were collected. Fish specimens were identified to the lowest possible taxonomic level on board and re-examined during two subsequent workshops involving this paper's authors. The most recent taxonomic references available were used: major works included Gomon et al. (2008) and Roberts et al. (2015), as well as more focussed taxonomic treatments in the ichthyological literature. To add more certainty to our identifications and compare taxa to those previously collected from nearby regions, we also examined additional preserved specimens from nearby regions in the Australian National Fish Collection (ANFC, Hobart).

Adopting an integrative taxonomic approach, we also analysed the Cytochrome Oxidase mitochondrial DNA barcode gene (COI). From each species where a muscle sample was extracted onboard the voyage or during the workshops, DNA was extracted (see Supplementary text of Osterhage et al. (2016)) and bi-directionally sequenced (using the FishF1, FishF2 and FishR2 primers of Ward et al. (2005); sequencing was undertaken at the Ramaciotti Centre for Genomics, University of New South Wales - <http://www.ramaciotti.unsw.edu.au/> and CSIRO Marine Laboratories on 3730xl and 3130xl DNA Analyzers, Thermo Fisher Scientific, USA, respectively, at least one specimen

from each taxon. Forward and reverse sequences were trimmed, *de novo* assembled, checked by eye and then converted into consensus sequences using Geneious (Biomatters Ltd, New Zealand) vers R8.1.4. Consensus sequences for each sample were compared using the Barcode of Life Data Systems v4 (BOLD) identification system

(http://www.boldsystems.org/index.php/IDS_OpenIdEngine) and GenBank BLASTn (via an internal application in Geneious) to check the similarity of sample sequences against existing database sequences. Species identification was based on a percentage of sequence identity, with homology of $\geq 99\%$ as the criterion used here for species confirmation. Sequences from this survey will be available in BOLD.

From the specimens that were morphologically and genetically examined, 108 species were recorded. All but 31 specimens were identified to a species-level taxon (herein referred to as species). The 31 specimens, which were too small or badly damaged for positive identification to species-level, accounted for only 0.25 kg and were excluded from analyses. Accurate comparisons of taxa across surveys (specifically comparison of this survey with Williams et al., 1996) was possible through a re-examination of current names of databased voucher specimens deposited into the CSIRO Australian National Fish Collection, Hobart and comparison with names in Roberts et al. (2015). Listed voucher specimen registration numbers for names used by Williams et al. (1996) enabled tracking to current names, especially when original species were provisional or thought to be undescribed.

8.2.3 Physical covariate data

A set of environmental data were generated for each sampling station from data that were compiled and spatially assigned to a 0.01 degree grid for modelling in other projects mainly from a variety of sources (Table 8.2) (Pitcher et al., 2016 and references therein):

1. Bathymetry (slope and aspect) — based on model bathymetry combined from several sources. The data set uses the Geoscience Australia (GA) GA2009 250 m bathymetric product as a background (Whiteway, 2009). The Western Australian state's official coastline (mean tide) was used to define 0 depth and islands. Commercial partners provided bathymetric data based upon LiDAR/LADS surveys and CSIRO and GA provided surveys based on acoustic systems. Australian Hydrographic Service (AHO) and the Western Australian Department of Primary Industries (WA DPI) provided historical soundings. These were integrated and processed in swath mapper processing software (CSIRO) into a 0.01 degree gridded product.

2. Sediment: gravel, sand, mud, carbonate — data sourced from the Australian MARine Sediments Database (MARS), GA (Passlow et al., 2005).
3. Bottom water attributes (annual average and seasonal range): temperature, salinity, oxygen, nitrate, phosphate, silicate — data sourced from the CSIRO Atlas of Regional Seas (CARS) (Dunn and Ridgway, 2002; Ridgeway et al., 2002).
4. NASA Ocean colour (SeaWiFS and MODIS): chlorophyll, SST, surface PAR — satellite derived datasets were processed for the period of 2003-2014 by the Integrated Marine Observing System (IMOS) (Edward King; IMOS, 2017).
5. Derived variables: benthic irradiance, primary productivity, exported POC (Particulate Organic Carbon) — calculated from ocean colour variables using published algorithms.
6. Bottom stress: averaged over a two-year hydrodynamic model simulation (2013-2014); maximum and standard deviation were also recorded (Middleton, 2017, GABRP Project 1.1.)

Each sampling station was assigned to the 0.01 degree spatial grid in a GIS based on the mid- point between the gear touching bottom and being lifted off seafloor, and the environmental data from this grid cell was used. A total of 36 environmental predictor variables (including the deployment depth, latitude and longitude) were available (Table 8.2).

8.2.4 Analysis methods

Because only demersal fishes were sampled quantitatively, 44 taxa (187 individuals, 2.12 kg) reported in the literature as epi-, meso or bathypelagic, or midwater juveniles of benthic taxa that could not be accurately identified were excluded from all analyses – these were selected species or genera from families Alepocephalidae, Anotopteridae, Ceratiidae, Chauliodontidae, Epigonidae, Gonostomatidae, Howellidae, Idiacanthidae, Macrouridae (juveniles), Malacosteidae, Melamphaidae, Melanocetidae, Moridae, Myctophidae, Phosichthyidae, Sternoptychidae.

The swept area of each tow was used to calculate standardised estimates of abundance for each sample individually: biomass (gm^{-2}) and density ($\text{individuals.m}^{-2}$). These estimates were combined to calculate an average biomass and density for each species (and family) for each depth stratum; this was done separately for the 30 transect samples and ‘all’ samples – the transect samples plus those from sites adjacent to potential seep zones (SZ), volcanic seamounts (VSM), areas with outcropping rocky bottom (OR) or unstructured sediment (S) (Table 8.1). The 30 transect samples presented a balanced design of samples on six depth strata by 5 transects. Average richness, biomass and density in those samples were compared between depth strata and transects using 2-way ANOVA without replication (assumption of no interaction between the two factors). Bonferroni post-hoc tests were

used to identify any pairwise differences for significant main effects. Analyses were done using GraphPad Rism v5.02 software (<http://www.graphpad.com/>).

Species richness was examined using summary statistics and randomly permuted species accumulation in PRIMER v7 (Clarke and Gorley, 2015). Differences in the assemblage structure were examined using comparison between dissimilarity matrices (RELATE) (Clarke and Gorley, 2015), permutational multivariate analysis of variance (PERMANOVA; Anderson, 2001) and non-metric multi-dimensional scaling (nMDS) (Kruskal, 1964; Clarke et al., 2014).

Distance-based linear models (DISTLM) with distance-based redundancy analysis (dbRDA) (Legendre and Anderson, 1999; McArdle and Anderson, 2001; Anderson et al., 2008) were used to examine the relationship between assemblage structure and the environmental predictor variables. The set of 36 variables was *a priori* reduced to 30 by removing measures of variability, seasonal range (SR) or standard deviation (SD), in an environmental factor, where these were highly correlated ($R > |0.9|$) with another measure of the same factor. Thus BIR_SR, SST SR, NPP SR, PAR_SR, EPOC_SR and BST_SD were excluded. All multi-variate analyses were performed on Bray-Curtis similarities of square-root transformed data in PRIMER v7 (Clarke and Gorley, 2015) and PERMANOVA+ for PRIMER (Anderson et al., 2008).

8.3 Results

8.3.1 Patterns of diversity and abundance (biomass and density)

A total of 108 species in 49 families were represented in the 1973 individual benthic fish collected (Table 8.1; see Appendix, Section 20.2 for full list). Most species occurred infrequently: 42 occurred in only one sample (39%), 13 occurred twice (12%), and only 53 species (49%) were captured more than twice (Figure 8.2). A rarefaction curve showing the accumulation of species with increasing number of samples showed no asymptote, indicating the total species pool had not been sampled (Figure 8.3).

The distribution of samples was even across depth horizons from the standard transect survey samples (5 each), but uneven across depths for the topography survey (Table 8.1). The average number of species (richness) in the transect survey sites shows a peak at 1000 m depth, and marked decline to the lowest richness at 3000 m (Figure 8.4). Compared to the transect sites, topography sites had relatively high richness at the 1500 m seamount (VSM) site, but comparable richness at 1000 m; seep sites at both depths (1000 and 2000 m) are comparable to transects; richness was comparatively very low at the outcropping rock (OR) sites – but these were the 5 deepest sites sampled (3000 and 4000 m) (Figure 8.4).

Estimates of average total biomass in different depths showed consistent patterns for transect sites, and all sites (transect + topography sites combined) (Figure 8.5a). Estimates were relatively very low ($\sim 0.5 \text{ gm}^{-2}$) at 200 m depth, highest at 400 m ($\sim 3.4 \text{ gm}^{-2}$), then showed a steady decline with increasing depth to about 0.4 gm^{-2} at 3000 m depth (Figure 8.5a). Estimates of average total density in different depths also showed consistent patterns for transect sites, and transect + topography sites combined (Figure 8.5b). Overall, the pattern was similar to the pattern with biomass, with density highest ($\sim 0.1 \text{ individuals.m}^{-2}$) at 400 m depth, and low estimates in deeper depths; however, the estimate at 200 m was relatively high ($0.05 \text{ individuals.m}^{-2}$) compared to biomass, and the decline in deeper depths more sudden and evenly low ($>0.02 \text{ individuals.m}^{-2}$) at 1000 m depth and below (Figure 8.5b). In combination, these data indicate an overall larger average size of fish species in depths $>1000 \text{ m}$ compared to shallower depths, especially at 1000 m depth where, compared to adjacent depths (400 and 1500 m) the decline in density is great for a relatively small decline in biomass (Figure 8.5a, b). In contrast, the relatively high density and low biomass at 200 m indicates the average size of fish at that depth is relatively small compared to all other depths (Figure 8.5a, b). Two-way ANOVA of the transect samples showed that depth had a significant effect on the distribution of fish species ($F_{4,5}=5.641$, $P = 0.0021$), biomass ($F_{4,5}=9.156$, $P = 0.0001$) and density ($F_{4,5}=5.249$, $P = 0.0031$); there was no significant transect effect.

The rattails (Macrouridae) were the dominant family by all measures of abundance. In the total catch across all sites, the Macrouridae was represented by 21 species, occurred most frequently (38/51 samples), made up 29% of total catch weight (53.9 kg) and 31% of abundance (668 individuals), and was top ranked by biomass and density in standardised data for all samples, and transect samples (Table 8.3). Two other deep-sea families were also dominant in terms of species diversity and catch weight. The basketwork eels (Synphobranchidae) and morid cods (Moridae) were the next ranked for species diversity (each with 7 species), had relatively high total catch weights (33.2 kg and 14.8 kg, ranked 2nd and 4th, respectively) and were highly ranked in standardised data. Three other deep-sea families were highly ranked by catch weight and biomass, but had relatively low density: the oreo dories (Oreosomatidae) with a total catch weight of 20.0 kg (ranked 3rd) but represented by only 2 species (mostly *Allocyttus verrucosus*); cusk eels (Ophidiidae) with a total catch of 11.5 kg (ranked 6th) and 4 species; and halosaurs (Halosauridae) with 12.7 kg (ranked 5th) and only 2 species. The relatively shallow (shelf break) families of ghost flathead (Hoplichthyidae) and temperate seabasses (Acropomatidae) were notable in having, respectively, the second highest biomass (11.8%), and second highest abundance (162 individuals) overall, being highly ranked in both biomass and density in transect samples. Both families were represented by single species, *Hoplichthys haswelli*, and *Verilus anomalus* (Table 8.3).

The composition of ichthyofauna changed markedly with depth, as measured by the 10 dominant families (ranked by average biomass and density) in each depth stratum (Figure 8.6). Family-level composition at the shelf break (200 m) sites stood out from all other depths in having the majority of biomass and density made up by 'Other' families, i.e. relatively high diversity, and only 2 conspicuously dominant families: temperate seabasses (Acropomatidae) (biomass and density), and bellowsfishes (Macroramphosidae) (density). In contrast, the dominant families in the upper slope (400 m) stratum, where biomass and density was highest overall, were ghost flatheads (Hoplichthyidae) (biomass) and Macrouridae (mostly species of *Coelorinchus*) (density). Two other families were also prominent at 400 m depth: cusk eels Ophidiidae (biomass – based on 2 large specimens) and Eucla cod Euclichthyidae (density). There were similarities in dominance at the mid-continental slope sites (1000, 1500 and 2000 m depths) where rattails (Macrouridae) (biomass and density) and basketwork eels (Synaphobranchidae) (biomass) were dominant. In this depth range, oreo dories (Oreosomatidae), morid cods (Moridae), and halosaurs (Halosauridae) were all prominent (biomass), the latter 2 families more so in 1500-2000 m depths. At 3000 m depth the cusk eels (Ophidiidae) were the overwhelmingly dominant family by biomass. Density was relatively very low at all sites ≥ 1000 m and entirely dominated by rattails (Macrouridae) and a mix of 'other' species. The pattern of relatively lower density than biomass in depths ≥ 1000 m indicated a generally larger body size of individuals compared to the upper slope and shelf break, especially for cusk eels (Ophidiidae) (Figure 8.6).

A comparison of the highest ranked 15 species separately by biomass and density showed little overlap (6 species) (Table 8.4). The overall trend was for species ranked highly by density to be small-bodied fishes and relatively shallow (<400 m depth) and for species ranked highly by biomass to be larger-bodied and deeper (>1000 m). Of the six species highly ranked on both metrics, 5 are relatively shallow (< 400 m depth) and small-bodied (<~200 mm). The only deeper species highly ranked by both biomass and density was *Cetonus globiceps*, which was highly abundant at sites around 1000 m depth. Only two other species had high density ranking at great depths: the bathygadid (*Bathygadus cottoides*) (14), and macrourid (*Coryphaenoides filicauda*) (15), at ~1300 and 2000 m depths respectively. The high biomass ranking (7) of the ophidiid, *Spectrunculus grandis*, was due to the capture of one very large specimen (and accounts for its correspondingly low density – ranked 77) (Table 8.4).

8.3.2 Assemblage structure

Fish assemblages were most strongly structured by depth: ordination using square-root transformed biomass or density data shows virtually no overlap in depth-related groups (Figure 8.7), after the outlier sample from T2-3000 was removed. The outlier sample from 3000 m depth on Transect 2

contained a single fish specimen of *Spectrunculus grandis*, a species not observed in any other sample. There was no clear distinction between sites from the transect survey and topography survey, and there was no consistent pattern discernible between the longitudinally separated arranged transects, within depth strata (Figure 8.7). Similarity patterns based on biomass and density data are highly correlated (RELATE analysis: $\text{Rho} = 0.982$, $P = 0.1\%$); thus we only show results for the biomass data.

PERMANOVA of the balanced-design transect data showed a highly significant depth effect for the biomass data (pseudo- $F_{5,4} = 5.465$, $P = 0.0001$). The pair-wise tests showed there were only few instances with no differences ($P > 0.01$). These were between 3000 m and all depth strata except 400 m, and between 1500 and each of 1000 and 2000 m. Transect had no significant effect (pseudo- $F_{5,4} = 0.829$, $P = 0.8647$).

The marginal tests of the DISTLM analysis showed a significant ($P = 0.001$) contribution by 25 of the 30 tested predictor variables, each contributing between 7% (GA_SLOPE) and 16% (CRS_O2_AV) to explaining the variation in the assemblage data. For sets of highly correlated ($R > |0.9|$) variables, only the one ranked highest in the marginal tests was retained in the final DISTLM analysis (Table 8.5). The best solution (based on all possible combinations of predictor variables) for explaining the pattern in the fish community structure is reached by using 11 of the 21 tested predictor variables (adjusted $R^2 = 0.44$; $R^2 = 0.57$) (Table 8.5). The most influential variables in the analyses were the average oxygen, salinity and temperature and seasonal range in nitrate, together accounting for 42% of the variance in the biomass model. The first two of these are both proxies for a range of chemical characteristics of bottom water (Table 8.5). The first two axes of the associated dbRDA explained 32.5% of the individual variation and 56.5% of the fitted model (Figure 8.8).

8.3.3 Biogeographic affinities

Distribution data were summarised for 104 of the 108 total species-level OTUs; 104 were identified to known species, of these 4 were determined as undescribed species with documented distributions: *Halargyreus* sp. (of Struthers et al., 2015), *Lepidotrigla* sp. (of Gomon et al., 2008), *Nesogobius* sp. and *Cataetys* sp. 1. Three were identified only to genus (*Leptoderma* sp., *Dicrolene* sp., *Paracetonurus* sp.), and 1 only to family (Zoarcidae).

The great majority of fishes in this collection have previously been recorded from Australian waters (90%), and the GAB (75%) (Table 8.6). The proportions of recorded species were broadly similar between shelf break (~200-240 m depths), upper slope (280-600 m) and mid-slope depths (950-1550 m): (91-100% in Australian waters, 86-89% in GAB waters). A markedly lower proportion of

recorded species occurred at greater depths (1700-3000 m) where there had been virtually no previous sampling: 74% in Australian waters, and 30% in GAB waters (Table 8.6).

The ichthyofauna had three major biogeographic elements that were strongly modified by depth (Table 8.7). There was (1) a strong affinity of fishes from shelf break to mid-slope depths to the Indo-west-Pacific and the broader Pacific Ocean region; (2) fishes from mid-slope and lower slope/rise depths contained a high proportion of circum-globally or southern circum-globally distributed species relative to shelf break and upper slope fishes; and (3) fishes from the shelf break and upper slope contained a high proportion (about half) of endemic species, whilst endemic species were scarce in deeper depths, especially the lower slope (Table 8.7).

8.4 Discussion

8.4.1 Diversity assemblage structure and biogeography of the ichthyofauna

Biogeographical analysis of Australia's marine fish fauna (Last et al., 2005; 2011) identified a large temperate continental slope (c. 270-1095 m) "Southern Province" bounded by Cape Leeuwin in the west and the South Australian (SA) gulfs region in the east (Figure 8.1); 366 species were recorded from depths > 200 m. The vast majority (85-90%) of shelf break and upper to mid-slope species collected in our study had previously been recorded from this region. However, around 70% (16 of 23) of fishes from the lower continental slope/ rise (1700-3000 m) are new records, highlighting the lack of previous sampling from these depths. Endemic species were most prevalent in shelf break and upper to mid-slope depths (both 52%), and declined with increasing depth (upper to mid-slope species 25%; lower slope/ rise 4%). This trend is consistent with a general pattern in the Australian ichthyofauna (Last et al., 2011).

The predominant patterns of biogeographical affinities of our collection (Table 8.7) are broadly similar to those described for slope fishes of the Southern Province (Last et al., 2011): dominated by a mix of Australian endemics (33%), circumglobal and southern circumglobal species (14% each), South-west Pacific and East-Indo-west Pacific combined (16% - equivalent to East-Indo-west Pacific of this study) plus a variety of other minor categories. The only notable difference appears to be a lower fraction of endemics in the GAB, reflecting the deeper (> 1600 m) components of fauna sampled for the first time in our study.

When compared to adjacent marine areas, the Australian deep temperate fish fauna has a strong affinity to the NZ fauna, and relatively lower affinity to the adjacent Australian west coast. Of the 166 fish species recorded from depths of 312-1192 m in deep-sea fisheries data from the GAB (Newton and Klaer, 1991), there were high overlaps of families (94%) and genera (88%) with NZ.

Although additional fishes have been recognised and described in the intervening period, our survey from approximately 200 to 3000 m depths recorded almost identical proportions of families (96%), genera (91%) and species (61%) shared with NZ. Collectively across surveys, the deep GAB genera not shared with NZ (*Heptranchias*, *Figaro*, *Ebinania*, *Luciobrotula*, *Brachionichthys*, *Platycephalus*, *Kuiterichthys*, *Nesogobius* and *Verilus* (recently moved from genus *Apogonops*), are typified by outer shelf or upper slope species (~200-500 m depths). Genera from the lower slope/ rise (1500-3000 m) recorded from this study but not NZ (*Dicrolene*, *Ipnops* and *Paracetonurus*) are known from multiple ocean basins and some species are widespread. The faunal overlap between our GAB collection and the adjacent western seaboard (shelf break to lower slope in 200-1500 m) – 85% families, 69% genera, 55% species (Williams et al., 1996; 2001) – was lower than that between the GAB and NZ. This was despite the much larger latitudinal range sampled in NZ waters (GAB c. 33 to 36° S; NZ c. 25 to 56° S; west coast c. 20-35° S). The greater difference between Australia's southern and western coasts is explained by the existence of four distinct west coast provinces: two each on the shelf-break and slope (Last et al., 2011) and the strong affinities of the northerly provinces with the tropical Indo-West Pacific fauna. A comparison of our collection with the Southern Ocean fish fauna shows that 14 of 21 (67%) demersal families occurring below 200 m are shared between our study and the sub-Antarctic Southern Ocean (Gon and Heemstra, 1990).

Success in the extreme environments of the deep-sea appear to be best achieved by the rattails (family Macrouridae); these are dominant in all measures of diversity and abundance in Australia's deep-sea (this study; Newton and Klaer, 1991; Williams et al., 2001). In our collection the Macrouridae was most diverse, occurred most frequently, abundant (density) in 400 m and all deeper strata, and top-ranked by biomass and density in standardised data for all samples, and transect samples alike. A similar pattern was noted on the adjacent western Australian margin where Williams et al. (1996) identified that macrourids made up 40-50% of individuals in all depth strata between 600 m and 1400 m, with around 50 species recorded in total. The Macrouridae was also dominant (with Alepocephalidae) in the deep Tasman Sea (Zintzen et al., 2011). Other dominant families at greater depth (> 800 m) in the GAB (Oreosomatidae, Moridae and Synphobranchidae) were very similar to the Australian west coast (Williams et al., 1996) and dominate the species pool in northern hemisphere deep-sea environments (e.g. the Mid-Atlantic Ridge, Bergstad, 2013). A study of the mid-slope fish fauna off south-eastern Australia (Koslow et al., 1994) showed species composition affinities with the North Atlantic (Haedrich and Merrett 1998) that were absent when compared to the North-east Pacific (Pearcy et al., 1982) and attributed these potentially to ocean circulation at intermediate depths. This suggestion is well supported by the absence in Percy et al's (1982) study of two families with long-lived leptocephalus larvae, the

Synphobranchidae and Halosauridae. Most species in these two families have a broad circumglobal distribution in tropical and/or temperate waters, often encompassing both the Western Pacific (including GAB) and the North Atlantic, but are rare or absent from the northeastern Pacific (e.g. see Sulak and Shcherbachev 1997 for Synphobranchidae). Below 1000 m depth in our study, the Synphobranchidae were particularly dominant in terms of species diversity and catch weight; *Synphobranchus brevidorsalis* had the highest biomass of any species beyond 1050 m in our study (recorded from 1005-2014 m) and was also abundant in 880-1500 m and wide-ranging by latitude (21-35° S) off the Australian west coast. The Halosauridae, especially *Halosauropsis macrochir*, also an abundant and wide-ranging group in 800-1500 m depths off the west coast (Williams et al., 1996) was also a significant component by weight in this study. The Moridae were a significant diversity (7 species), biomass and density component and their diversity has been noted in other studies of deepwater fishes of the southern (Williams et al., 1996; 13 species) and northern hemisphere (Bergstad et al., 2008; 7 species).

The faunal affinities of the contemporary GAB ichthyofauna will be partly influenced by dispersal in ocean currents. For groups with eggs or larvae that ascend to near surface waters (e.g. depths < 500 m from sea surface) – such as macrourids (Fukui et al., 2010) – there will be strong effects by two boundary currents: the Leeuwin Current which flows eastwards across the GAB region in depths to 300 m (McClatchie et al. 2006), and the deeper (to 600 m) Flinders Current (McClatchie et al. 2006) which runs westward (Coleman et al. 2013). Boundary currents influence global patterns of diversity because they play an important role in physical transport, and processes such as larval retention and dispersal (Coleman et al. 2013). Larval fish found within the Leeuwin Current comprise a mixture of oceanic, slope, tropical and temperate coastal species (Beckley et al. 2009): the effect on the eastward distribution of commercial fishes, and of tropical and submarine canyon fauna into the GAB has been noted previously (Maxwell and Cresswell 1981; Beckley et al. 2009; Kool et al. 2015). The connection provided by the Flinders Current is thought to contribute to a perceived homogenous species composition of fishes along the southern Australian margin (Last et al. 2005; McClatchie et al. 2006). A number of water masses in deeper (~700 to 3000 m) water also characterise the GAB region including Antarctic Intermediate Water and Circumpolar Deep Water (Schodlok et al. 1997). These are circumpolar in nature and thought to connect a number of bathyal provinces in both hemispheres, which may play a role in the higher proportions of circumglobal and southern circumglobal species we found in the GAB's mid-slope and lower slope/rise (Watling et al. 2013). The vertical distribution of fish communities in the GAB may also be influenced by water masses, with Currie et al (2012) finding fish assemblages in a GAB submarine canyon coincided with

depth distributions of Antarctic Intermediate Water, the Flinders Current, and well-mixed surface waters.

Numerous other studies have also highlighted an apparent trend toward more widespread distributions of demersal fish species with increasing depth; this is assumed to be due to the relative stability of the deep-sea and limited barriers to dispersal (e.g. Koslow et al., 1997). For this reason, Koslow et al. (1997), suggested that continued sampling will encounter a progressive decline in the discovery of new species. However, our data (Figure 8.3) show that considerable additional species accumulation can be expected with further sampling in the deep GAB. Recent studies of population structure of widely distributed demersal fishes show less than expected demographic connectivity and considerable spatial genetic heterogeneity and complexity for some species; in other species, genetic homogeneity across wide ranges was discovered (Bergstad, 2013). The family Liparidae is an example of deep-sea species discovery in the modern era, with at least 140 new species described between 1998 and 2017 (Eschmeyer and Fong, 2017; Fricke, 2017). Other deep-sea families undergoing significant expansion in diversity due to new species descriptions include Zoarcidae, Bythitidae and Ophidiidae. The impact of regional-scale re-evaluation of species identifications is highlighted by recent (between 1989 and 2013) investigation of the NZ fish fauna (Roberts et al., 2015). These authors showed a reduction in widespread species from 494 (47% of total) to 374 (30% of total) due to the increasing recognition of endemic and narrower-ranging species, often likely restricted to a single ocean basin or the Tasman Sea. Additional scrutiny, including with molecular techniques, may show similar patterns in the Australian deep ichthyofauna. There are some indications of cryptic speciation or unrecognised species in some genera (e.g. *Aldrovandia*) from the DNA barcoding undertaken as part of this study, however, the great majority of GAB species separated using morphological techniques were validated by DNA barcoding.

Depth-related patterns (zonation or continual replacement of species, Haedrich and Merrett, 1988) typically dominate fish assemblage structure in regional scale studies (e.g. New Zealand, Tracey et al., 2004; the North Atlantic, Haedrich and Merrett 1988; North Pacific, Percy et al., 1982). Patterns are sufficiently consistent at the shelf-break and on the continental slope around the Australian continent to identify characteristic depth-related zones of ichthyofauna at a national scale (Last et al., 2011). Unsurprisingly, our data from a set of widely spaced depth horizons, also identified depth as the main factor explaining assemblage structure (for analysis of both fish biomass and fish density). However, it was of interest that the lower slope and continental rise (>1500 m depths), that had not previously been sampled in Australian waters, showed relatively little difference to the mid-slope sites (< 1500 m depths). Also of interest was the lack of clear distinction between sites

from the transect survey and topography survey, although sampling in the topography survey was on sediment habitats adjacent to either seamounts or rocky bottom, whilst no strongly active seeps were identified in the potential seep zones. Differences in productivity between the central and eastern GAB driven by summertime upwelling in the east (Rogers et al., 2013) were not reflected in differences between the longitudinally separated arranged transects (central transects (T1-T3) and eastern transects (T4-T5). Chemical and physical characteristics of the bottom waters (average of oxygen, salinity and temperature and seasonal range in nitrate) were the most influential environmental predictors for the GAB demersal fish assemblage structure, while depth, or its proxy average silicate, was not selected in the final model. This finding is consistent with other studies where salinity, temperature, oxygen and depth were highly influential variables in structuring fish assemblages in the Tasman Sea (Zintzen et al. 2011) and on seamounts globally (Clark et al. 2010). Peak fish biomass in the Mediterranean was linked by Fanelli et al. (2013) to low temperature and high oxygen concentration in bottom waters; similarly Fujita et al. (2013) highlight temperature as an important factor in structuring deep fish communities in Japanese waters.

8.4.2 Abundance of the ichthyofauna

Gear selectivity will significantly influence estimation of biomass by net sampling (Cartes et al 2009), with smaller gears such as beam trawls thought to underestimate biomass due to lower sampling efficiency of large, faster swimming fishes – particularly in upper to mid-slope environments (Pearcy et al. 1982; Gordon and Duncan 1985). For example, beam trawls may catch a lower percentage by weight of chondrichthyans compared with larger commercial fish trawls; Gordon and Duncan (1985) found no sharks represented in beam trawl catches despite being relatively abundant in commercial fish trawls. Our beam trawl catches suggest such bias had occurred because only 3 chondrichthyan species were captured in 50 samples compared to much larger collections by commercial fish trawls in nearby areas: 30 chondrichthyan species in 147 trawls (GAB, Newton and Klaer, 1991); 15 species in 12 trawls (South Australia, Currie et al 2012); and 70 species in 151 trawls (Australian west coast, Williams et al., 1996). Thus, our data provide comparative estimates of biomass between sites, but were expected to have under-estimated absolute biomass.

The extent of the under-estimation of biomass in the GAB beam trawls was examined by comparing them to commercial fish trawl and beam trawl data from other Australian and global studies (Figure 8.5). Between-region comparisons of beam trawl data showed the GAB fish biomass was generally higher than in the SW Pacific Ocean, and somewhat lower than in the NE Pacific Ocean in depths >2000 m (Figure 8.5). However, the GAB beam trawl estimates were unexpectedly higher than many of those from fish trawls (Figure 8.5). Estimates from productive areas of the NE Atlantic Ocean (data

sets 11 and 12) were higher than the GAB, as were some estimates from Australia. However, the Australian data sets (1, 3 and 4) were elevated by aggregated commercial species and sharks and otherwise estimates from several other studies were lower than the GAB. The relatively high estimates from GAB beam trawls appear to have two possible explanations. First, whilst the small mesh size of beam trawl nets will positively select toward species of small adult size (Merrett et al 1991), it may also select for elongate fishes such as eels (Gordon and Duncan 1985; Merrett et al 1991). In the GAB data, the biomass at upper slope depths was dominated by small-bodied species of macrourids and *Hoplichthys haswelli*, but at mid-slope sites and beyond (>1000 m) by synphobranchid eels and halosaurs. This appears to show that biomass estimates from the GAB are driven by small-bodied species but elevated by relatively high abundance of elongate species. It also raises the possibility that fish trawl catches may substantially under-estimate biomass when small and elongate species are not retained – as may have been the case in the comparable Australian studies (Figure 8.5).

8.4.3 Relevance to management

The GAB is one region that is experiencing the widespread pattern of accelerating anthropogenic activity and impacts in deep areas of world oceans (Halpern et al., 2008; Ramirez-Ilodra et al., 2011). In the GAB, bottom trawling for orange roughy over the last two decades extended the spatial footprint of commercial fishing to about 1500 m, while oil and gas exploration is presently being considered in several active lease blocks that all extend far beyond the continental shelf break, with the deepest including seabed areas beyond 4000 m depths. Benthic biodiversity conservation in the deep sea of the Australian Marine Jurisdiction includes ecosystem based fisheries management (EBFM) (Smith et al., 2007), and seabed protection within a national network of marine reserves that typically extend beyond abyssal depths (> 4000 m) (DEE, 2017). Somewhat paradoxically, the knowledge of deep-sea benthic fauna, including fishes, is generally sparse, and in the GAB there had been virtually no systematic scientific survey of benthic fauna beyond the shelf break prior to the work reported here (except see Newton and Klaer, 1991). As a consequence, there was very little information on deep-sea fauna available to inform fisheries management, to inform and assess environmental approvals for oil and gas development, or even produce an inventory of species occurring within marine reserves. This was reflected in the consensus view of GAB stakeholders that the region's conservation values and key ecological elements and processes should be assessed during oil and gas exploration and before production begins to fill key knowledge gaps. These gaps include the distribution, biodiversity and ecological responses to oceanographic processes and environmental gradients of demersal fishes – especially in depths below about 1500 m that were unsampled (Rogers et al., 2013).

There are several applications of the data presented here to both marine reserve management and ecological monitoring in the context of oil and gas industry development (Table 8.8) because the current data set includes samples from within and immediately adjacent to the GAB CMR and six active lease blocks (Figure 8.1). Its value is further enhanced by including the deepest sites in any systematic survey of fishes in Australian waters, and being the only systematic survey of deep-sea fishes in the GAB in which all specimens have been identified to species-level.

Most obviously, and because of the quality assured nature of the taxonomic identifications, the data inform the conservation performance of the GAB CMR by building on the inventory of species contained or likely to be present in the reserve. This information is fundamental to understanding the diversity and ecological traits of the species and assemblages being protected, and identifying whether or not there are threatened or vulnerable species represented. Similarly, species-level identifications are the foundation for baseline assessment of the regional species pool and evaluation of potential species or higher level taxa as indicators of change in a monitoring program. The species-level information is also the basis for understanding the broader distributions (biogeography) of the species present to understand the representivity of reserves and spatial context for designing a monitoring program. Our data show assemblages change most markedly with depth (richness, diversity, biomass, endemism) but insignificantly across the GAB, indicating the GAB CMR is likely to represent all assemblages because it covers the entire deep-sea depth range extending to the limit of the Australian marine jurisdiction. Representation in the GAB CMR can be placed in the context of the reserve network when inventories and biogeographic data are available for other reserves, and understood in a broader ocean basin perspective. These spatial patterns inform the design of an ecological monitoring program through mapping species distributions and associations with habitats in the area of interest – including identifying potential sites of impact and suitable control sites inside and outside reserves.

8.5 Tables

Table 8.1 Number and distribution of beam trawl samples by depth and site type. Analyses are based on either the subset of 30 'transect' samples, or 'All' samples – the transect samples plus those from sites adjacent to potential seep zones (SZ), volcanic seamounts (VSM), areas with outcropping rocky bottom (OR) or unstructured sediment (S).

DEPTH (M)	ALL SAMPLES	TRANSECT (T)	SEEP ZONE (SZ)	VOLCANIC SEAMOUNT (VSM)	OUTCROP ROCK (OR)	SEDIMENT (S)
200	6	5				1
400	6	5				1
1000	12	5	4	1		2
1500	7	5		2		

2000	10	5	5			
3000	6	5			1	
4000	4				4	
GRAND TOTAL	51	30	9	3	5	4

Table 8.2 Environmental variables compiled for consideration as explanatory factors in community analyses. Numbers in the Source column refer to corresponding points in Section 8.2.3.

Variable	Description	Units	Source
DPTH_AV	Average of start and end depth of gear deployment	m	Survey data
LAT_MID	Latitude of midpoint of gear deployment	°	Survey data
LONG_MID	Longitude of midpoint of gear deployment	°	Survey data
GA_SLOPE	Slope derived from bathymetry DEM	°	1 Bathymetry DEM
GA_ASPECT	Aspect of slope derived from bathymetry DEM	°	1 Bathymetry DEM
GA_CRBNT	Sediment carbonate (CaCO ₃) composition	%CaCO ₃	2 MARS
GA_GRAVEL	Sediment gravel grainsize fraction, ($\phi > 2$ mm)	%	2 MARS
GA_SAND	Sediment sand grainsize fraction, ($63 \mu\text{m} < \phi < 2$ mm)	%	2 MARS
GA_MUD	Sediment mud grainsize fraction, ($\phi < 63 \mu\text{m}$)	%	2 MARS
CRS_NO3_AV	Nitrate bottom water annual average NO ₃	μM	3 CARS
CRS_NO3_SR	Nitrate Seasonal Range	μM	3 CARS
CRS_PO4_AV	Phosphate bottom water annual average PO ₄	μM	3 CARS
CRS_PO4_SR	Phosphate Seasonal Range	μM	3 CARS
CRS_O2_AV	Oxygen bottom water annual average O ₂	mL L^{-1}	3 CARS
CRS_O2_SR	Oxygen Seasonal Range	mL L^{-1}	3 CARS
CRS_S_AV	Salinity bottom water annual average S	‰	3 CARS
CRS_S_SR	Salinity Seasonal Range	‰	3 CARS
CRS_T_AV	Temperature bottom water annual average T	°C	3 CARS
CRS_T_SR	Temperature Seasonal Range	°C	3 CARS
CRS_SI_AV	Silicate bottom water annual average Si	μM	3 CARS
CRS_SI_SR	Silicate Seasonal Range	μM	3 CARS
CHLA_AV	Chlorophyll annual average from SeaWiFS	mg m^{-3}	4 NASA Ocean colour
CHLA_SR	Chlorophyll Seasonal Range	mg m^{-3}	4 NASA Ocean colour
NPP_AV	Net Primary Production annual average from SeaWiFS	$\text{mg C m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
NPP_SR	Net Primary Production seasonal range	$\text{mg C m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
PAR_AV	Photosynthetically Active Radiation (PAR) from MODIS	$\text{E m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
PAR_SR	Photosynthetically Active Radiation seasonal range	$\text{E m}^{-2} \text{day}^{-1}$	4 NASA Ocean colour
SST_AV	Sea Surface Temperature annual average from Modis	°C	4 NASA Ocean colour
SST_MAX	Sea Surface Temperature maximum monthly average	°C	4 NASA Ocean colour
BIR_AV	Benthic Irradiance annual average, $\text{BIR} = \text{PAR} \times e^{-\text{K} \times \text{Depth}}$	$\text{E m}^{-2} \text{day}^{-1}$	5 Derived variables
BIR_SR	Benthic Irradiance Seasonal Range	$\text{E m}^{-2} \text{day}^{-1}$	5 Derived variables
EPOC_AV	Export Particulate Organic Carbon flux annual average from SeaWiFS	$\text{mg C m}^{-2} \text{day}^{-1}$	5 Derived variables
EPOC_SR	Export Particulate Organic Carbon seasonal range	$\text{mg C m}^{-2} \text{day}^{-1}$	5 Derived variables
BSTR_AV	Bottom stress Average - mean over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)
BSTR_MAX	Bottom stress Maximum over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)
BSTR_SD	Bottom stress Standard Deviation of mean over 2 year model simulation	N m^{-2}	6 BENTHIS (BPRP 1.1)

Table 8.3 List of Families of deep-sea benthic fishes collected by beam trawl in the Great Australian Bight showing occurrence, number of species, unstandardized catch (weight and individuals), and percentage of total biomass and density standardised by beam trawl swept area. Top-ranked Families **bolded** (those contributing to 90% of biomass or density).

FAMILY	All samples				All samples				Transect samples (30)			
	Occurrence (in 51 samples)	No. Species	Total catch (kg)	Total individuals	Total biomass (g.m ⁻²)	Total density (ind.m ⁻²)	% biomass	% density	Total biomass (g.m ⁻²)	Total density (ind.m ⁻²)	% biomass	% density
Scyliorhinidae	1	1	0.01	1	0.00	0.00	0.00	0.03	0.00	0.00	0.01	0.03
Rajidae	1	1	0.01	1	0.01	0.00	0.01	0.07	0.01	0.00	0.02	0.09
Chimaeridae	1	1	2.43	1	0.72	0.00	0.86	0.02	0.00	0.00	--	--
Nettastomatidae	5	1	0.29	5	0.12	0.00	0.14	0.16	0.06	0.00	0.13	0.12
Congridae	6	3	0.96	27	0.80	0.02	0.96	1.76	0.44	0.02	0.92	2.15
Synaphobranchidae	29	7	33.19	99	12.78	0.04	15.37	3.17	6.41	0.02	13.53	1.84
Halosauridae	20	2	12.74	70	4.26	0.02	5.12	1.99	2.64	0.02	5.56	1.66
Notacanthidae	9	2	1.07	12	0.43	0.00	0.52	0.40	0.21	0.00	0.45	0.25
Argentinidae	2	1	0.01	5	0.01	0.00	0.01	0.34	0.01	0.00	0.02	0.43
Phosichthyidae	1	1	0.00	1	0.00	0.00	0.00	0.07	0.00	0.00	--	--
Alepocephalidae	5	6	2.43	7	0.84	0.00	1.00	0.21	0.67	0.00	1.42	0.19
Platyroctidae	1	1	0.00	1	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.03
Bathysauridae	7	1	4.51	11	1.58	0.00	1.90	0.31	0.88	0.00	1.86	0.18
Bathysauropsidae	14	1	1.39	47	0.44	0.02	0.53	1.27	0.22	0.01	0.46	1.02
Paraulopidae	9	2	0.82	35	0.70	0.03	0.84	2.47	0.65	0.03	1.37	2.96
Ipnopidae	5	2	0.31	26	0.10	0.01	0.12	0.71	0.10	0.01	0.21	0.88
Brachionichthyidae	1	1	0.00	2	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.21
Antennariidae	1	1	0.01	2	0.01	0.00	0.01	0.14	0.01	0.00	0.01	0.17
Chaunacidae	1	1	0.01	1	0.00	0.00	0.00	0.02	0.00	0.00	--	--
Eulichthyidae	6	1	2.28	118	1.84	0.10	2.22	8.04	1.49	0.08	3.15	8.75
Melanonidae	1	1	0.66	1	0.23	0.00	0.27	0.03	0.23	0.00	0.48	0.04
Moridae	26	7	14.84	103	4.88	0.04	5.87	3.30	1.48	0.02	3.13	2.25
Bythitidae	3	2	0.11	3	0.05	0.00	0.06	0.10	0.04	0.00	0.08	0.09
Ophidiidae	14	4	11.52	42	6.51	0.02	7.82	1.45	6.41	0.01	13.52	0.85
Carapidae	2	2	0.04	6	0.03	0.01	0.04	0.44	0.01	0.00	0.02	0.09
Zoarcidae	1	1	0.02	1	0.01	0.00	0.01	0.03	0.01	0.00	0.02	0.04
Bathygadidae	14	3	3.14	114	1.06	0.04	1.28	2.99	0.34	0.02	0.72	2.26
Macrouridae	38	21	53.88	668	21.04	0.37	25.31	30.84	10.20	0.27	21.53	28.20
Trachichthyidae	4	2	3.44	5	1.58	0.00	1.90	0.25	0.00	0.00	0.01	0.09
Oreosomatidae	13	2	19.96	42	7.40	0.02	8.90	1.30	3.30	0.01	6.97	0.69
Macroramphosidae	5	1	0.18	40	0.16	0.04	0.20	2.96	0.16	0.04	0.35	3.78
Syngnathidae	1	1	0.00	4	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.32
Scorpaenidae	1	1	0.00	1	0.00	0.00	0.00	0.08	0.00	0.00	--	--
Sebastidae	9	3	1.17	27	1.10	0.03	1.32	2.07	0.57	0.02	1.20	1.82
Triglidae	7	2	0.20	16	0.15	0.01	0.19	1.23	0.15	0.01	0.33	1.57
Platycephalidae	4	1	0.40	5	0.39	0.01	0.47	0.46	0.39	0.01	0.83	0.58
Hoplichthyidae	7	1	9.07	77	9.77	0.07	11.75	5.97	7.66	0.06	16.15	6.11
Cottidae	1	1	0.00	1	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.20
Psychrolutidae	1	1	2.08	1	1.05	0.00	1.26	0.04	0.00	0.00	--	--
Acropomatidae	5	1	1.30	162	1.06	0.13	1.27	10.51	1.05	0.13	2.21	13.33
Serranidae	2	2	0.07	7	0.06	0.01	0.07	0.52	0.00	0.00	0.01	0.08
Epigonidae	4	3	0.33	29	0.27	0.02	0.32	1.91	0.26	0.02	0.56	2.40
Pentacerotidae	3	1	1.10	3	0.92	0.00	1.11	0.21	0.57	0.00	1.21	0.17
Labridae	1	1	0.00	1	0.00	0.00	0.00	0.08	0.00	0.00	--	--
Pinguipedidae	4	1	0.13	11	0.17	0.01	0.20	0.85	0.17	0.01	0.36	1.09
Callionymidae	7	2	0.22	69	0.26	0.08	0.31	6.20	0.26	0.07	0.54	7.73
Gobiidae	1	1	0.00	1	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.08
Pleuronectidae	5	1	0.36	39	0.27	0.03	0.33	2.43	0.24	0.03	0.50	2.72
Tetraodontidae	4	1	0.07	22	0.07	0.02	0.09	1.91	0.07	0.02	0.16	2.44
Grand Total	47	108	186.73	1973	83.15	1.22			47.39	0.95		

Table 8.4 Top ranked 15 species in total average biomass (B), density (D) or both biomass and density (BandD) in 30 transect samples. Species are ordered by the mid-point of their depth range in samples and account for 80% of total biomass and 76% of density.

Family	Species		Total biomass (g.m ⁻²)	% Biomass	Rank Biomass	Total density (ind.m ⁻²)	% Density	Rank Density	Min. Depth	Max. Depth	Mid- depth range
Macroramphosidae	<i>Macroramphosus scolopax</i>	D	0.1647	0.00	39	0.0360	0.04	7	189	283	236
Acropomatidae	<i>Verilus anomalus</i>	B&D	1.0483	0.02	11	0.1269	0.13	1	189	426	307
Hoplichthyidae	<i>Hoplichthys haswelli</i>	B&D	7.6554	0.16	1	0.0582	0.06	5	189	426	307
Paraulopidae	<i>Paraulopus nigripinnis</i>	B&D	0.6499	0.01	15	0.0282	0.03	10	199	426	312
Ophidiidae	<i>Dannevigia tusca</i>	B	4.2141	0.09	3	0.0017	0.00	53	383	383	383
Pleuronectidae	<i>Azygopus pinnifasciatus</i>	D	0.2389	0.01	28	0.0259	0.03	11	383	412	397
Epigonidae	<i>Epigonus denticulatus</i>	D	0.2648	0.01	26	0.0226	0.02	13	388	410	399
Macrouridae	<i>Coelorinchus amydrozosterus</i>	B&D	0.7122	0.02	14	0.0926	0.10	2	383	426	404
Euclichthyidae	<i>Euclichthys polynemus</i>	B&D	1.4929	0.03	9	0.0833	0.09	3	383	426	404
Callionymidae	<i>Foetorepus apricus</i>	D	0.2548	0.01	27	0.0720	0.08	4	383	426	404
Macrouridae	<i>Coelorinchus mirus</i>	D	0.4102	0.01	20	0.0533	0.06	6	388	426	407
Macrouridae	<i>Hymenocephalus longibarbis</i>	D	0.0390	0.00	60	0.0308	0.03	8	388	426	407
Tetraodontidae	<i>Omegophora armilla</i>	D	0.0740	0.00	51	0.0232	0.02	12	189	1027	608
Macrouridae	<i>Cetonurus globiceps</i>	B&D	5.5406	0.12	2	0.0289	0.03	9	996	1027	1011
Macrouridae	<i>Coryphaenoides serrulatus</i>	B	1.4659	0.03	10	0.0068	0.01	28	996	1027	1011
Oreosomatidae	<i>Alloctytus verrucosus</i>	B	3.3020	0.07	5	0.0065	0.01	29	996	1527	1261
Synphobranchidae	<i>Diastobanchus capensis</i>	B	1.8610	0.04	8	0.0031	0.00	41	1021	1527	1274
Bathygadidae	<i>Bathygadus cottoides</i>	D	0.1317	0.00	43	0.0196	0.02	15	1021	1553	1287
Moridae	<i>Antimora rostrata</i>	B	1.0004	0.02	12	0.0074	0.01	26	996	2014	1505
Synphobranchidae	<i>Synphobranchus brevidorsalis</i>	B	3.6696	0.08	4	0.0057	0.01	31	1005	2014	1509
Bathysauridae	<i>Bathysaurus ferox</i>	B	0.8793	0.02	13	0.0017	0.00	51	1005	2037	1521
Macrouridae	<i>Coryphaenoides filicauda</i>	D	0.2898	0.01	23	0.0206	0.02	14	1006	3021	2014
Halosauridae	<i>Halosaurus macrochir</i>	B	2.5118	0.05	6	0.0141	0.01	16	1468	2840	2154
Ophidiidae	<i>Spectrunculus grandis</i>	B	2.1148	0.04	7	0.0004	0.00	77	3002	3002	3002

Table 8.5 The marginal test results from the DISTLM analysis showing the proportion of variation in the assemblage structure explained by environmental predictor variables tested. Variables with correlation of $>|0.9|$ to a higher ranked variable were excluded from the DISTLM model run (grey cells). The selection of variables resulting in the 'best' result $\text{adj.}R^2 = 0.44$, $R^2 = 0.57$ are ranked by their relative influence on the model.

Variable	Proportion	P	Selection (best)	Represented by (correlation $> 0.9 $)
CRS_O2_AV	0.165	0.001	1	
CRS_PO4_AV	0.159	0.001		CRS_O2_AV, CRS_T_AV
CRS_NO3_AV	0.153	0.001		CRS_O2_AV, CRS_T_AV
CRS_S_AV	0.149	0.001	2	
CRS_O2_SR	0.147	0.001	6	
CRS_S_SR	0.145	0.001		CRS_O2_AV, CRS_T_AV
CRS_T_AV	0.145	0.001	3	
CRS_NO3_SR	0.142	0.001	4	
EPOC_AV	0.138	0.001		CRS_T_AV
CRS_T_SR	0.136	0.001		CRS_O2_AV
CRS_SI_AV	0.135	0.001		
CRS_PO4_SR	0.134	0.001		CRS_NO3_SR
NPP_AV	0.129	0.001		
GA_SAND	0.113	0.001		
Dpth (ave)	0.113	0.001		CRS_SI_AV
SST_AV	0.108	0.001		
GA_MUD	0.105	0.001		GA_SAND
CHLA_AV	0.097	0.001		
GA_CRBNT	0.095	0.001	7	
BIR_AV	0.085	0.001	8	
CRS_SI_SR	0.085	0.001	5	
BSTR_AV	0.080	0.001	9	
PAR_AV	0.078	0.001		SST_AV
BSTR_Max	0.075	0.001	11	
GA_SLOPE	0.071	0.002	10	
lat (mid)	0.060	0.003		
CHLA_SR	0.018	0.623		
long (mid)	0.016	0.726		
GA_ASPECT	0.016	0.752		
GA_GRAVEL	0.015	0.848		

Table 8.6 Summary of fishes collected by beam trawl in this study compared to previous records of deep-sea benthic fishes in the Great Australian Bight; shown by depth range.

Depth range	Species	Previously recorded from			
		GAB	%	Australia	%
Shelf break (~200-240 m)	19	17	89	19	100
Upper slope (280-600 m)	23	20	87	22	96
Mid slope (950-1550 m)	43	37	86	39	91
Lower slope/ rise (1700-3000 m)	23	7	30	17	74
Total species	108	81	75	97	90

Table 8.7 Documented geographical distributional ranges of deep-sea benthic fishes collected by beam trawl in the Great Australian Bight shown by depth range.

Distribution	Species	Depth range			
		Shelf break	Upper slope	Mid-slope	Lower slope/ rise
East-Indo-west Pacific	22	5	7	9	1
Indo-west Pacific	6	2		3	1
East Atlantic Indo-west Pacific	4		1	2	1
Indo-Pacific	1	1			
West Pacific	1				1
Pacific	1		1		
Atlantic-Indo-west Pacific	3			2	1
Atlantic-Indo-west-central Pacific	3			1	2
Indian	1			1	
East Indian	1				1
Circumglobal	17	1	1	11	4
Southern circumglobal	11			6	5
Circumtropical	1				1
Antitropical	2			1	1
Unknown	7		1	3	3
Endemic	27	10	12	4	1
Total	108	19	23	43	23

Table 8.8 Potential applications of data on deep-sea fishes to marine management in the Great Australian Bight.

	Reserve management	Ecological monitoring
Composition & diversity (Quality assured species level taxonomy)	<ul style="list-style-type: none"> > Inventory of species present > Robust indices of diversity > Key species identified (e.g. endemic, keystone) > Threatened/ vulnerable species identified 	<ul style="list-style-type: none"> > Baseline data > Selection of species-level indicators > Assessment of taxonomic sufficiency, i.e. monitoring at higher taxonomic levels
Biogeography (Quality assured species level taxonomy)	<ul style="list-style-type: none"> > Representivity assessed at scale of main planning regions > Representivity assessed in relation to broad affinities of fauna 	<ul style="list-style-type: none"> > Understanding of relevant spatial scales for monitoring program
Spatial patterns	<ul style="list-style-type: none"> > Representivity assessed in relation to depth and east-west gradient > Species associations with environment (habitats) > Species, communities and habitats identified at 'control' sites within reserves 	<ul style="list-style-type: none"> > Species associations with environment (habitats) identified for selection of monitoring sites > Species, communities and habitats identified at 'disturbed' and/ or 'contrasting' sites, e.g. active lease blocks

8.6 Figures

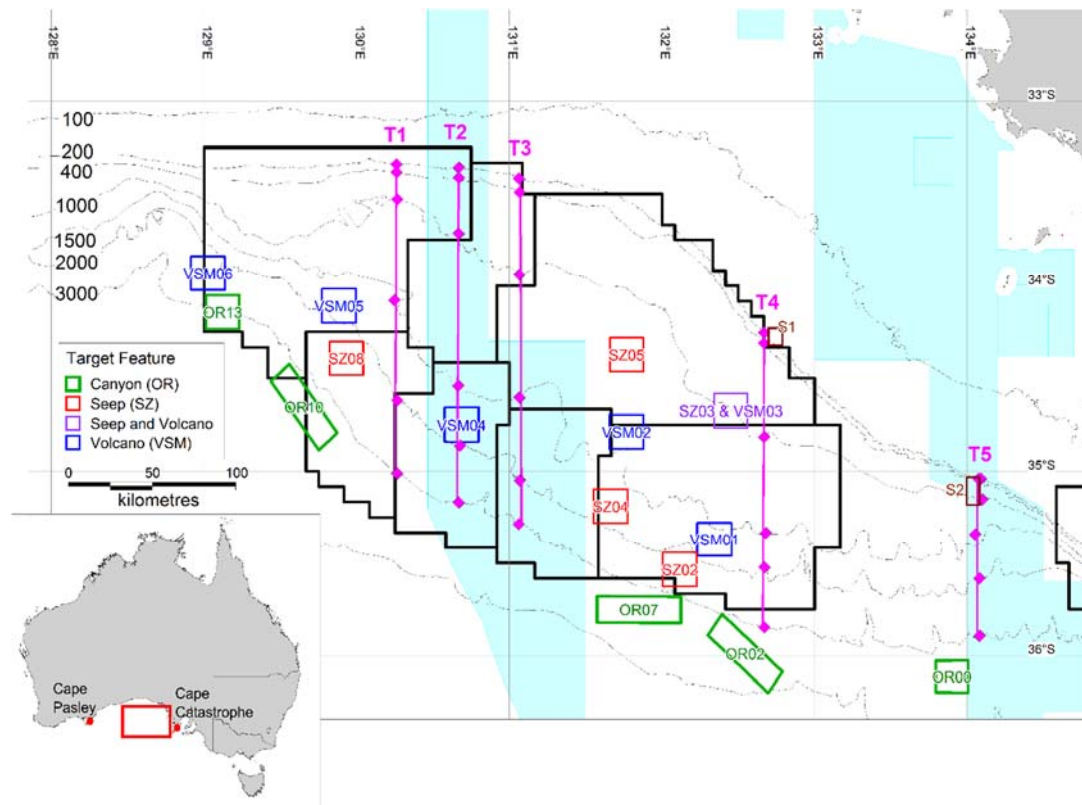


Figure 8.1 Map showing the study area in the central Great Australian Bight (GAB): sampling sites occur on transects T1 to T5, arranged from west to east, at six depth strata: 200, 400, 1000, 1500, 2000 and 3000 m, and at sites chosen based on local topography (SZ, VSM, OR and S see key).. Also shown: relevant isobaths (labelled); proclaimed Commonwealth Marine Reserves (shaded light blue); active oil and gas lease blocks (black boundaries). Inset: Sampling location in relation to Australia.

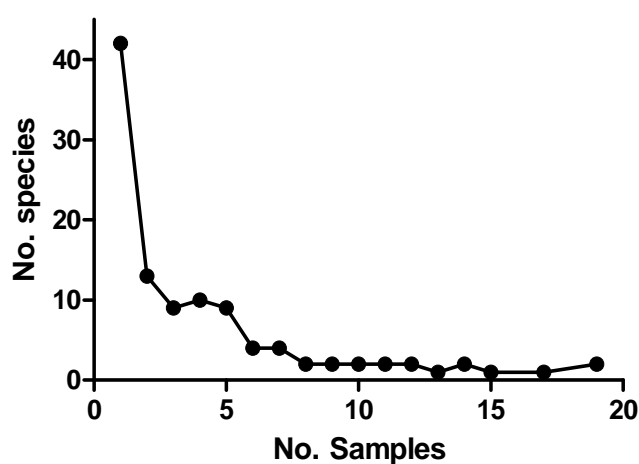


Figure 8.2 Frequency of occurrence of individual taxa in 51 beam trawl samples from the GAB.

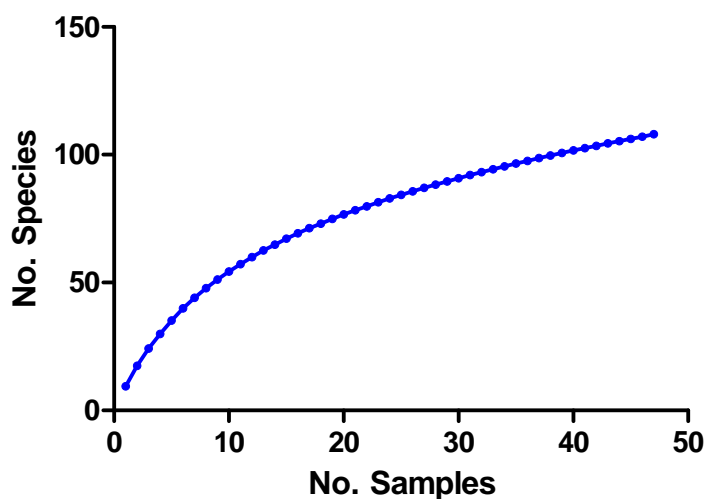


Figure 8.3 Species accumulation curve for fish in the GAB (999 permutations).

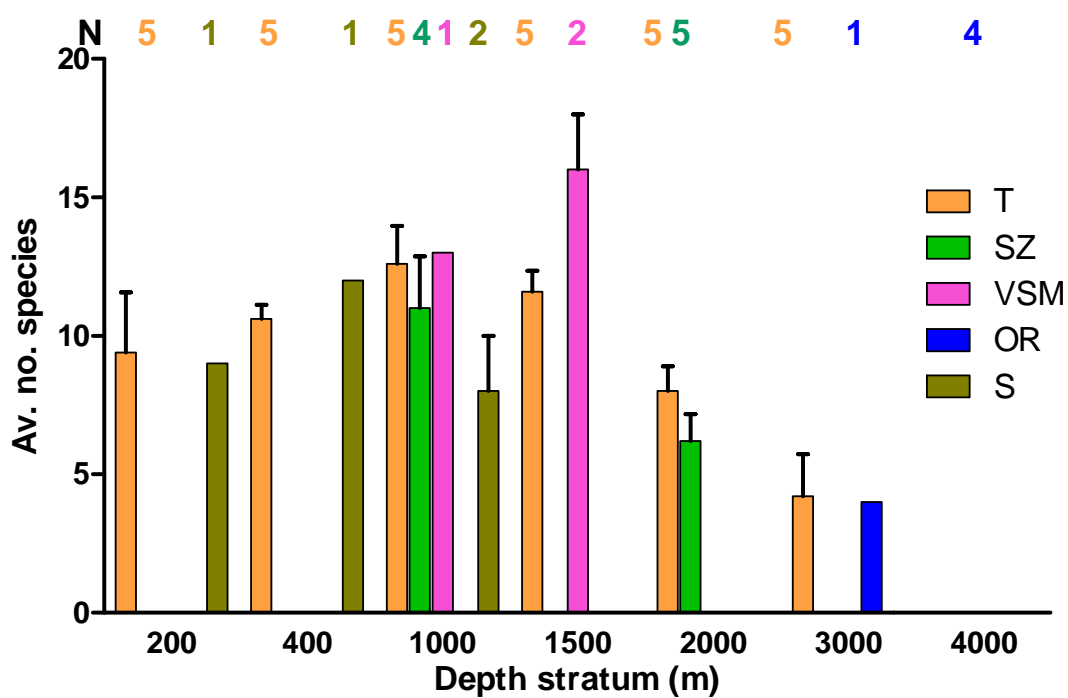


Figure 8.4 Richness of benthic fishes shown by the average number of species collected per sample by depth stratum and site type (T – standard transects (one sample per transect-depth); S – unstructured sediments; SZ – potential seep sites; VSM – volcanic seamount sites; OR – outcropping rock sites). Number of samples per depth (N); bar = standard error.

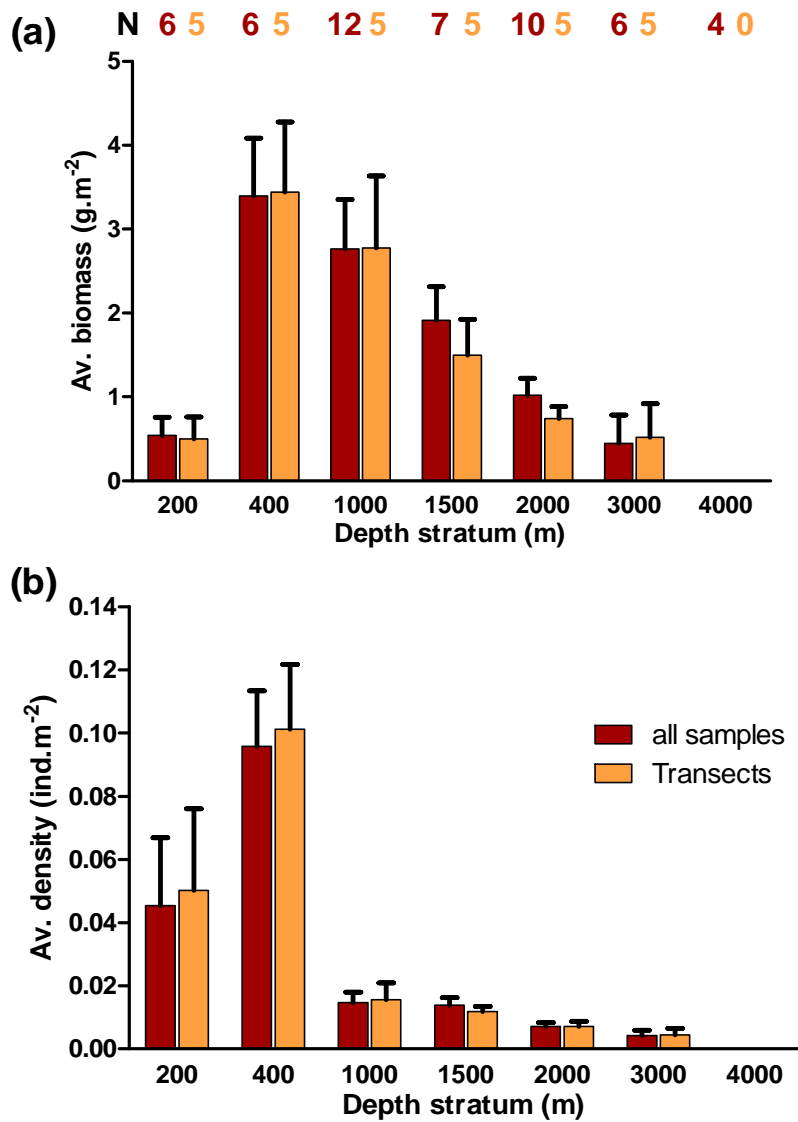


Figure 8.5 Abundance of benthic fishes in beam trawl samples by depth stratum for transect samples and transect + topography (all) samples: (a) average biomass and (b) average density. Number of samples per depth (N); bar = standard error.

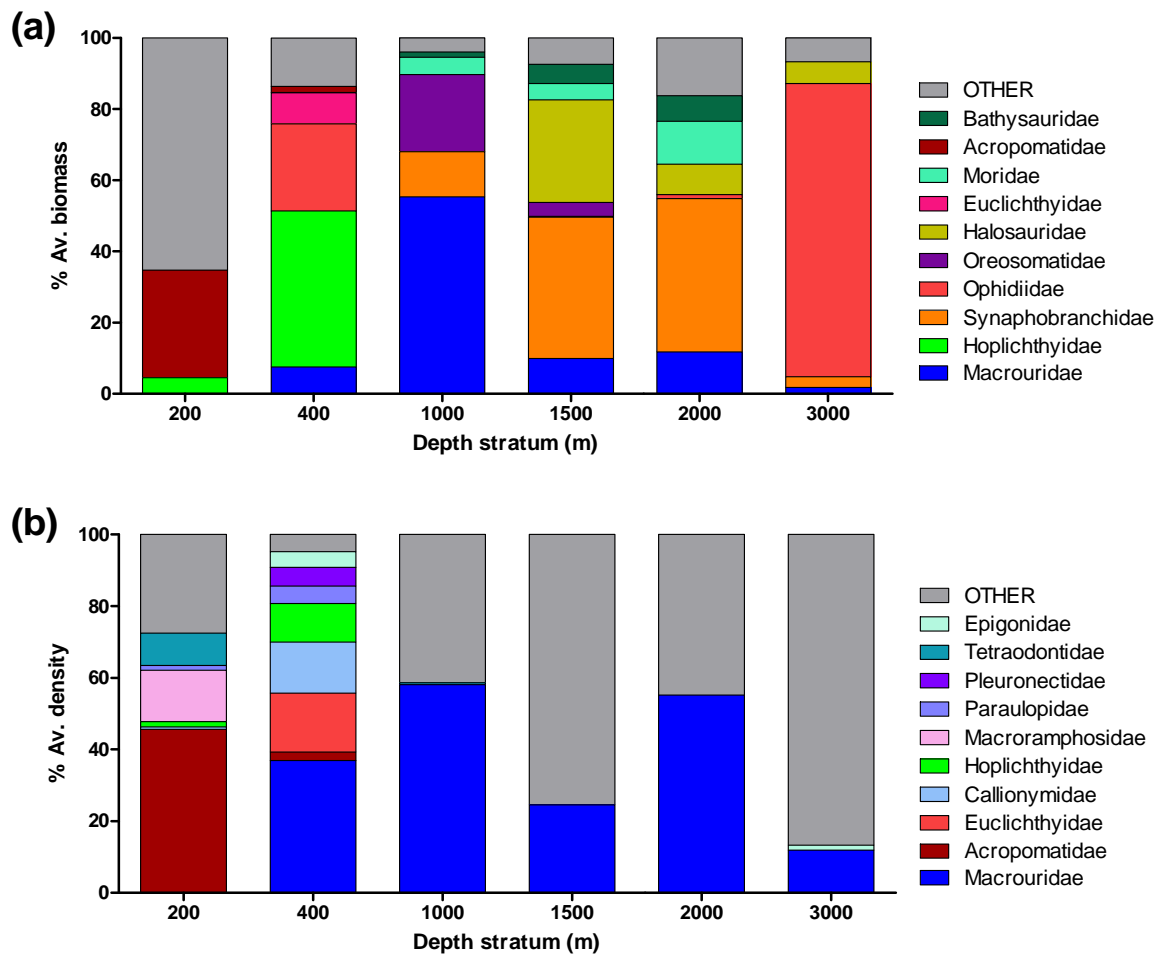


Figure 8.6 Percentage of (a) biomass and (b) density distribution in the transect samples of the 10 top ranked fish families by depth stratum. Data shown for the 10 highest ranked families making up >88% of the standardised biomass, with the remaining families summed into 'others'.

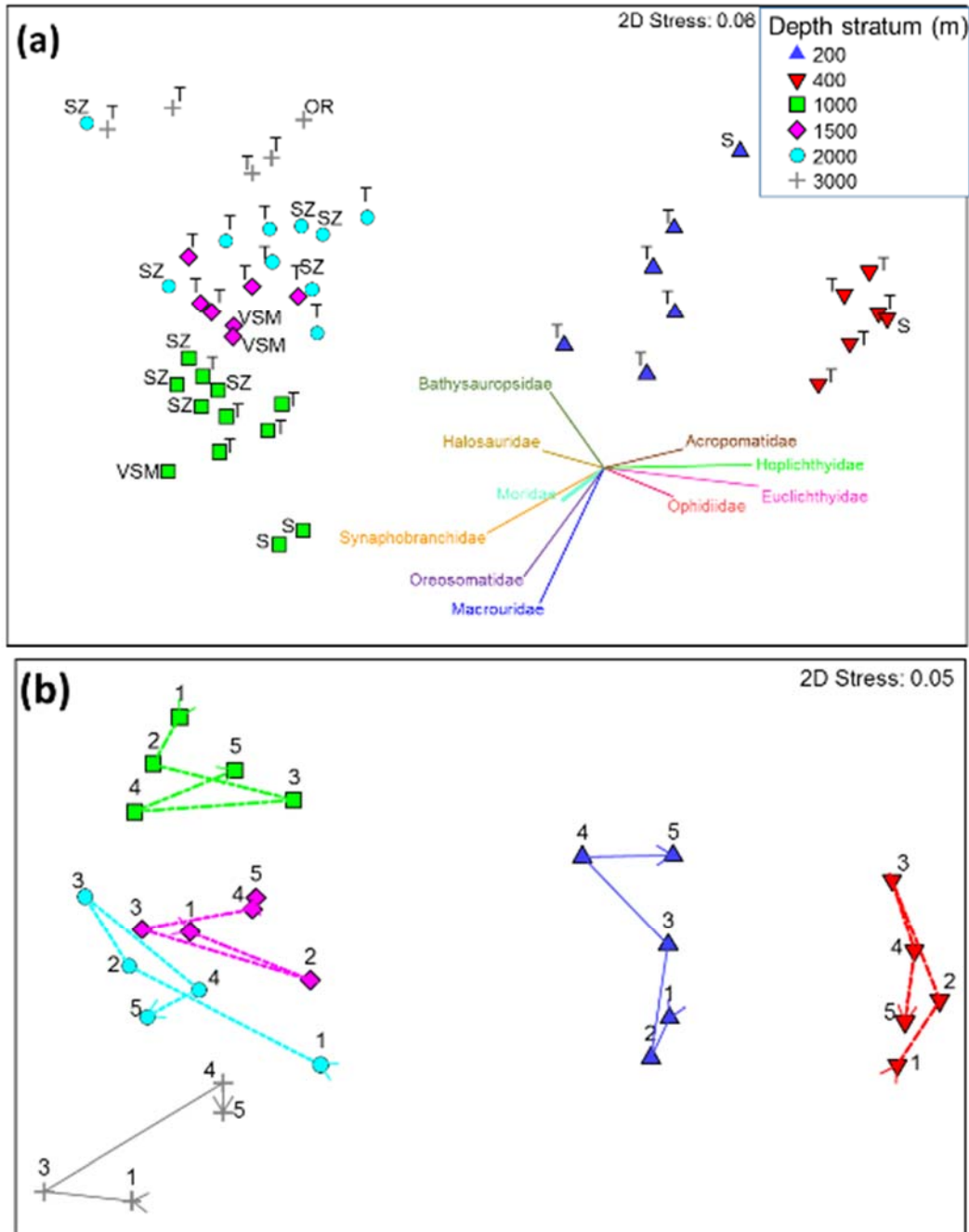


Figure 8.7 Ordination (2D-nMDS) plot showing the Bray-Curtis similarity between fish catches (square-root transformed biomass) from (a) all samples (transect and topography samples combined; and (b) the transect sites only. (a) The data are coloured by depth strata and labelled by site type; the overlay graph is based on the Pearson's correlation of the 10 top-ranked families with the first 2 MDS axes, showing the direction line angle and size (length) of the correlation. (b) The data is coloured by depth strata and labelled by transect number with trajectories from west to east (transects 1 to 5 as labelled) overlaid within each depth stratum.

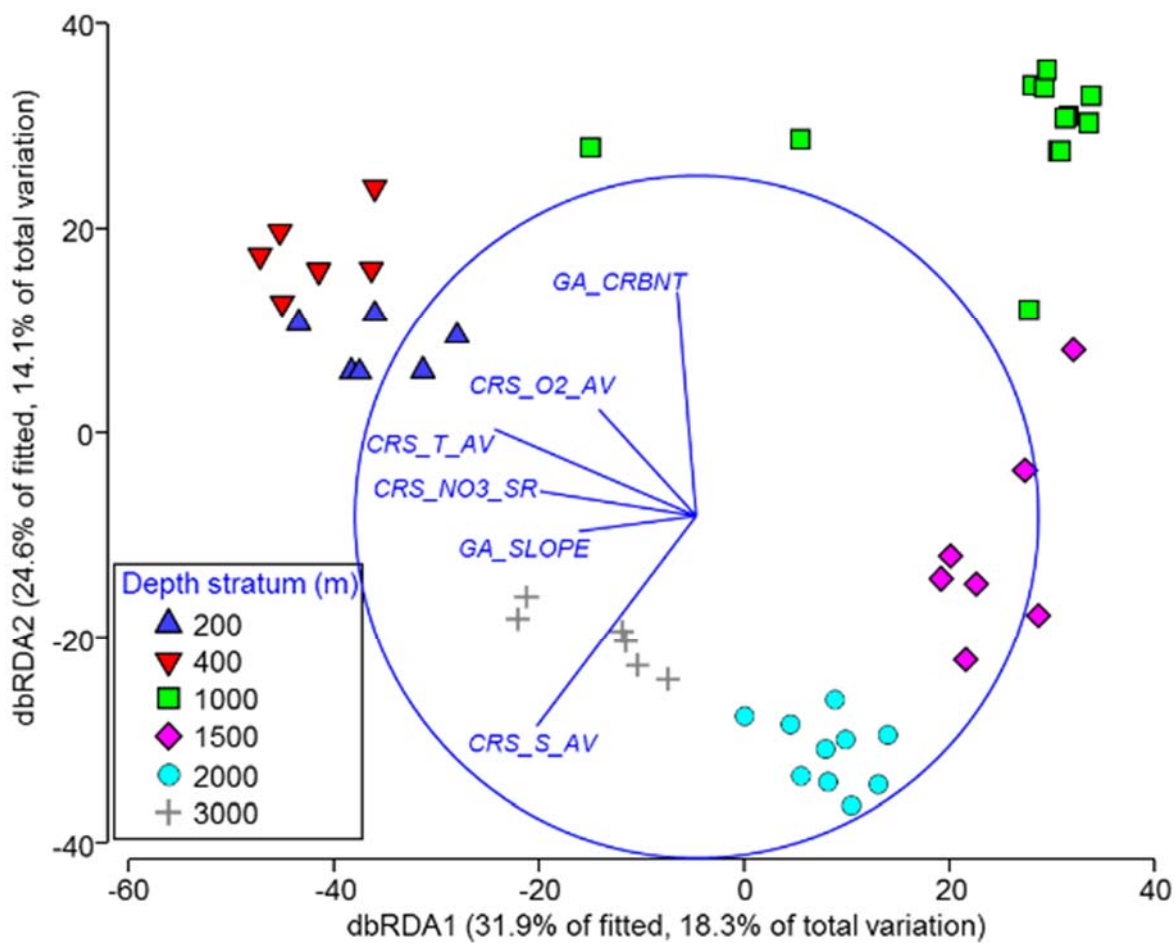


Figure 8.8 Distance based RDA based on the selected predictor variables from the DISTLM on the fish biomass data. The overlay graph is limited to the variables that have a correlation to the RDA axes of >0.2 .

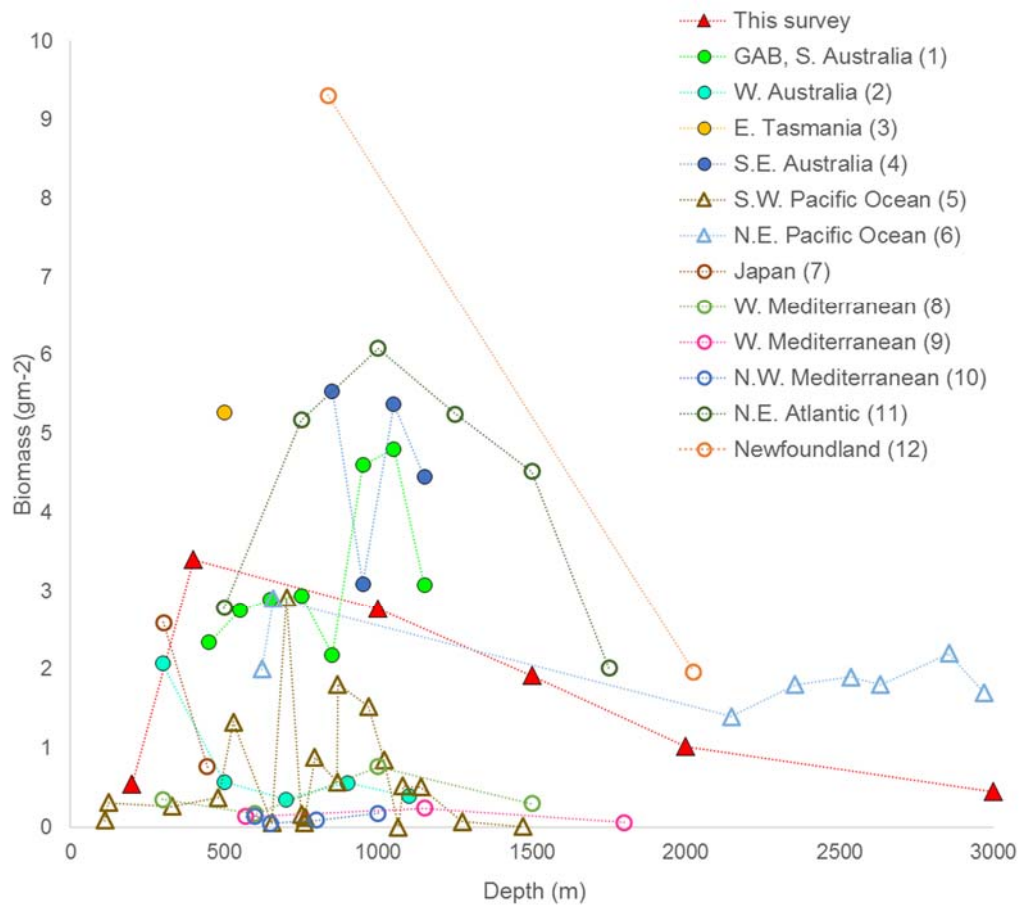


Figure 8.9 Comparative estimates of benthic fish biomass from trawl surveys, displayed by depth strata. Survey data from beam trawl collections (triangles), commercial-type trawls (circles). Solid markers from Australian waters, hollow markers from other regions. 1 = Newton and Klaer 1991, 2 = Williams et al. 2001, 3 = May and Blaber 1989, 4 = Koslow et al. 1994, 5 = unpublished data from NORFANZ voyage Tan20030 (an outlier of 63.6 g/m² at 1338 m was removed from this data), 6 = Percy et al 1982, 7 = Fujita et al. 1995, 8 = Moranta et al. 1998, 9 = Fanelli et al. 2013, 10 = Papiol et al. 2012, 11 = Gordon and Duncan 1985, 12 = Snelgrove and Haedrich 1985.

9 Biogeography of the southern Australian continental slope: Do comprehensive surveys accord with museum records

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9.1 Introduction

Biogeographic affiliations in the deep sea are often poorly understood, due to the difficulty and expense in collecting comprehensive data on the assemblages present in these areas. In 3000 m water depth, a single trawl shot can take almost half a day, and cost \$50,000 or more if using a dedicated offshore research vessel with the capability of supporting a scientific team that can process the sample. Where historical catch data are available, it may not be comprehensive, as many surveys only target particular taxa of interest, or the resources were not available to undertake high level taxonomic identifications.

An alternative source of data are historical records from museums. These records often result from ad hoc sample collection, or surveys that only document certain components of the fauna. Even when records stem from a comprehensive survey effort, often the associated metadata have not been archived in a way that can be matched to individual specimen records, and/or the comprehensive survey data are simply not available for re-use. In addition, many of the samples were collected well before the advent of modern navigational technology, and thus location and depth data may be inaccurate. Finally, many specimens have not been subject to rigorous taxonomic scrutiny, or this may have been based on what is now a well out-dated taxonomy. As a consequence of these potential issues, it is not clear how useful these historical records are for generating a modern biogeography of assemblages.

Biogeographic patterns in shallow waters are often better understood than those in the deep sea (e.g. Colgan, 2016), as they are more accessible and thus have been the focus of much more intensive sampling, with Australian studies dating back to at least the 1950s. However, as the physical environment, and subsequently the life-histories of the organisms living there, can differ substantially between the shallow and deep oceans, it is not possible to extrapolate shallow-water biogeographic patterns to the deep. Biogeography and patterns in diversity are known to differ with depth (Macpherson et al., 2010; Williams et al., 2011; Woolley et al., 2016), and it is generally considered that deep-sea species are widely distributed compared to their shallow-water counterparts (McClain and Hardy, 2010; Gooday and Jorissen, 2012). However, recent work on benthic and particle-attached microbes suggests that many 'species' in the deep sea have a

relatively restricted distribution, leading to substantial geographic structuring in assemblages (Zinger et al., 2011; Bienhold et al., 2016; Salazar et al., 2016).

Here, we generate a biogeography of the southern Australian deep-sea (200-3000 m depth), based on specimen records held by major Australian museums. To determine how well this historical data set does at defining the assemblages present, we include in our analysis depth integrated data from a series of comprehensive beam trawl surveys conducted in the central GAB in late 2015. This is a particularly data poor region, thus providing a challenging test of the ability to describe biogeographic affiliations using historical data.

To date, there have been few studies published that provide a detailed quantitative examination of the biogeography of Australian marine waters, with two on fish (Commonwealth of Australia, 2006; Last et al., 2005), one on ophiuroids (O'Hara, 2008), one on sponges (Hooper and Ekins, 2004) and one on algae (Waters et al., 2010). Only Last et al. (2005) and O'Hara (2008) consider deep (> 200 m) waters off southern Australia. The first four of these studies involved comprehensive collation of records from a wide range of museums, along with published literature, followed by re-examination of many specimens. For each individual taxon considered, taxon distributions were then modelled based on the available point data, interpolating species occurrence between these points, before the final biogeographic analysis was undertaken. While this approach provides a gold standard, it is also very labour intensive and slow, and thus we were interested in determining if similar results could be obtained from a much less exhaustive process. A similar approach to ours is taken by Waters et al. (2010), although they test for distinctions between the existing Integrated Marine and Coastal Biogeographic Regionalisation of Australia (IMCRA) bioregions (Commonwealth of Australia, 2006).

9.2 Methods

Database extracts were requested from museums throughout Australia for all specimen lots with collection depth >200 m from temperate Australia (collection location between 32°S and 44°S). Database extracts were received from the Australian Museum (AM), Museum Victoria (MV), Queensland Museum (QM), Western Australian Museum (WAM) and the Northern Territory Museum of Arts and Sciences (NTM). Although the South Australian Museum had substantial holdings of relevant specimens, very few had been databased. Consequently, a systematic search of the museum shelves was undertaken, and all relevant specimen records databased, with the exception of arthropods, of which only the decapods and pycnogonids were entered. Large deepwater collections, particularly from waters east of Tasmania, are held by the Tasmanian Museum, but it was not possible to extract the relevant records from their system. Due to time constraints, analysis was restricted to the 8 major taxa listed in Table 4.3.

Once a collated data set was obtained, it was subject to comprehensive screening and taxonomic updating. 1966 records that were identified in the original data downloads as having a spatial precision > 10 km were discarded, along with 188 that had no spatial position, and 174 that were identified as being > 4000 m. The remaining records were then mapped in ArcGIS (v10.3.1 ESRI Inc.), along with a comprehensive bathymetry of Australia, an integrated product produced at CSIRO (G. Keith), based on the Geoscience Australia (GA) GA2009 250 m bathymetric product (Whiteway, 2009) refined with bathymetric data based upon LiDAR/LADS surveys and surveys based on acoustic systems provided by CSIRO and GA, and historical soundings provided by the Australian Hydrographic Service (AHO) and the Western Australian Department of Primary Industries (WA DPI). Those records that mapped on land (412), in water shallower than 180 m (1260), or in water > 3000 m (430) were also discarded, along with 3 records that mapped well outside the southern Australian continental slope (1 each from Africa, the North-West Shelf and the Chatham Rise).

The remaining 20327 records were then cross-checked against the World Register of Marine Species (WoRMS) to obtain full current taxonomies. Specimens that had not been identified to species level were not re-examined, but were instead retained at the taxonomic level recorded. All tentative species designations (sp 1, cf sp y, sp z? etc) were moved up to genus level. Species that could not be found in WoRMS were carefully checked for possible mis-spellings, and if no species name could be confirmed, also moved up to the genus level. The final 'species' list contained 3496 taxa (at the lowest taxonomic level recorded). Of these, 1248 were represented by a single record, although 1 record may have equated to multiple individuals. A total of 2993 taxa (85.6%) were represented by 10 or fewer records. The most abundant taxon was *Sassia kampyla* (a triton mollusc), with 233 records. A total of 25 taxa had 50 or more records, although 3 of these were undifferentiated groupings at the family, order or class level.

For analysis, records were grouped by splitting the region into 40 geographic segments based on latitude and longitude, each split with ~ 508 records (Figure 9.1). This often split records that appeared to be from a single station between two adjacent groups. In this case, the split point was moved to avoid this (so range in sample size was 368-533). 33 of the 40 segments were on the east coast of Australia, with the remaining segments spread over the much larger south and west coasts.

In addition, a comprehensive beam trawl survey data set from the GAB obtained under the Great Australian Bight Research Program (GABRP) from the Marine National Facility RV *Investigator* in December 2015 (IN2015_C02), was included in the analysis to ascertain how comparable the ad-hoc museum data are to such a survey. Briefly, beam trawls were conducted at predetermined depths (200, 400, 1000, 1500, 2000 and 3000 m) along each of five north-south transects in the central GAB

(See Figure 9.1). All fauna caught in each trawl were sorted, classified and enumerated on retrieval, and representative samples kept for further detailed taxonomy by specialist taxonomists. For the purpose of the analysis presented here, the detailed taxonomy is utilized, and each transect is treated as a single depth-integrated sample (as the museum data are depth-integrated). Again, we have restricted the analysis to the groups listed in Table 9.1. This data set contains 1853 records from 617 taxa, 264 with only a single record. Of these 617 taxa, only 359 are present in the museum data set. The two most abundant species in the museum data set (and 6 of the 7 most abundant) were absent from the survey data set.

To assess spatial patterns in deep-sea assemblage structure, we used non-metric multidimensional scaling (nMDS), and cluster analysis with a similarity profiles analysis to indicate significant groupings at the 5% level. All analyses were performed on presence/absence data, as the museum data are unlikely to provide a good indication of abundance. Bray-Curtis dissimilarities were used to eliminate the influence of joint absences, as neither the museum nor the survey data sets can be considered to provide a comprehensive list of taxa present. To determine whether patterns were consistent between different taxonomic levels, we repeated the analyses at the species, genus, family, class and phylum levels. In each case, specimens that had not been classified down to the level being analysed were retained in the analysis at the taxonomic level recorded. A 2-stage nMDS was then used to assess concordance between the patterns at each level. Multivariate analyses were undertaken in Primer (v7.0.11, Primer-E Ltd.).

9.3 Results

There were clear geographic patterns present in the museum data, with the ordination showing the south-west and south coasts grouping with south-east Tasmania, a second grouping covering north-east Tasmania through to about the border between Victoria and New South Wales, and a third grouping of New South Wales sites (Figure 9.2). This is supported by the cluster analysis, which also splits off the south-west segments from the southern segments and shows more detailed structuring along the east coast (Figure 9.3 and Figure 9.4). The survey data forms a tight grouping in both the ordination and the cluster analysis, lying very close to geographic segments d and e, within which they lie. These patterns persist at the genus and family levels, start to break down at the class level, and are entirely absent at the phylum level (Figure 9.2 and Figure 9.3). The concordance of patterns at the species, genus and family levels is confirmed by the second stage nMDS (Figure 9.5), which shows these 3 levels all lying close together in the ordination, with class and phylum lying in substantially different parts of the plot.

Species level patterns do not appear to be driven by geographic patterns in the level of taxonomic identification, as all taxa with a correlation >0.8 with the nMDS axes are identified to species level (Figure 9.2). However, at the genus level, a number of the taxa with high correlations are only identified to the family level or higher. The grouping of segments off the New South Wales coast are characterized by gastropods, particularly those in the genus *Columbarium* and the family *Olividae*. Those of north-east Tasmania and Victoria are characterized by the presence of a range of isopod taxa, including the families *Dendrotonidae*, *Janiridae* and *Munnidae*, as well as the cumacean family *Gynodiastylidae*. Southern and south-western segments are typified by *Sipuncula*, anemones in the family *Hormathiidae*, sponges of the families *Suberitidae* and *Leucaltidae*, ophiuroids in the genera *Amphiophiura* and *Ophiomusium*, and octocorals of the genus *Umbellula*.

When individual phyla were analysed, only the Arthropoda produced similar results to the all taxa analysis (Figure 9.6 and Figure 9.7). Similar groupings could also be seen in the ordination for Echinodermata (Figure 9.6), although the second stage ordination suggests that this pattern is less similar to the all taxa pattern than those produced for Chordata, Cnidaria and Mollusca. The Porifera, Bryozoa and *Sipuncula* produced the most dissimilar results, although these three phyla all had very low sample sizes (Table 4.3).

9.4 Discussion

There was a clear concordance between the historical museum data and the newly collected beam trawl survey data, with the latter grouping with geographic segments within which they were contained in both the ordinations and the cluster analyses at the species, genus and family levels. Although less obvious, this pattern persisted at the class and even phylum level, despite the analyses being based on the presence/absence of only 8 phyla. While the survey data only have very limited spatial coverage in comparison to the museum data, this concordance suggests that biogeographic patterns based on the latter are likely to be robust, despite the ad hoc nature of the data collection, and the disparate taxonomic treatment of the resulting samples. Given the time and expense of collecting dedicated survey data from deep waters, and the subsequent effort required to work up the taxonomy, the use of existing data is really the only feasible option for examining deep-sea biogeographic patterns over any meaningful spatial scale.

The assemblages present in the central GAB (d, e) were most closely related to those further east on the southern Australian continental slope (f, g, h), and then to the western GAB (c) and south-west corner of Australia (a, b). Assemblages off south-eastern Tasmania (i) appeared to be intermediate between southern Australia and the south-east (j-r), although the cluster analysis indicates that the transition between h and i is the biggest break point. There is another transition around the border

between Victoria and New South Wales (NSW) (r-u), with the remainder of the NSW coast forming a distinct and fairly tight group. The one exception was segment ab, which was an outlier in the species, genus and family level analyses. This segment had the lowest number of records (368, compared to the next lowest being 441), possibly indicating that this is insufficient to properly characterize it. The transition between h and i appears to correspond to the bifurcation between the eastward flowing Zeehan Current, and the south flowing East Australian Current (EAC) (Middleton and Cirano, 2005). The former would promote dispersal of the southern Australian fauna around to the south-east of Tasmania, while the latter would act as a barrier to dispersal further up the Tasmanian coast. The EAC would promote strong connectivity between north-east Tasmania and the east coast of mainland Australia. With the strength of the EAC increasing in recent times, it is possible that this eastern Australian fauna will move further south, as has already been well documented in shallower waters (e.g. Ling et al., 2009). The differences between the fauna off north-east Tasmania and Victoria on the one hand, and NSW on the other, may relate to the Bass Strait Cascade, which results in an outflow of warm salty water down the slope in this region (Middleton and Black, 1994).

There have been two previous studies of biogeographic patterns in southern Australian deepwater fauna, one for fish (Last et al., 2005), and the other for ophiuroids (O'Hara, 2008). The patterns found here are broadly in agreement with these two single taxon analyses, although with some differences. Both indicate a southern Australian province that extends further west than our central GAB province, incorporating segment c, and for fish some of segment b, and then a south-west zone in segment b, with segment a being part of a larger central western province. To the east, the southern province and for fish a transition zone, includes segment f and some of g. There is then a Tasmanian province roughly corresponding to segments g and h (and into l for fish). The east coast of Tasmania and the NSW coasts then form 2 additional provinces. Both of these previous studies used point source data to model the distribution of each species considered, and put considerable effort into examining specimens to ensure consistent taxonomy, whereas we were interested in determining if museum data were sufficiently robust to determine biogeographic patterns without this extra work, although it should be noted that our analyses would have benefited from updated taxonomies of fish and ophiuroids that resulted from the previous studies. Our patterns are also broadly consistent with the global biogeographic provinces proposed for the lower bathyal (800-3500 m) by Watling et al. (2013) based purely on modelled environmental variables (temperature salinity, dissolved oxygen and particulate organic carbon flux). They propose an Indian province that extends across western and southern Australia, a subantarctic province that includes southern Tasmania, and a New Zealand-Kermadec province that includes temperate and sub-tropical eastern

Australia. In intertidal and shallow subtidal waters, there are well documented phylogeographic breaks off eastern Victoria, southern NSW, south-eastern Tasmania and between the central and eastern GAB (Colgan, 2016). Interestingly, these all appear to coincide with biogeographic breaks found here, including the two major breaks off south-eastern Tasmania and eastern Victoria.

In Section 11, we take another approach to using existing data, in this case historical catch data, to examine the distribution of assemblages in the GAB itself. This analysis is consistent with what we present here, with the central GAB being distinct from the eastern and western GAB, and by chance, the break points are identified as where the boundary between segments c and d in the west and e and f in the east occur.

A clearly obvious pattern in the museum data is the vast preponderance of records from the eastern coast of Australia compared to the south and south-west. Of the 20327 records used in total, <3000 were from the extensive southern coastline, while >16000 were from the east coast. Particularly well sampled areas lie off the central east coast of Victoria and the NSW coast between Jervis Bay and Sydney. The additional 1853 records from the beam trawl survey thus represent almost half of the data available from southern Australia, although only covering a very small proportion of this region. As a consequence, the resolution along the southern coast is very low, and the boundaries between different biogeographic provinces may not be well demarcated. This lack of resolution may also account for the identification of a single large south-western province, compared to several smaller provinces in previous biogeographic analyses based on single taxonomic groups (Last et al., 2005; O'Hara, 2008). There is clearly a need for a substantial increase in survey effort in the southern and south-western Australian region if we are to properly understand the fauna present. This bias is likely to be related to Australia's major population centers, and hence largest museums and other marine research organisations, and its longest standing fishery all lying on the east coast.

We have not considered the potential for different depth biomes to be present in our analyses, primarily due to the rapid decline in number of records as depth increases making sample sizes potentially inadequate along the southern Australian coastline. Biogeographic provinces along southern Australia, which are based on demersal fishes, differ substantially between the shelf (<200 m deep) and upper slope (200-1200 m) (Commonwealth of Australia, 2006). However, while there were substantial differences in taxa present in different depth biomes (50-1500 m depth), O'Hara (2008) found broadly consistent biogeographic patterns for ophiuroids. Similar results have been found for galatheid squat lobsters in the Pacific Ocean, with factors structuring biogeography apparently the same on the continental slope (200-900 m depth) and continental rise (>900 m)

(Macpherson et al., 2010). In contrast, at a global scale, there are substantial differences in diversity pattern in ophiuroids above and below 2000 m depth (Woolley et al., 2016).

Classification of a fauna into biogeographic provinces depends very much on the scale of the study. For example, although O'Hara (2008) identifies a number of provinces in southern Australia, based on Australian data only, O'Hara et al. (2011) identify only 2 depth dependent strata when undertaking an analysis across the broader Australasian region, with the bathyal province being shared with New Zealand. Similarly, a global analysis of seamount fishes groups south-eastern Australia with New Zealand (Clark et al., 2010).

At the individual phylum level the Arthropoda produced the most similar patterns to those seen in the all taxa analysis. While this may be partly explained by sample size, there were more mollusc records in the data set than arthropods. Each of these phyla had approximately double the number of records as the next two most common (Echinodermata and Chordata (fish)), although both of these groups were as good as the molluscs at replicating the overall pattern. Even the Cnidaria, with 8-9 times fewer records than the Mollusca and Arthropoda, replicated the overall pattern as well as the Mollusca. Thus rather than being an artefact of sample size, it appears that the differences between phyla may be real differences in biogeographic structure, although this needs to be confirmed by more detailed analysis of these phyla along the lines of those that have been conducted for fishes (Last et al., 2005) and ophiuroids (O'Hara, 2008). The lack of biogeographic patterns in the Porifera, Bryozoa and Sipuncula is likely to be related to low sample size, however, with all of these taxa accounting for <1.5% of the total number of records used. As different taxa can differ in their life-history strategies, it is not axiomatic that all will show similar biogeographic patterns. For example, O'Hara and Poore (2000) showed some differences between echinoderms and decapods in southern Australia, and Piacenza et al. (2015) have shown different patterns of diversity between taxa on the United States west coast.

Overall, there are strong similarities between the biogeographic grouping found here, and those found in previous detailed studies of fishes and ophiuroids, and the limited comprehensive survey data available for analysis also suggests that the patterns found are real. An alternative explanation is a bias in the availability of electronic records towards different taxa in different regions. For example, the dominant influence of gastropods on the grouping of east coast segments may be related to either sampling in this region being influenced by a strong interest in this group, or alternatively subsequent taxonomic work-up, and databasing, being influenced in this way. Differences in substrate type sampled in different regions may also play a role. The survey data from the central GAB used here all came from soft sediment areas, but the museum data includes

specimens collected off hard substrate, although this information is often absent from the record and can only be confirmed if records can be matched to a publication (for example, data from hard substrates on seamounts off south-eastern Tasmania (Koslow et al., 2001; Dunstan et al., 2012) and canyons in the GAB (Currie and Sorokin, 2014) are included in the analysis). Confirmation that the patterns documented represent biogeographic patterns will require additional survey data integrated across the 200-3000 m depth range examined here, especially from the east coast of Australia. Based on the results presented here, the central deep GAB appears to be unique, albeit with affinities with the fauna found in the eastern GAB, and around south-western Australia. There is a very clear distinction between the faunas in the south and south-west, and those present along the east coast.

9.5 Tables

Table 9.1 Data for holdings of deepwater temperate invertebrates (7 phyla) and fishes at Australian museums and used in the analysis.

Phylum	AM	MV	NTM	QM	SAM	WAM	Total
Arthropoda	2385	35	9	12	364	43	6313
Bryozoa	80	11		1	68		160
Cnidaria	225	114	38	18	351	4	750
Echinodermata	1090	1266			394	46	2796
Mollusca	5083	1202	7		127	226	6645
Porifera	35	6	3	126	93	17	280
Sipuncula	22	4			7		33
Fishes	3343			7			3350
Total	12263	2638	57	164	1404	336	20327

9.6 Figures

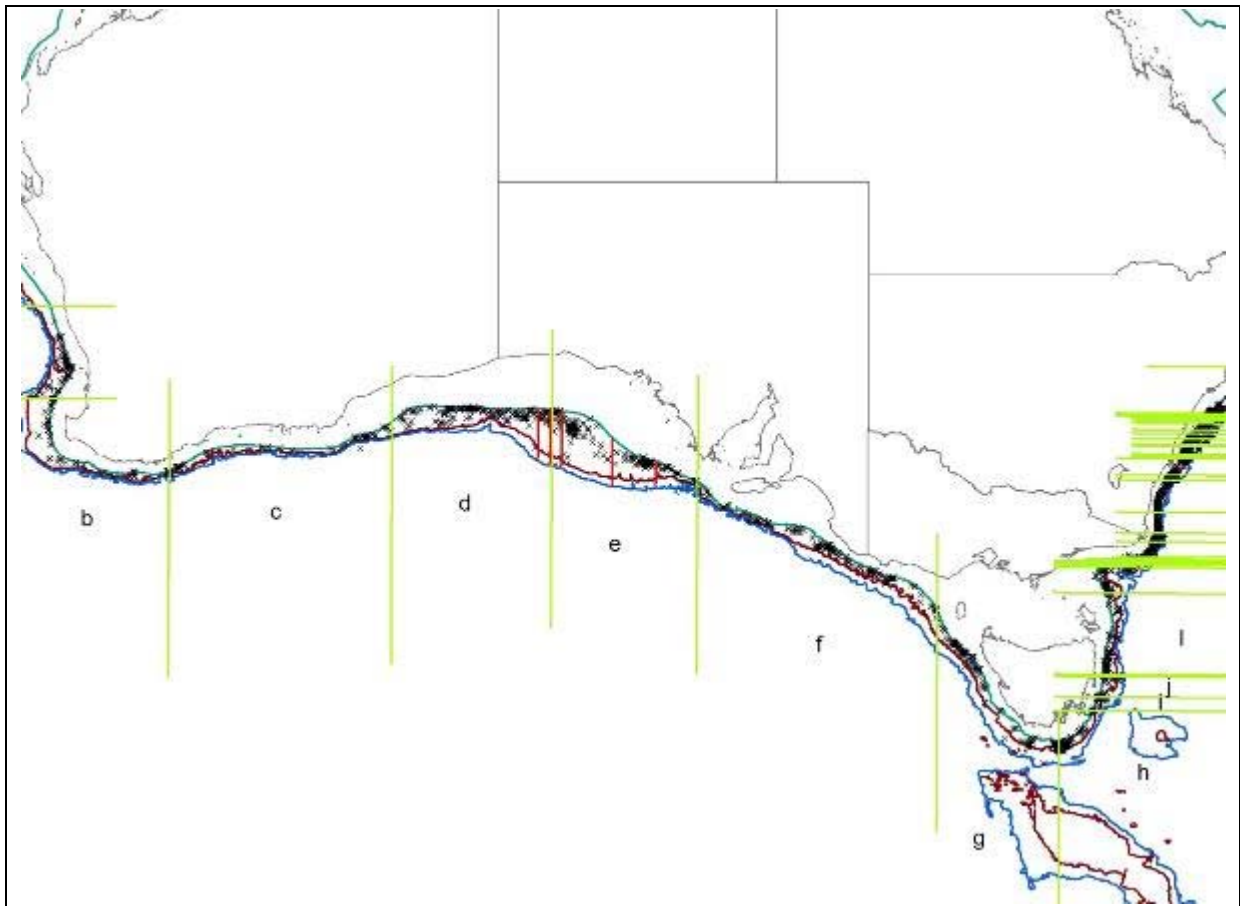


Figure 9.1 Map of southern Australia showing geographic distribution of samples represented in museum collections (black crosses), with geographic segments used for multivariate analysis (indicated by green vertical/horizontal lines and letters – missing letters indicate that the segment is too small to label). Inner, mid and outer bathymetry contours are 200, 2000 and 3000m respectively. Red vertical lines in segments d and e indicate location of the GAB benthic transects (T1 to west, T5 to east).

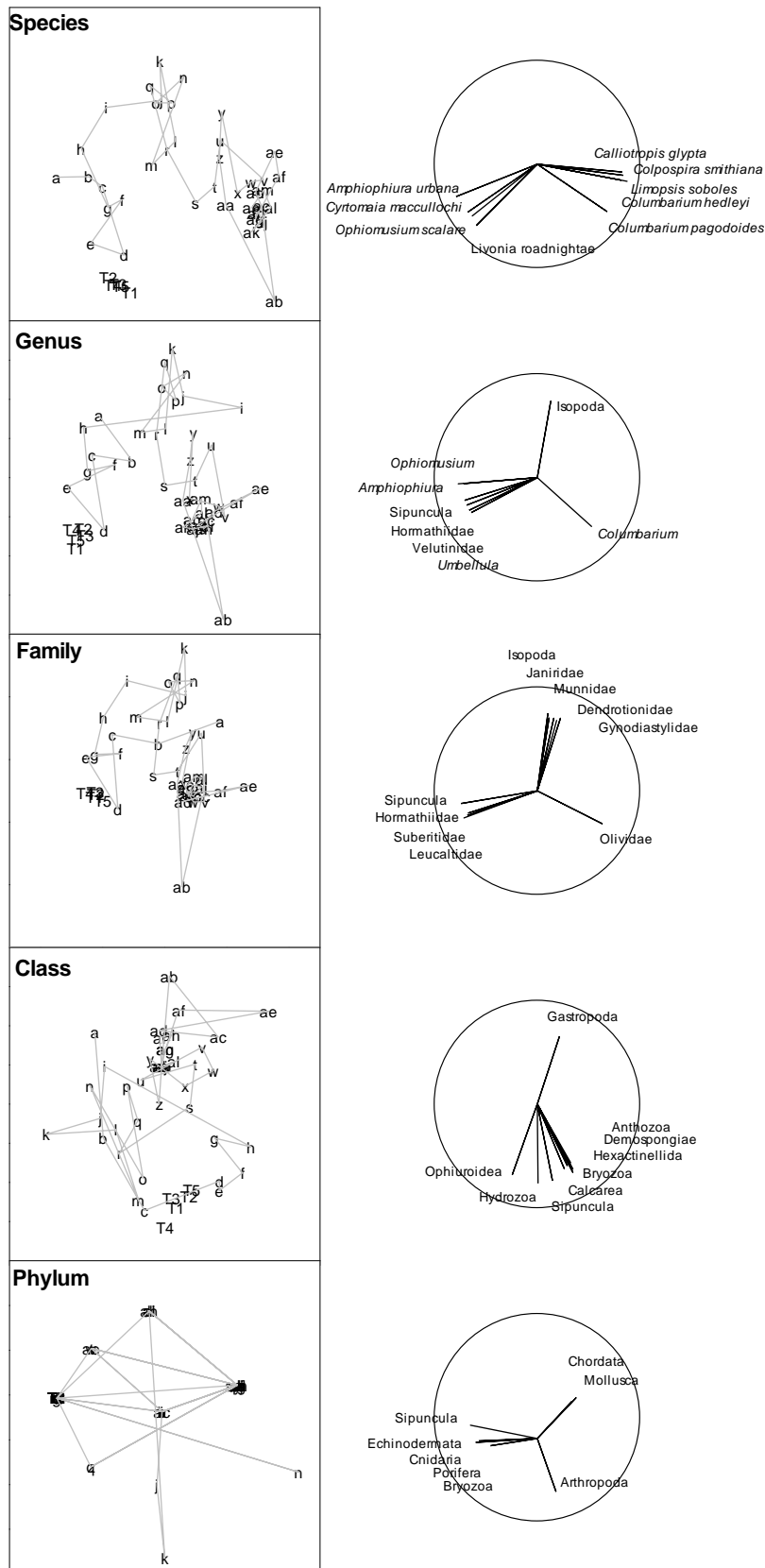
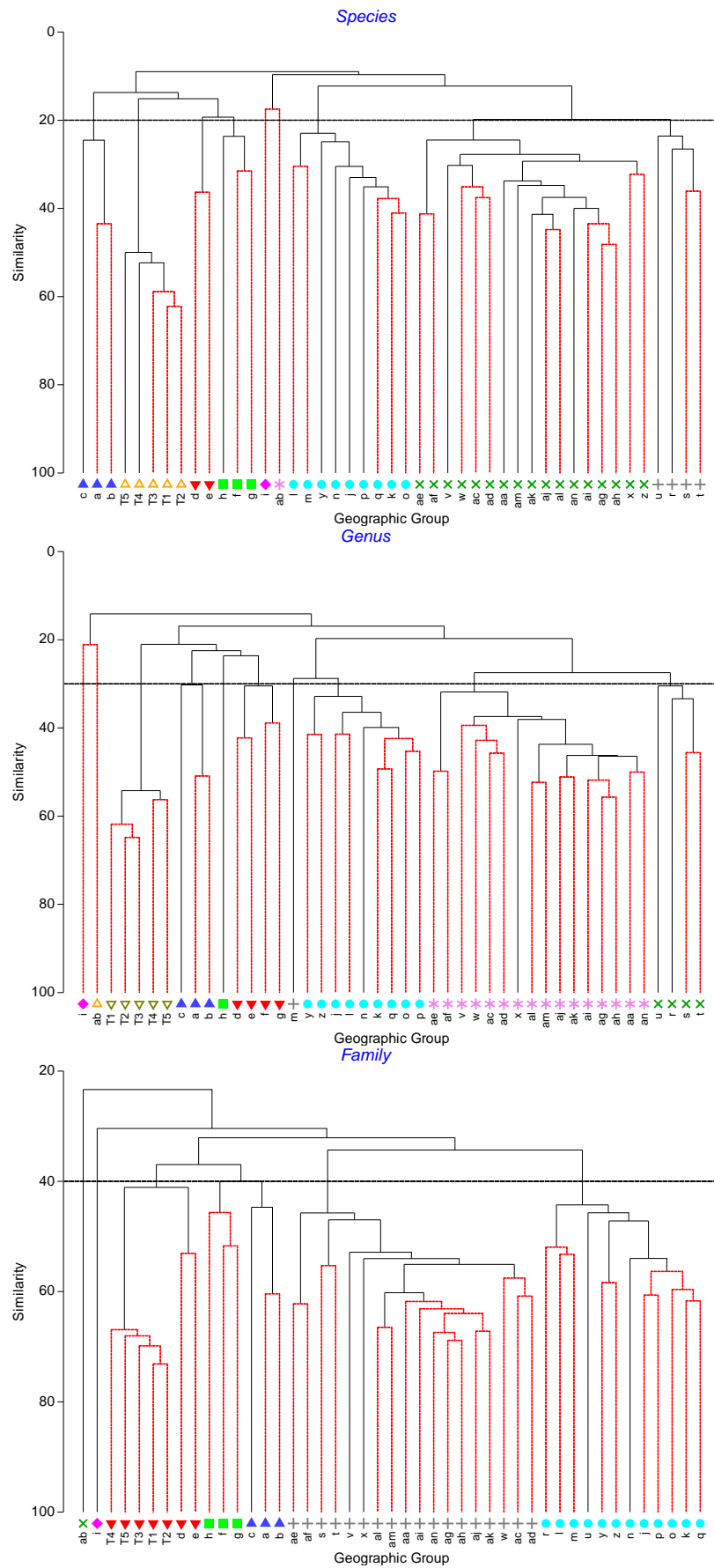


Figure 9.2 Nonmetric Multidimensional Scaling ordination plots showing biogeographic patterns in deep-sea benthic assemblages around southern Australia (see Figure 9.1 for geographic locations of each point). Biplots indicate taxa most highly correlated to the nMDS axes, with the circle representing a correlation of 1.



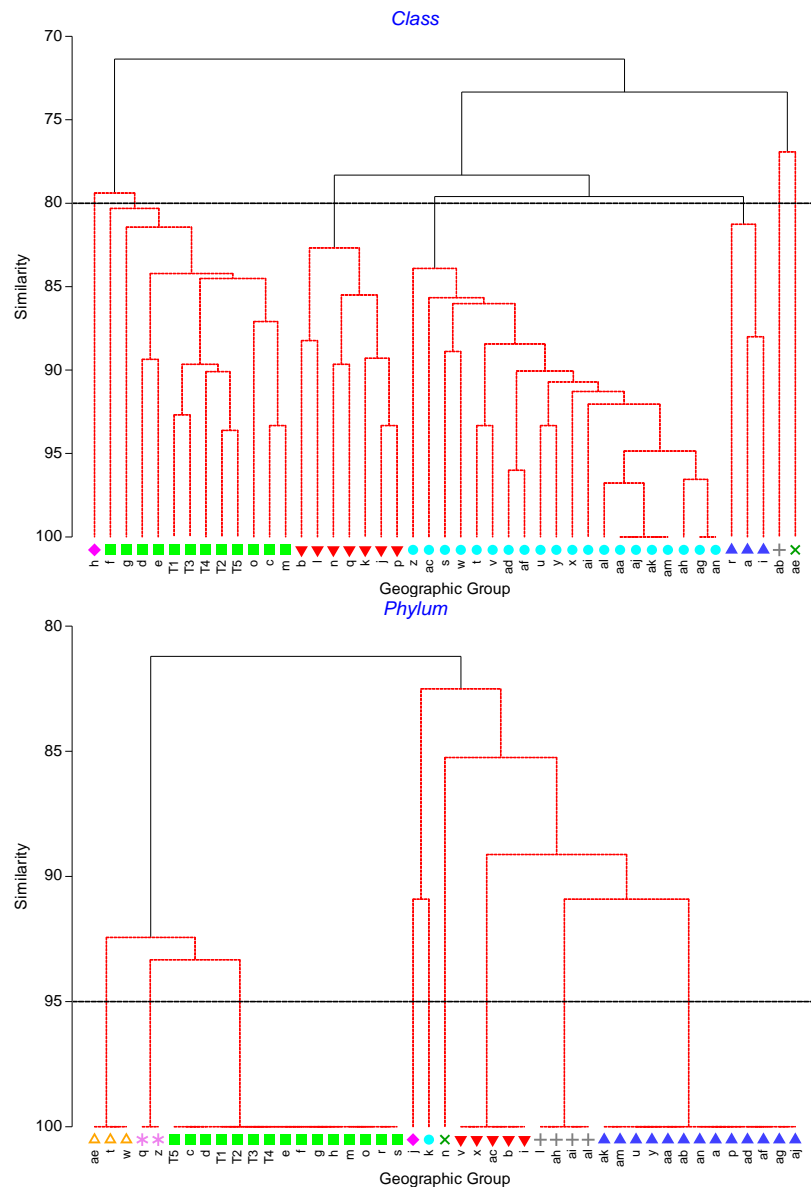


Figure 9.3 Cluster analysis of southern Australian deep-sea benthos at different taxonomic levels. Red lines indicate groupings that do not differ at the 5% significance level.

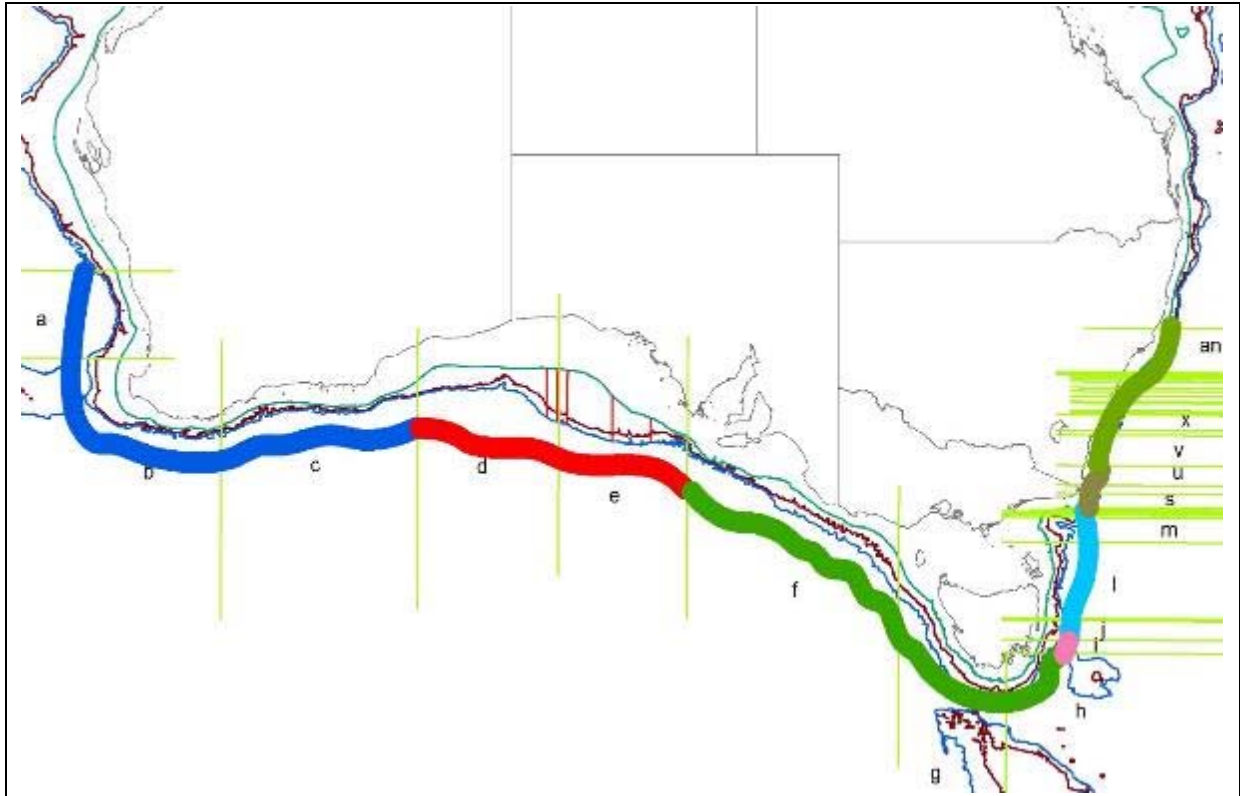


Figure 9.4 Map of southern Australia showing biogeographic zones based on the multivariate analyses at the species level. Zone boundaries are based on a similarity cut-off of 20% in the cluster analysis (Figure 9.3).

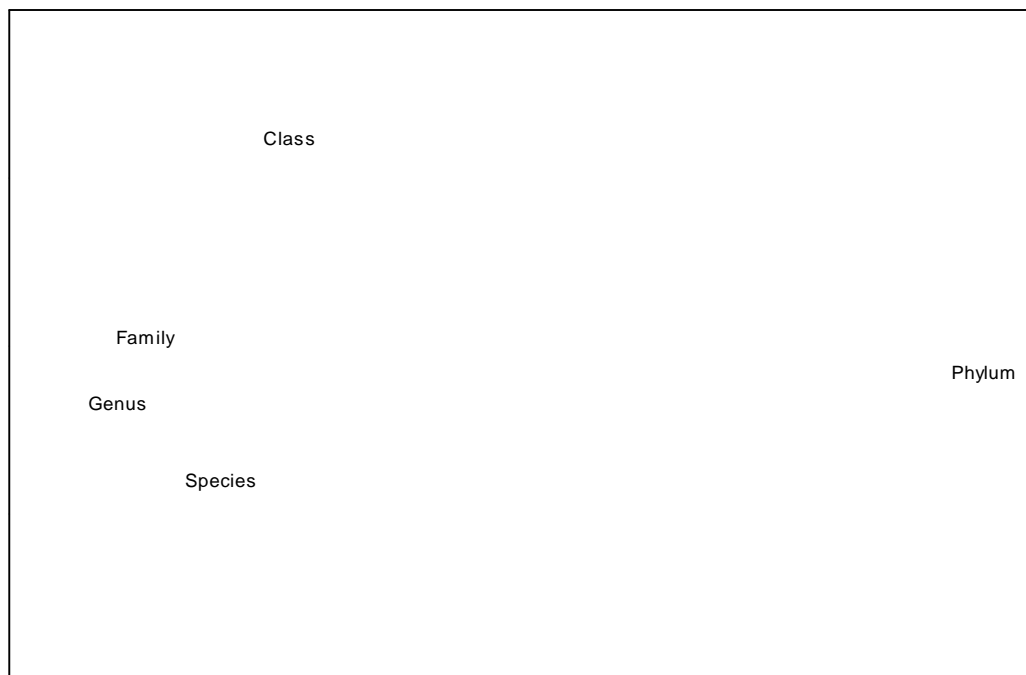


Figure 9.5 Results of the second stage nMDS showing degree of concordance in biogeographic patterns at different taxonomic levels. Points that are close together indicate that the analyses at the respective taxonomic levels (i.e. the plots in Figure 9.2) show very similar patterns, while those that are more distant do not show similar patterns.

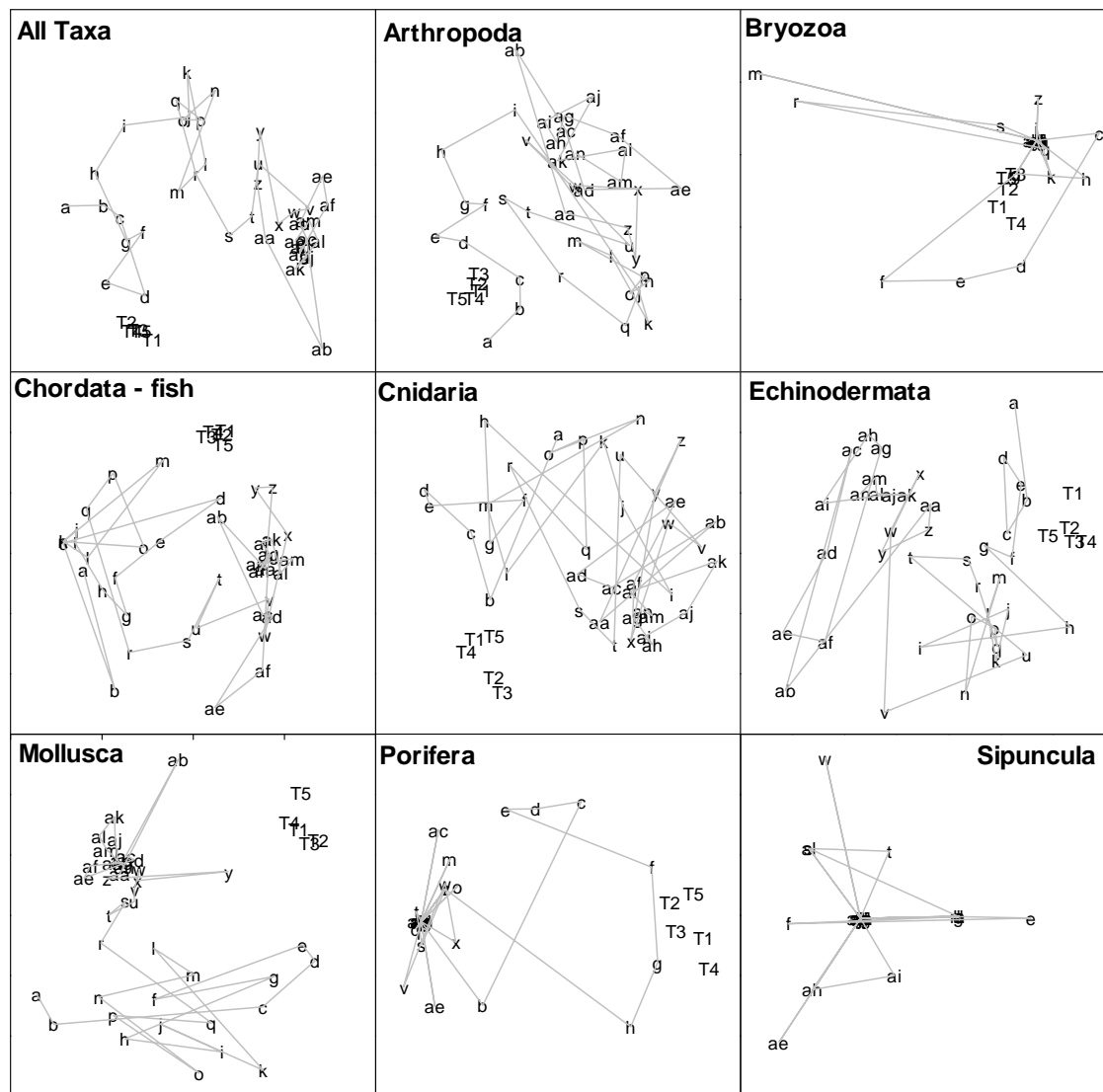


Figure 9.6 Nonmetric Multidimensional Scaling ordination plots showing biogeographic patterns in individual phyla around southern Australia (see Figure 9.1 for geographic locations of each point).

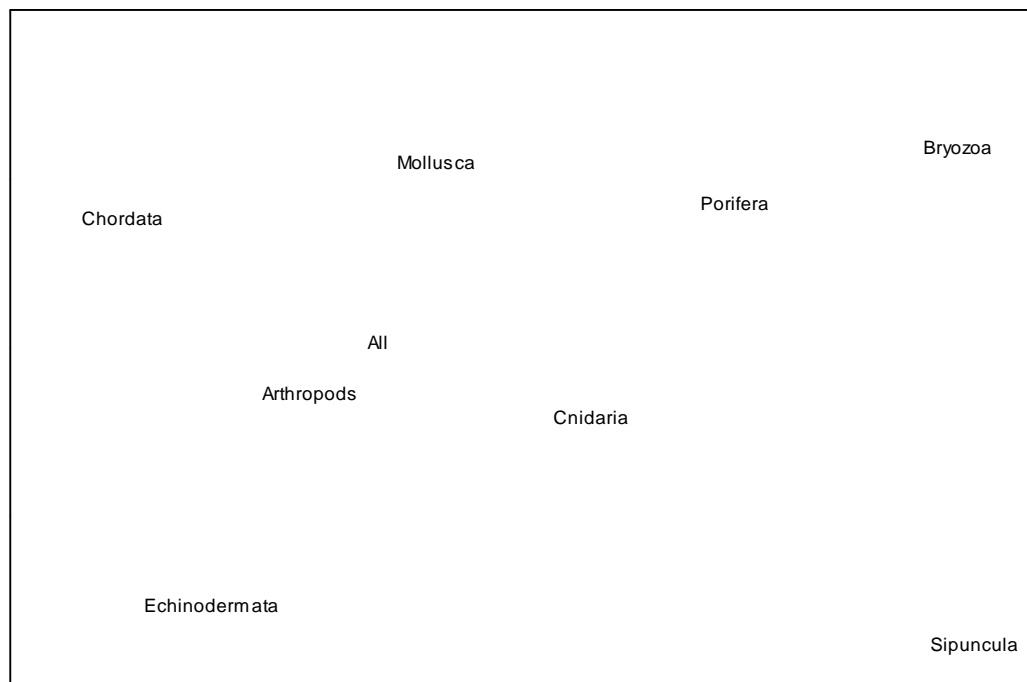


Figure 9.7 Results of the second stage nMDS showing degree of concordance in biogeographic patterns in different phyla. Points that are close together indicate that the analyses at the respective taxonomic levels (i.e. the plots in Figure 9.6) show very similar patterns, while those that are more distant do not show similar patterns.

10 Assessing environmental suitability of the GAB region for key deep-sea benthic taxa using species distribution modelling

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10.1 Introduction

10.1.1 Background

As part of the Great Australian Bight Research Program (GABRP) benthic biodiversity characterisation research project, existing information on the deep-sea (>200 m depth) epibenthos and demersal fish present in both the Great Australian Bight (GAB) region and other temperate Australian deep water biomes was collated (see Sections 4 and 9). These historical data were supplemented with faunal collections made from the RV *Investigator* (IN2015_C02; see Section 2.3) in late 2015. These efforts have increased our understanding of the assemblages that occur in the GAB, but sampling of the entire region is unfeasible, so some areas remain poorly characterised.

Species distribution modelling (SDM), where models are developed based on recorded species presences linked to environmental data, can be used to predict habitat suitability of unsampled areas (reviewed below). SDM was employed for several representative taxa using the collated historical data and GAB survey data, supplemented with records from online databases, to predict the potential distribution of key benthic fauna across temperate Australia, including the GAB region.

10.1.2 Objectives

Our aim was to produce species distribution models for key taxa representing common components of deep water benthic assemblages that may be important for informing biogeographical patterns. Specific objectives were:

- Identification of regions of suitable habitat for one or more species;
- Comparison of habitat suitability of the GAB region with broader temperate Australia for key benthic taxa;
- Identifying informative environmental indicators of species distributions.

10.2 Review of Species Distribution Modelling

Species Distribution Modelling (SDM) has become a common technique to predict the distribution of terrestrial species at different scales (over 300 citations per year in 2008 (Robinson et al., 2011)), but is still relatively uncommon for marine species (only ~ 100 citations total by 2008, the vast majority

for fish and mammals (Robinson et al. 2011)). There have been 18 SDM studies in the deep sea to date, primarily focused on corals (Vierod et al., 2014), with one on sea urchins (Gonzalez-Irusta et al., 2015), one on canyon associated fish (Sigler et al., 2015) and another on snapper (Gomez et al., 2015). SDM is also variously referred to in the literature as Environmental Suitability Modelling (Azzurro et al., 2013), Habitat Suitability Modelling (Bellamy et al., 2013), and Ecological Niche Modelling (Drake, 2014) among other names. SDM is also broadly equivalent to used-available analysis, which examines habitat use of individuals at a fine scale in more detail (for example, what habitats might be preferred within a home range - e.g. Warton and Aarts, 2013). A good overview of SDM without any technical or methodological details is given by Elith and Leathwick (2009). In the GAB, we are interested in the potential for SDM to be used to analyze the records of benthic invertebrate taxa collated from Australian museums, supplemented by our own collection efforts. SDMs can be used to predict where a species will occur, predict the potential distribution of an invasive species (e.g. Azzurro et al., 2013), and predict how a species distribution might change with changing environmental factors (such as with climate change e.g. Fand et al., 2014). These predictions fall into two broad categories – interpolation and extrapolation, with the latter being more problematic as it goes beyond the range of the data used to build the models (Elith and Leathwick, 2009; Merow et al., 2013). An alternative (or complementary) approach would be to model the distribution of community-level characteristics (e.g. species richness), rather than the distribution of individual taxa (reviewed in Ferrier and Guisan, 2006).

SDMs can be categorized in various ways, with two of the major dichotomies being based on their modelling approach and the type of data used. Models can be broadly classified as correlative, mechanistic or hybrid (Robinson et al., 2011). As the name implies, correlative models correlate the known species distribution with a range of (typically) environmental factors for which data are broadly available over the area of interest (generally in GIS format). Conversely, mechanistic models employ detailed knowledge of the biotic mechanisms that underpin a species distribution (for e.g. temperature and salinity tolerance), while hybrid models combine both approaches. Most published SDMs utilize presence/absence data, and therefore rely on the availability of comprehensive survey data that provides not only reliable documentation of where a species is present, but also where it is absent. Increasingly, however, SDMs are being developed with presence-background data (sometimes also erroneously called presence-only, or presence-pseudoabsence). These models take advantage of large databases available from museums and herbaria that provide extensive records of where individual species are found, but generally lack any details about where it has been looked for and not found. They also utilize data on the physical habitat at both the locations where the species has been documented, and at a broad range of locations where no information is available

(the background). Data are usually aggregated into equal-sized grid cells for analysis. True presence-only models only utilize environmental data from where the species is found, and do not include any background data in model development (e.g. Drake, 2014). A limited number of models also use abundance data, again generally relying on comprehensive surveys to provide this, which can substantially improve performance (e.g. Howard et al., 2014). Bradley (2016) compares presence only models to abundance models, and shows that high probability of species occurrence does not necessarily equal high probability that the species will be abundant. A good overview of how to match SDMs to their intended purpose is provided by Guillera-Aroita et al. (2015), who also point out that the common practice of converting continuous output into a presence/absence map is often not justified.

In the context of the benthic theme of the GAB Research Program, the primary interest is in presence-background modelling, since we have access to occurrence data but explicit data on absences is lacking, so the focus of this review is on this approach. The discussion is restricted to correlative techniques, as we know little about the species of interest and do not have sufficient data to develop mechanistic or hybrid models.

The most common approach to correlative SDM with presence-background data is to use maximum entropy modelling (reviewed in Elith et al., 2011; Merow et al., 2013), typically implemented in the Java software MaxEnt (Phillips et al., 2006; 2017), either directly, or via R packages (e.g. dismo; Hijmans et al., 2016). MaxEnt provides more accurate predictions than other methods, is relatively easy to use (Merow et al., 2013; Gomez et al., 2015), and can be as good as presence-absence methods in some cases (Gonzalez-Irusta et al., 2015). Yackulic et al. (2013) review the shortcomings of a range of published MaxEnt studies. Multivariate Adaptive Regression Splines (MARS - Elith and Leathwick, 2007; Gomez et al., 2015), Spatial Point Process Models (Dorazio, 2012), Low-Bias Bagging (Drake, 2014), Bayesian linear logistic regression (Tonini et al., 2014), Boosted Regression Trees (BRT - Elith et al., 2006; Elith et al., 2008), Bayesian Networks (Tantipisanuh et al., 2014), Classification Tree Analysis (Gomez et al., 2015) and Random Forests (RF - Howard et al., 2014) have also attracted some interest, although are less well developed, especially in the latter two cases for presence-background data. Elith et al. (2006) compare and review a range of other methods. One potential advantage of MARS is that it can be used for multiresponse modelling (i.e. for multiple species at once), which has been found to perform slightly better than single species models (Elith and Leathwick, 2007). This can be particularly useful in cases with limited data for a number of species. Point Process Models (PPMs) have been proposed as having advantages for model fitting, and unlike other methods, don't require the region of interest to be divided into a set of grid cells, but work directly on the spatial location of each presence record; they also provide a theoretical

basis for choosing the number of background points to include in the analysis (Renner et al., 2015). MaxEnt is a special case of PPM.

Data required include the locations of known occurrences of the species of interest, and environmental data as GIS layers. Typical environmental data utilized for marine SDM include depth, surface salinity, sea surface temperature (SST), SST Standard Deviation, Chl a, Chl a SD. These parameters for example, explained 80% of the variation in the distribution of an invasive fish species in the Mediterranean (Azzurro et al., 2013). Correlation between explanatory variables (collinearity) causes several issues with model fitting and interpretation of SDMs (Braunisch et al., 2013; Dormann et al., 2013). The preferred approach for selection of environmental variables is based on ecological knowledge (Dormann et al., 2013), but where this is lacking, the variable with greatest predictive power from each correlated set can be used (Dormann et al., 2013; Merow et al., 2013; Syfert et al., 2013).

A major issue for SDM using existing ad-hoc data is that the geographic (and hence likely the environmental) distribution of samples is likely to be biased (Yackulic et al., 2013). In marine systems, for example, it is easier to sample shallow waters close to the coast and population centers than it is to sample remote deep waters (e.g. Robinson et al., 2011). This is only a problem for presence-background models, and not presence-absence, as in the latter both presences and absences are similarly biased, cancelling each other out. If this bias is not accounted for, it can generate bias in the predicted distributions (Phillips et al., 2009). If the bias is known, it can be accounted for directly (e.g. if we know sampling effort decrease linearly with depth, we can include this in the model) (e.g. Warton et al., 2013). For most situations, however, including the GAB, this bias is not known. Instead, a target-group background can be used, where rather than randomly selecting background points, points are only chosen from those at which other similar species have been collected, also known as inventory pseudo-absences (Elith and Leathwick, 2007; Phillips et al., 2009; Elith et al., 2011; Merow et al., 2013). A key assumption in doing this is that the survey methodology is approximately the same for all species in the target group. This is likely to be broadly true with the macro-invertebrates and within the fish, but there is some potential for it to differ between these groups, particularly if surveys only document one or the other group. The target group should be as broad as possible, however, since having too few background points (less than ~6,000) can lead to dampened predicted responses of the modelled species (Phillips and Dudík, 2008; Phillips et al., 2009; Merow et al., 2013).

Another approach to help deal with sampling bias, and take advantage of extensive presence only data sets along with smaller presence-absence data sets is to pool both (Fithian et al., 2015). This

requires that sampling bias is the same across all species being considered. As well as helping correct for sampling bias, this technique can improve precision even when no bias exists, and can be utilized when there are presence-absence data for only some species of interest. MARS allows a different approach to combining both types of data into a single analysis (Choe et al., 2016; Hermoso et al., 2015). Hui et al. (2013) present another approach to modelling community data, using Species Archetype Models to jointly model multiple species, including two marine data sets, based on either presence-absence or abundance data. This approach improves model accuracy and discriminatory capacity compared to multiple single-species SDMs, especially for rarer species. D'Amen et al. (2015) extend stacked SDMs for community modelling by incorporating information on species traits to reduce over-prediction of species richness. Spatial factor analysis is another alternative, although requires actual assemblage data, so may be suitable for survey data, but not for the museum data, and again is more accurate than a series of single species SDMs (Thorson et al., 2015). Given the limited sampling effort at each site, and the fact that we have sampled only ~25% of the number of species that our data suggest are there, our sampling effort is unlikely to be sufficient for us to have any confidence that species not sampled are actually absent. Warton et al. (2015) provide an overview of joint SDM.

A second important consideration in selecting the background is in determining its spatial extent. If the spatial extent is too large and takes in habitats that are not available, then the models may not be accurate (Elith et al., 2011; Merow et al., 2013). In the GAB context, this means that we need to be careful in setting latitudinal limits along the east and west coasts of Australia, to ensure that we don't include subtropical/tropical habitats. It also means that we should restrict models to southern Australia, and not include for example New Zealand or South Africa.

One consideration with presence-background SDM is that without strong assumptions (or data) about prevalence (i.e. the proportion of available sites that a species occupies), the outputs can only be interpreted as relative indices of occurrence, and not absolute probabilities (e.g. Elith et al., 2011; Phillips and Elith, 2013; Yackulic et al., 2013). While newer techniques can reportedly overcome this issue (Merow and Silander, 2014), they are reliant on a large number of samples (~ 2000). A logistic output option is available in MaxEnt (Phillips and Dudík, 2008) but the assumptions behind this conversion have been criticised, and it should not be interpreted as probability of presence despite being on the scale 0-1 (Royle et al., 2012; Merow et al., 2013; Yackulic et al., 2013; Merow and Silander, 2014). The raw output is therefore recommended where MaxEnt is used, but as it is dependent on the number of points (presence and background) used, it is not comparable between models built with different numbers of points (Merow et al., 2013; Yackulic et al., 2013). The raw

output can, however, be scaled using the number of points to allow comparison. This output has been termed probability-ratio output (PRO) (Halvorsen, 2013; Halvorsen et al., 2015)

Imperfect detection can also cause problems with SDM, leading to bias in model predictions (Lahoz-Monfort et al., 2014; Yackulic et al., 2013). This is particularly so if detection is related to a covariate that is independent of those driving occupancy, as the former will then be included in the SDM leading to poor model performance. If detection probability is constant or positively correlated with occupancy, then the SDM output will still give valid rankings for habitat quality. For the GAB, detection probability is probably fairly constant for our data, but likely highly variable for the museum data. Testing and correcting for this issue relies on having multiple samples from each location – which we don't have.

The default methods employed by MaxEnt have sometimes been criticised for producing overly complex models, leading to poor transferability of the model over space or time, and difficulty in interpretation of ecological responses (Warren and Seifert, 2011; Syfert et al., 2013; Radosavljevic and Anderson, 2014; Halvorsen et al., 2015;). More parsimonious models may be produced by species-specific tuning of MaxEnt's regularisation parameter (Anderson and Gonzalez Jr, 2011; Muscarella et al., 2014; Radosavljevic and Anderson, 2014), restricting the types of transformation applied to environmental data ('feature types') within MaxEnt (Elith et al., 2010; Merow et al., 2013; Syfert et al., 2013), or using step-wise variable selection under a maximum likelihood (ML) interpretation of the maximum entropy algorithm (Halvorsen, 2013; Halvorsen et al., 2015; 2016; Mazzoni et al., 2015). Increasing regularisation simplifies models but results in biased parameter estimates (Royle et al., 2012; Dormann et al., 2013; Halvorsen et al., 2015) and can lead to over-generalised predictions (Ashford et al., 2014; Radosavljevic and Anderson, 2014). Species-specific tuning is generally impractical when developing models for a large number of species (Merow et al., 2013). There can sometimes be problems fitting SDMs when using ML estimates for Poisson point processes, including MaxEnt, when presence only data are used. Alternative estimators are available (Hefley and Hooten, 2015). There are also methods for assessing data quality and its influence on model performance (Fei and Yu, 2016).

For mobile taxa, it would be possible to undertake multiscale modelling, where environmental parameters are derived at different spatial scales to determine at what spatial scales they are responding to (e.g. Bellamy et al., 2013). This, however, is probably more relevant for inshore species where habitats change more quickly.

True presence-only (or one-class) SDM might also be applicable to our own data, where we have data on sediment composition that is not available more broadly, and thus cannot be incorporated

into presence-background (or two-class) models. These models are more appropriately called Ecological Niche Models (ENM), as they cannot be used to predict the species distribution, but rather its association with the environmental factors included. This can then be used to predict the probability of occurrence at a new site where those environmental factors have been measured. Traditionally these techniques have been considered inferior to presence-background techniques, but this appears to be changing. Drake (2014) proposes a technique called Low Bias Bagging for Once Class classification (LOBAG-OC), which performed almost as well as MaxEnt, and better than other true presence only methods (DOMAIN and BIOCLIM), for the single species studied. Maher et al., (2014) examine a range of alternative presence-only methods and compare them to presence-background methods, and show that they give similar performance.

Once you have constructed an SDM, it can be important to establish where the greatest uncertainty in predicted species distributions arises from. Watling et al., (2015) show that 70% of the variation in their study is due to choice of model algorithm, and that other factors such as uncertainty in the predictor variables or the presence of the species all produce relatively minor variation.

Consequently, they recommend using multiple algorithms and examining where their predictions intersect. Ochoa-Ochoa et al. (2016) echo this view, and actually found that a consensus model best predicted species ranges. An alternative to a consensus model is an ensemble model, which averages over different model runs (e.g. Chefaoui et al., 2016).

As an alternative to SDMs, we could also undertake community-level modelling to examine the geographic distribution of parameters such as species richness. For example, Ballesteros-Mejia et al. (2013) collated records of moths into 200 km x 200 km grid cells, then used rarefaction curves and species richness estimators to estimate total species richness in each cell, which they then mapped. They also used spatially explicit regression techniques to relate richness to environmental factors. Dunstan and Foster (2011) used Rank Abundance Distributions to predict benthic biodiversity at depths of 100-1500 m along the WA coast. More advanced techniques actually model the whole community, and not just summary statistics (reviewed in Ferrier and Guisan, 2006), and thus include predictions of individual species distributions. These data can then be subject to the broad suite of univariate and multivariate analyses typically used for community level data. This approach is considered particularly advantageous when there are a large number of species, many of them rare (Ovaskainen and Soininen, 2011).

10.3 Methods

10.3.1 Modelling methods

To achieve our specific aims of constructing multiple SDMs for key taxa to identify regions of suitable habitat, compare habitat suitability of the GAB region with broader temperate Australia, and identify informative environmental indicators of species distributions, we chose to use presence-background maximum entropy models. This modelling was designed to complement the community level modelling performed specifically for the GAB region (Section 11). Our review (section 10.2) identified other potential modelling methods, but some (e.g. ensemble modelling) were impractical to apply over a large number of species, while others require presence-absence, assemblage or abundance data, which were not available in our data set. In addition to being suitable for our aims, MaxEnt can be run via R, allowing for automated running of multiple models (e.g. Merow et al., 2016; Zeng et al., 2016), making this approach practical for generating SDMs for a larger number of species than other methods.

To compare the various approaches recommended to avoid overfitting in MaxEnt, we assessed model outputs for a subset of species using a range of modelling options: default MaxEnt settings, feature types restricted to linear and quadratic only (Merow et al., 2013; Syfert et al., 2013), increased regularisation (Anderson and Gonzalez Jr, 2011; Muscarella et al., 2014; Radosavljevic and Anderson, 2014), and the forward selection based on ML interpretation (Halvorsen, 2013; Halvorsen et al., 2015; 2016; Mazzoni et al., 2015). Based on Akaike Information Criterion with small sample correction (AICc), calculated based on Halvorsen (2013), and Area Under the Curve (AUC) statistics produced by MaxEnt, the ML forward selection models were the best performing across the tested species. This method was therefore applied across all selected species. Exploratory and final modelling was performed using MaxEnt v3.3.3 run from batch files generated in R (R Core Team, 2016) using custom code or, for the ML implementation, the R package MIAMaxent (Vollering et al., 2016).

The R package MIAMaxent produces derived variables outside MaxEnt to provide greater control over the variable transformations used in models. For each environmental variable, five derived variables were produced: one linear (L), one monotonic (M) zero-skew transform, and three deviation type transforms (D0.5, D1, D2). The transformation functions used are described in Halvorsen et al. (2015), and the numeric suffixes of the three deviation variables represent use of values of $a = 0.5, 1$ and 2 in the deviation transform. These transformations were repeated independently for each species, since the deviation transforms aim to describe the distribution around the empirical optimum value (=mean at presence locations) of each environmental variable

(Halvorsen, 2013; Halvorsen et al., 2015). Following derivation of transformed variables, models were built in two steps (following Halvorsen, 2013; Halvorsen et al., 2015; Mazzoni et al., 2015): firstly the most parsimonious set of transformed variables was selected for each environmental variable, and then models built using combinations of environmental variables (each represented by the selected transformed variable set). Nested models were compared using F-tests, and more complex models were selected only when their predictive power was significantly greater than simpler models using an alpha of 0.01. The F-statistic was calculated based on the fractional variation accounted for (FVA) in models (“gain” in the terminology of Phillips et al., 2006) and degrees of freedom dependent on the number of points used to build models and number of parameters (total number of derived variables used). Variables were added to models in decreasing order of F-statistic value in single variable models. We did not include interaction terms as the number of presence records available was too low to support this.

The default output produced by MIAMaxent is PRO. A predicted PRO value of 1 reflects environmental suitability equivalent to that of an average presence point. Predicted PRO values were generated for each species over the entire model domain, i.e. over all raster cells for which environmental data were available. Due to the slightly different extents of environmental variables (see Figure 10.2 and Figure 10.3), the extent of predictions varied between species, depending on the variables in each final model. For each species, the variables selected in the model are listed in order of their selection (i.e., variables with greater F-statistic value are first), with the transformed variables used to represent each shown. For assessment of model performance, we present the total FVA of the final model, the training AUC obtained by the full model, and test AUC calculated by running four models per species using geographically stratified sampling, following the ‘checkerboard2’ method of Muscarella et al., (2014).

To illustrate patterns of environmental suitability across species through the region, we reclassified PRO values to scores as follows: PRO 0-0.5, low suitability (0), PRO 0.5-2, average suitability (1), PRO 2-10, above average suitability (2), PRO 10-100, high suitability (3) and PRO>100, very high suitability (4). We averaged classified suitability scores over all species and over species within each phylum to produce rasters of average suitability class, and extracted the average score for each 100 m depth band. Reclassified scores were used rather than PRO values to down-weight the influence of very high PRO values that were obtained for some species in some areas, which were likely the result of extrapolation to environmental values outside the range used for training. The classified suitability scores also illustrate areas where suitability is above average for multiple species, which otherwise could not be easily distinguished from areas with very high PRO values for a single species. PRO scores should also not be considered additive across multiple species, since PRO is a scaled measure

of relative occurrence rate, not an estimate of prevalence or probability of occurrence (Ferrier and Guisan, 2006). Estimation of prevalence, and thereby probability of occurrence, requires survey presence-absence data, or a large number (>2,000) of presence records (Elith et al., 2011; Merow and Silander, 2014; Phillips and Elith, 2013), which were not available for the deep water species considered.

10.3.2 Species occurrence records

Species occurrence records for deep (>200 m) water benthic species were obtained from compiled historical museum and survey catch data as described in Section 4 (historical data) and from benthic sampling conducted in the GAB on the RV *Investigator* charter (IN2015_C02) in late 2015 (Section 2.3) (GAB data). These two data sets were checked for up to date taxonomy using the World Register of Marine Species (www.marinespecies.org), and formed the basis for selecting representative species for modelling. To obtain sufficient records for use as background in models (described further below), additional records were obtained from online databases, specifically GBIF, with records accessed using the R package *rgbif* (Chamberlain, 2016), and iOBIS (<http://www.iobis.org/>); these records were also used to supplement species occurrence data, and provided records for depths <200 m, which were not included in the historical data set. Records were downloaded from these two databases only for taxonomic classes represented in the museum and GAB data and for the target area (30° to 46°S and 110° to 155°E). As records may occur in more than one data set, and since only one record per site is used in modelling, spatial duplicates were removed from the online database records. From the combined species records, we extracted the set of species that had at least 20 deep water records (i.e. from the historical and GAB data sets combined) and total sufficient records for modelling (minimum 50 spatially unique). There were 96 species from 5 phyla and 11 classes in this extracted data set. We selected two representatives from each class, being the species with the overall most records and the species with the most GAB records, with the following exceptions: three representatives were selected for the very diverse classes Malacostraca (Arthropoda) and Actinopterygii (Chordata), and also for the Ophiuroidea (Echinodermata), being a class of specific interest; only one representative was selected for Ostracoda (Arthropoda), Elasmobranchii (Chordata), Echinoidea (Echinodermata) and Scaphopoda (Mollusca) as these classes had few representatives in the extracted data set, and either the species with the most GAB records was the species with most records overall, or there were no species with GAB records in the extracted set. The 21 selected species are listed in Table 10.1 with the number of records (deep water, total spatially unique and number used in models) shown. The number of occurrence records used to build models was often less than the total number of spatially unique records due to some records falling outside the range of available environmental data, or some records falling into the

same environmental grid cells despite being spatially unique and therefore being redundant in models. Presence point locations for each species are shown in maps accompanying the model results (Figure 10.5 to Figure 10.8). Note that some modelled species have more records in the GAB region than suggested by Table 10.1; the GAB records shown in Table 10.1 are those specifically from the 2015 survey, so this total does not include records in this region from the historical data set or online databases.

To account for sampling bias, we used target-group samples (TGS) from the compiled data set to characterise the background environment. TGS records used for each species were of selected classes of the same Phylum, with a maximum of 10,000 records used in each case. The classes selected were any represented within the museum and GAB data sets, except for Mollusca, where class Cephalopoda was excluded since these were not compiled in the historical data and may not be relevant as TGS to less motile Mollusca, and Chordata, where only classes representing fish taxa were regarded as relevant, i.e. Actinopterygii and Elasmobranchii, and all other classes excluded. The TGS records for each phylum are shown in Figure 10.1. Only TGS (and presence) points falling within the range of available environmental data were able to be used in models. There were only 5,705 TGS records with environmental data for Cnidaria, but >10,000 for all other phyla.

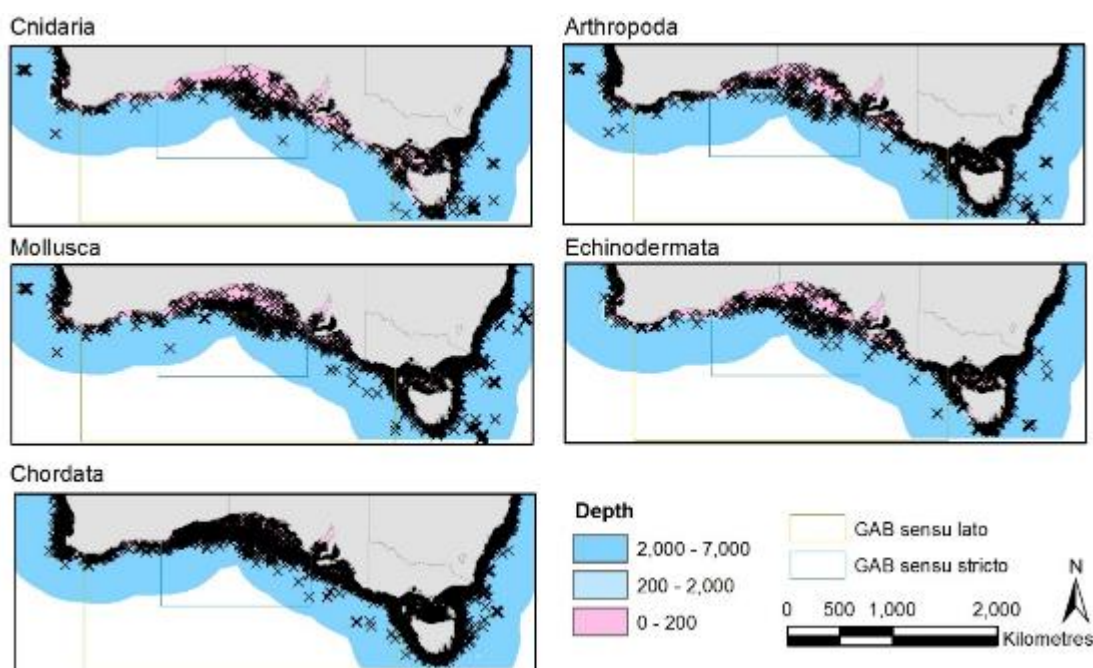


Figure 10.1. Maps of TGS locations for each Phylum used in models.

Table 10.1. Representative deep water taxa selected for modelling, showing taxonomy and number of deep water and total spatially unique records for use in SDM.

Phylum	Class	Order	Family	Species	Records >200 m (Historical/GAB)	Total records (used in models)
Cnidaria	Anthozoa	Scleractinia	Caryophylliidae	<i>Caryophyllia planilamellata</i>	30 (21/9)	67 (65)
			Flabellidae	<i>Flabellum hoffmeisteri</i>	49 (49/0)	93 (89)
Arthropoda	Malacostraca	Decapoda	Aristeidae	<i>Austropenaeus nitidus</i>	41 (28/13)	57 (54)
			Munididae	<i>Munida chydrea</i>	55 (55/0)	122 (119)
			Parapaguridae	<i>Parapagurus latimanus</i>	34 (19/15)	61 (61)
Mollusca	Bivalvia	Arcida	Limopsidae	<i>Limopsis soboles</i>	54 (54/0)	152 (147)
		Pectinida	Pectinidae	<i>Veprichlamys perillustris</i>	26 (21/5)	71 (69)
	Gastropoda	Neogastropoda	Borsoniidae	<i>Bathytoma agnata</i>	66 (61/5)	178 (168)
		Littorinimorpha	Ranellidae	<i>Sassia kampyla</i>	202 (202/0)	484 (460)
	Scaphopoda	Dentaliida	Dentaliidae	<i>Fissidentalium ponderi</i>	36 (33/3)	135 (134)
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	<i>Psilaster acuminatus</i>	50 (50/0)	114 (100)
		Forcipulatida	Zoroasteridae	<i>Zoroaster macracantha</i>	37 (35/2)	52 (51)
	Echinoidea	Camarodonta	Echinidae	<i>Echinus multidentatus</i>	68 (64/4)	103 (90)
	Holothuroidea	Elasipodida	Laetmogonidae	<i>Laetmogone violacea</i>	42 (42/0)	63 (63)
	Ophiuroidea	Euryalida	Asteronychidae	<i>Asteronyx loveni</i>	45 (45/0)	100 (93)
		Ophiurida	Ophiolepididae	<i>Ophiomusium lymani</i>	58 (24/34)	103 (103)
			Ophiuridae	<i>Ophiocten hastatum</i>	29 (15/14)	65 (65)
Chordata	Actinopterygii	Perciformes	Gempylidae	<i>Rexea solandri</i>	71 (71/0)	163 (137)
		Notacanthiformes	Halosauridae	<i>Halosauropsis macrochir</i>	22 (3/19)	56 (56)
		Gadiformes	Moridae	<i>Antimora rostrata</i>	28 (11/17)	59 (59)
	Elasmobranchii	Carcharhiniformes	Pentanchidae	<i>Apristurus australis</i>	29 (29/0)	71 (68)

10.3.3 Environmental data

Environmental data for southern Australia (latitude 30 - 46°S) was obtained from sources as described in Section 2 as 0.01° gridded data within Australia's 200 nm Exclusive Economic Zone (EEZ), and converted to raster files for use in MaxEnt models. The available data could be categorised as follows: bottom water parameters (temperature, salinity, water nutrients), satellite derived (light, chlorophyll, attenuation, sea surface temperature, and productivity variables calculated from these), sediment properties (carbonate, gravel, sand, mud content), bathymetry derived (depth, slope, aspect and terrain morphology probability categories) and seabed current stress. MaxEnt is able to use categorical variables, but we did not include the categorical terrain variables in the analysis since initial data exploration showed that they were almost invariable over the presence and background points, and would therefore not be informative. We also excluded current stress as the available data were of limited extent (depth <2,000 m); the benthic stress model outputs from GABRP Project 1.1 only covered the GAB, and so also could not be used. Bottom water data layers had some areas of missing data within the model domain, but these layers were retained as the missing data did not lead to the exclusion of many occurrence or TGS points. There are, however, gaps in model predictions corresponding to missing data locations where these variables were used in models.

Initial exploration of the environmental data showed that many of the variables were highly correlated ($|r| > 0.7$), and, given the large number of variables available (34 in total), a subset of candidate predictors should be selected for use in model building (Elith et al., 2011; Braunisch et al., 2013; Dormann et al., 2013). Knowledge of ecological importance of the available predictors to the modelled species is lacking, so we ran single-variable models across all selected species to determine the relative predictive power of each variable based on FVA. We selected the candidate set of environmental variables in order of predictive power, excluding variables that were correlated at $|r| > 0.7$ with any of greater predictive power. This resulted in a set of 16 candidate variables being selected for use in model building. These variables are shown in Table 10.2, and the scaled values of each of these predictors over the model domain is shown in Figure 10.2 and Figure 10.3. It should be noted that the selected variables are acting as proxies for the set of correlated variables, and the effects of these cannot be separated without additional data.

Table 10.2. Environmental variables included in the candidate set for modelling, and correlated excluded variables.

Variable used Name: Description	Correlated variables excluded ($ r > 0.7$)
<i>Bottom water parameters</i>	
TEMPav: Average temperature	Bottom temperature seasonal range, Depth, Average phosphate, Average nitrate, Average silicate, Average salinity, Oxygen seasonal range
O2av: Average oxygen	
SALsr: Salinity seasonal range	
PO4sr: Phosphate seasonal range	Nitrate seasonal range
SiO2sr: Silicate Seasonal range	
<i>Sediment properties</i>	
Crbnt: Sediment Carbonate%	
Sand: Sediment Sand%	Sediment Mud%
Gravel: Sediment Gravel%	
<i>Satellite derived</i>	
EPOCav: Average Exported Particulate Organic Carbon (EPOC)	EPOC seasonal range, Average benthic irradiance, Benthic irradiance seasonal range
K490av: Average diffuse attenuation coefficient	Diffuse attenuation seasonal range, Average Chlorophyll-a, Chlorophyll-a seasonal range
NPPav: Average Net Primary Productivity	
NPPsr: Net Primary Productivity seasonal range	
SSTmax: Sea surface temperature (SST) maximum monthly average	Annual average SST, Average photosynthetically active radiation (PAR), PAR seasonal range
<i>Bathymetry</i>	
Slope: Slope	
Ngrad/Egrad: Aspect (Northerly and Easterly components)	

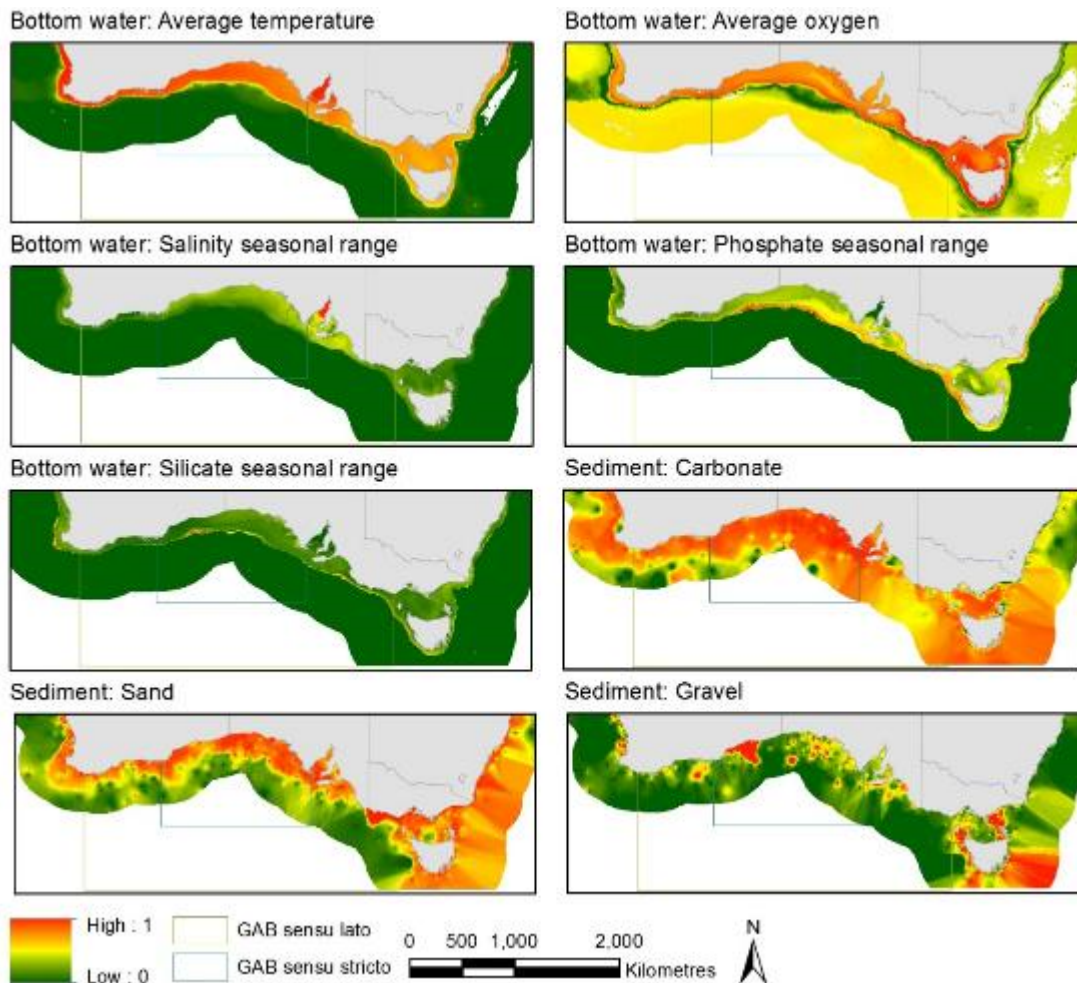


Figure 10.2. Maps of environmental data: Bottom water properties – average temperature, average oxygen, salinity seasonal range phosphate seasonal range and silicate seasonal range; Sediment properties – carbonate, sand and gravel content.

Model predictions may be unreliable when made to environmental data outside the range present in the training data (presence and background) (Elith et al., 2011; Radosavljevic and Anderson, 2014). To visualise regions where predictions are extrapolated to environmental data outside the training range, MaxEnt generates a multivariate environmental similarity surface and identifies the most dissimilar variable in areas of low similarity (Elith et al., 2010; 2011). We present these maps in the results to aid model interpretation.

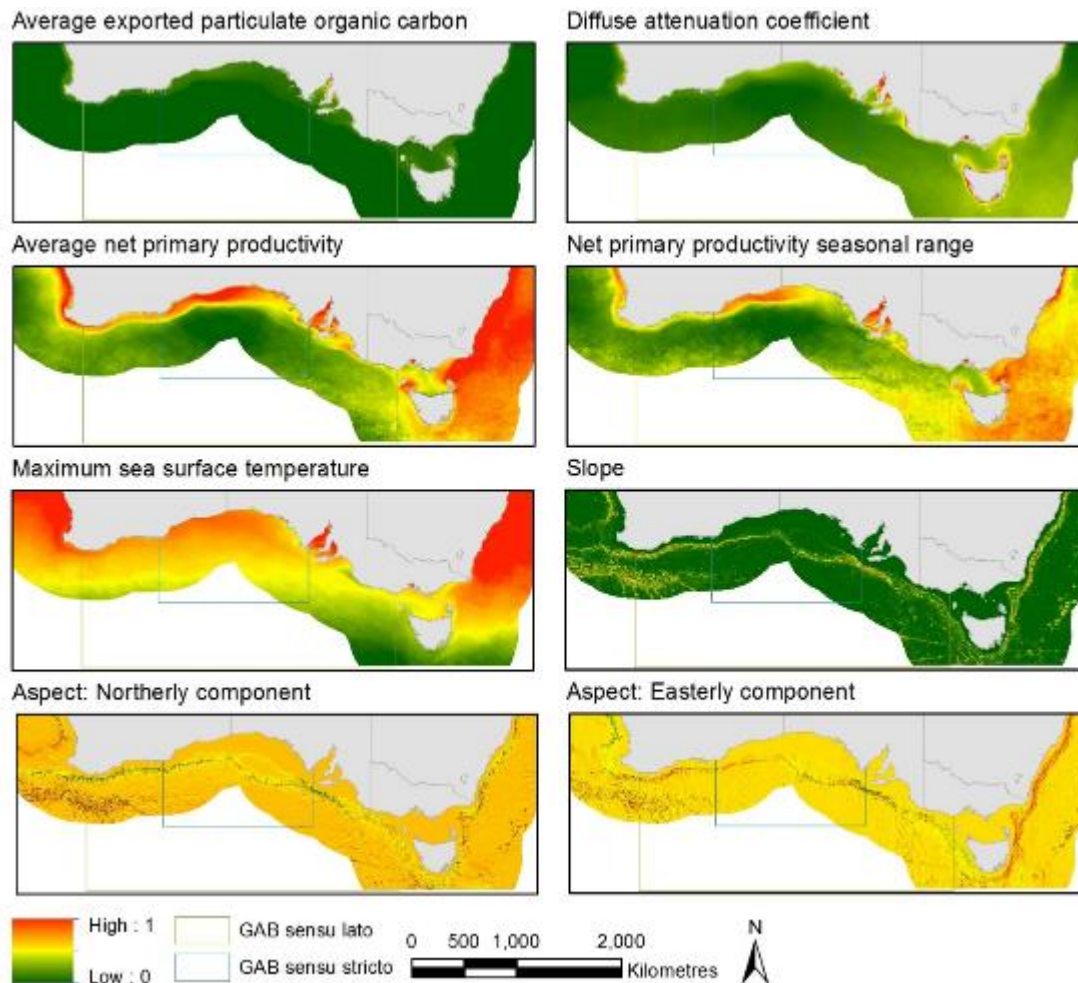


Figure 10.3. Maps of environmental data: Satellite derived average exported particulate organic carbon, diffuse attenuation coefficient, and net primary productivity, net primary productivity seasonal range and maximum sea surface temperature; Bathymetry derived slope and aspect (northerly and easterly components).

10.4 Results

The map of multivariate environmental similarity (Figure 10.4 top panel) shows that environmental conditions through most of the model domain have at least moderate similarity to the training data (grey colour, darker being higher similarity). Areas coloured yellow to red show moderate to high extrapolation to environmental variables outside the range used in training. The greatest dissimilarity is within Spencer Gulf (red colour), which is driven by the much greater salinity seasonal range in this area, as also seen in Figure 10.2. In deeper water off south-western Australia, average water temperature is the most dissimilar variable (Figure 10.4 bottom panel), but multivariate similarity in the area is only moderately low overall (yellow). There are two small areas with low values for sediment sand content, leading to moderately low multivariate similarity (yellow).

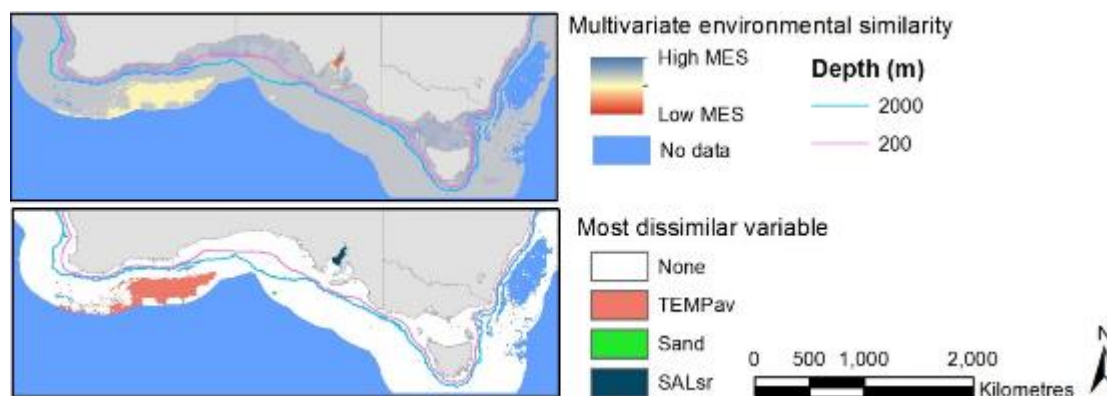


Figure 10.4. Multivariate environmental similarity surface (top) showing areas where environmental data is outside the range used in training models as yellow-red, and map of most dissimilar variable (bottom).

10.4.1 Individual species models

Most models showed good to excellent discrimination of presences (training AUC >0.8 or >0.9) and good transferability over space (test AUC >0.7 and difference between training and test AUC <0.1). Model FVA was >30% in most cases (Table 10.3).

Table 10.3. Model assessment results for MaxEnt models of 21 species.

Species	Training AUC	Test AUC	AUC difference	FVA (%)
<i>Caryophyllia planilamellata</i>	0.935	0.873	0.062	41.0
<i>Flabellum hoffmeisteri</i>	0.932	0.862	0.071	36.5
<i>Austropenaeus nitidus</i>	0.983	0.953	0.03	51.9
<i>Munida chydrea</i>	0.946	0.893	0.052	41.1
<i>Parapagurus latimanus</i>	0.948	0.819	0.129	30.9
<i>Limopsis soboles</i>	0.871	0.782	0.088	22.0
<i>Veprichlamys perillustris</i>	0.909	0.765	0.144	25.0
<i>Bathytoma agnata</i>	0.899	0.776	0.123	26.9
<i>Sassia kampyla</i>	0.852	0.771	0.081	24.8
<i>Fissidentalium ponderi</i>	0.933	0.858	0.075	34.3
<i>Psilaster acuminatus</i>	0.922	0.804	0.119	30.5
<i>Zoroaster macracantha</i>	0.928	0.616	0.312	21.2
<i>Echinus multidentatus</i>	0.891	0.753	0.138	21.1
<i>Laetmogone violacea</i>	0.957	0.808	0.149	34.4
<i>Asteronyx loveni</i>	0.911	0.774	0.137	27.5
<i>Ophiomusium lymani</i>	0.96	0.938	0.022	44.2
<i>Ophiocten hastatum</i>	0.955	0.924	0.031	36.4
<i>Rexea solandri</i>	0.812	0.614	0.198	12.3
<i>Halosauropsis macrochir</i>	0.958	0.894	0.065	43.9
<i>Antimora rostrata</i>	0.953	0.868	0.086	36.9
<i>Apristurus australis</i>	0.941	0.852	0.088	32.3

Cnidaria

Caryophyllia planilamellata (Anthozoa: Scleractinia: Caryophylliidae)

Caryophyllia are solitary hard corals without zooxanthellae (Kitahara et al., 2010). The area of greatest predicted suitability for *Caryophyllia planilamellata* was the upper continental slope (around 400-1,000 m depth) across southern Australia (Figure 10.5).

Variables used: EPOCav (D0.5), PO4sr (D0.5), SSTmax (D0.5,L,M), Slope (L,M), K490av (D0.5), Egrad (D0.5,L), SALsr (D2,L), TEMPav (D0.5,D2), NPPsr (D0.5,L), Sand (D0.5,M),

Flabellum hoffmeisteri (Anthozoa: Scleractinia: Flabellidae)

The Flabellidae are solitary hard corals without zooxanthellae (ALA, 2017). Greatest predicted suitability for *Flabellum hoffmeisteri* was along the continental slope, particularly at depths around 300-900 m on the east coast (Figure 10.5).

Variables used: TEMPav (D1), NPPsr (D0.5), SiO2sr (D0.5,D2,M), O2av (D1), Sand (D0.5,L), Crbnt (D2,L), EPOCav (D0.5), NPPav (D0.5,L).

Arthropoda

Austropenaeus nitidus (Malacostraca: Decapoda: Aristeidae)

Aristeidae is a family of deepwater prawn species (ALA, 2017). The continental slope area (especially 1,000-1,500 m) within the GAB region was predicted to be very highly suitable for *Austropenaeus nitidus*, with other slope areas also showing high suitability (Figure 10.5).

Variables used: K490av (D0.5), TEMPav (D0.5,D1,L), O2av (D1,M), Ngrad (D0.5), Egrad (D0.5), NPPsr (D0.5,D1), SiO2sr (D0.5,M), Crbnt (D0.5,D2,L,M), PO4sr (D0.5,D2,M), Sand (D0.5,D2).

Munida chydaea (Malacostraca: Decapoda: Munididae)

The Munididae is a family of squat lobsters (ALA, 2017). The area of greatest predicted suitability for *Munida chydaea* was the continental slope, especially 300-900 m depth, around south-eastern Australia (Figure 10.5).

Variables used: TEMPav (D0.5,D1,M), O2av (D0.5,D1,D2,M), SiO2sr (D2,L), SSTmax (D0.5,D2), Slope (L,M), Sand (D1,M), Crbnt (D0.5,D2,M), NPPav (D0.5,D2).

Parapagurus latimanus (Malacostraca: Decapoda: Parapaguridae)

The family Parapaguridae are deepwater hermit crabs (ALA, 2017). Large areas of the continental slope, especially around 1,000-1,500 m depth, and some deeper areas were predicted to be highly suitable for *Parapagurus latimanus*, including much of the GAB region (Figure 10.5).

Variables used: O2av (D2), Crbnt (D2,L), K490av (D0.5,M), TEMPav (D1,D2,L), Sand (D0.5,D2,M), Slope (L,M), SiO2sr (D1,M), PO4sr (D0.5,D2,L), SSTmax (D2,M).

Mollusca

Limopsis soboles (Bivalvia: Arcida: Limopsidae)

Limopsis bivalves are known from seamounts (ALA, 2017). The area of greatest predicted suitability for *Limopsis soboles* was along the east coast of Australia, especially at depths of 300-1,000 m (Figure 10.5).

Variables used: Egrad (D2), O2av (D2,L), TEMPav (D0.5,D1,M), SSTmax (D0.5,D2), PO4sr (D2,M), NPPav (D0.5,D2,M), SiO2sr (D2,L), SALsr (D1,D2,M).

Veprichlamys perillustris (Bivalvia: Pectinida: Pectinidae)

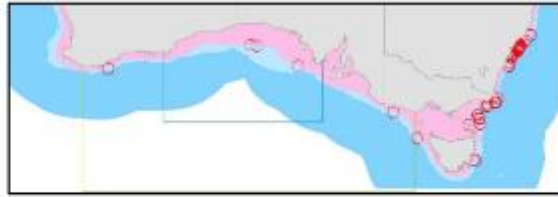
The family Pectinidae (scallops) contains over 250 species, with *Veprichlamys* species typically found in water deeper than 75 m (ALA, 2017). Continental slope areas, especially around 300-800 m, were predicted to be highly suitable for *Veprichlamys perillustris*, along with some deeper areas (>5,000 m), particularly in the GAB region (Figure 10.6). Data transformation of some variables for this species resulted in missing data at the deeper edge of available data in this region, with adjacent very high values. These are likely to be artefacts of extrapolation; although variables values in this area are only slightly outside the training data range, the modelled response to K490av is exponential and approaches infinity as K490av nears zero, leading to very high predictions.

Variables used: TEMPav (D1,D2,L), Sand (D0.5), K490av (D0.5,M), Egrad (D0.5), SSTmax (D0.5,L), O2av (D0.5,D1), EPOCav (D0.5,L,M), Ngrad (D0.5,D2), PO4sr (D0.5,D1,L), Slope (D2,L,M).

Caryophyllia planilamellata



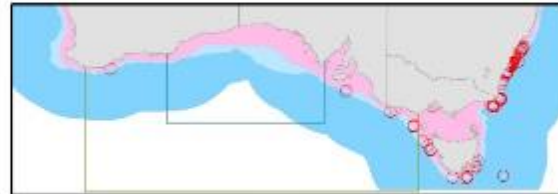
Flabellum hoffmeisteri



Austropenaeus nitidus



Munida chydea



Parapagurus latimanus



Limopsis soboles

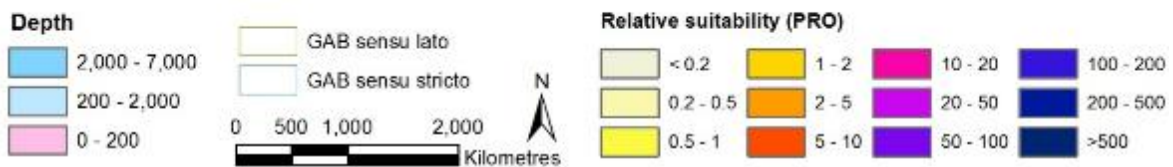
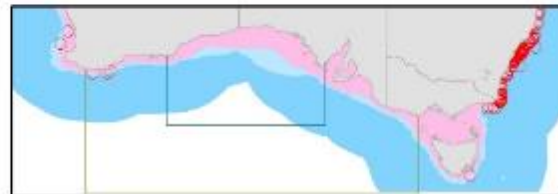


Figure 10.5. Maps of presences and model results for Cnidaria: *Caryophyllia planilamellata*, *Flabellum hoffmeisteri*; Arthropoda: *Austropenaeus nitidus*, *Munida chydea*, *Parapagurus latimanus* and Mollusca: *Limopsis soboles*. Presences (red circles) are shown in the top panel and model results in the lower panel for each species.

Bathytoma agnata (Gastropoda: Neogastropoda: Borsoniidae)

Borsoniidae is a family of predatory marine snails within the same order as the cone snails (ALA, 2017). The area of greatest predicted suitability for *Bathytoma agnata* was along the east coast, particularly the continental slope at 400-1,000 m, with the upper slope around south-western Australia having average suitability (Figure 10.6).

Variables used: TEMPav (D1,L), O2av (D1,L), SSTmax (D0.5,D2,M), SALsr (D1), Slope (L,M), Gravel (D0.5), Crbnt (D0.5,M).

Sassia kampyla (Gastropoda: Littorinimorpha: Ranellidae)

The family Ranellidae, known as triton shells, are medium to large predatory marine snails (ALA, 2017). The upper continental slope (300-900 m) around temperature Australia was predicted to be suitable for *Sassia kampyla* (Figure 10.6).

Variables used: TEMPav (D2,M), NPPsr (D1), EPOCav (D0.5,M), Egrad (D2,L), O2av (D0.5,D2,L), K490av (D0.5,D1,L), SiO2sr (D0.5,D2,L), Crbnt (D2,L).

Fissidentalium ponderi (Scaphopoda: Dentallida: Dentaliidae)

Scaphopoda, also known as tusk shells, are infaunal molluscs that occur in surface sediments (to a few centimetres) at depths of up to 6,000 m and beyond (Lamprell and Healy, 1998). Waters of Spencer Gulf appear to be highly suitable for *Fissidentalium ponderi*, but this is likely to be an artefact of extrapolation to high values of salinity seasonal range. Likely greatest suitability for this species is the upper continental slope, especially 500-1,000 m in eastern Australia (Figure 10.6).

Variables used: TEMPav (D1,M), SSTmax (D0.5,L), O2av (D0.5,L), Slope (D2,L,M), SALsr (D0.5,D1,L), Sand (D1,L), SiO2sr (D1,L), NPPav (D0.5,D2,M).

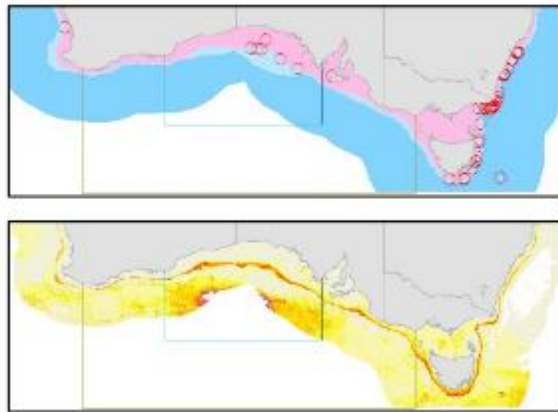
Echinodermata

Psilaster acuminatus (Asteroidea: Paxillosida: Astropectinidae)

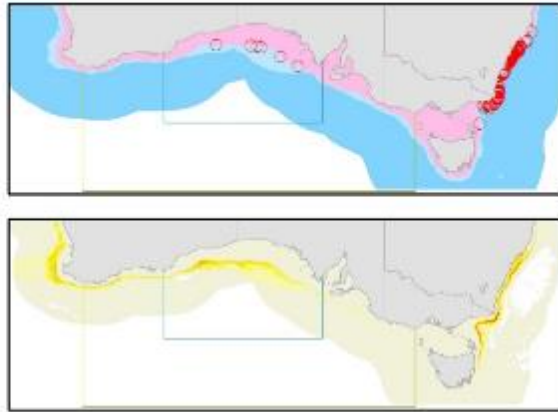
Psilaster acuminatus is a sea star known from continental shelf and slope areas from 150 to beyond 1100 m depth (ALA, 2017). Slope areas around south-western and eastern Australia had highest predicted suitability for this species, especially in 400-900 m, with some deeper areas having above average suitability (Figure 10.6).

Variables used: TEMPav (D1,L), NPPav (D0.5,L), O2av (D0.5,D1), SSTmax (D1,M), Crbnt (D0.5,D2), Ngrad (D2), Egrad (D0.5,D2), SiO2sr (D1), PO4sr (D2,L).

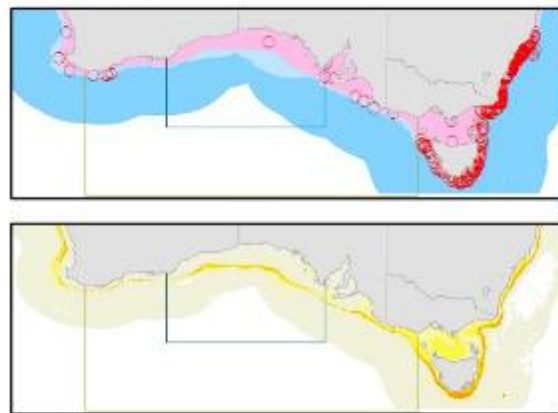
Veprichlamys perillustris



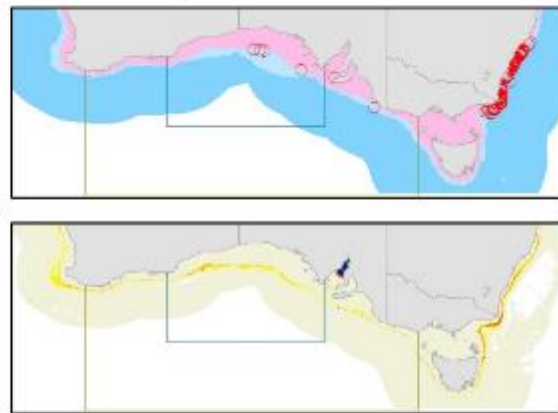
Bathytoma agnata



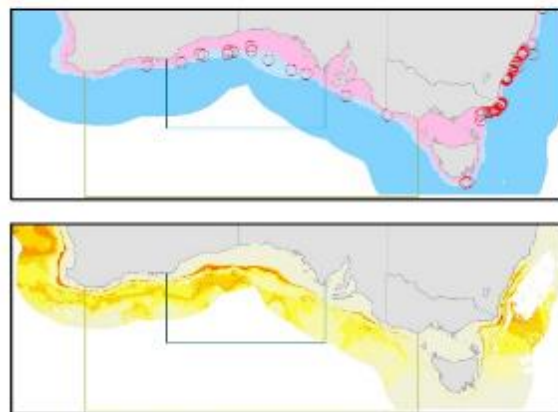
Sassia kampyla



Fissidentalium ponderi



Psilaster acuminatus



Zoroaster macracantha

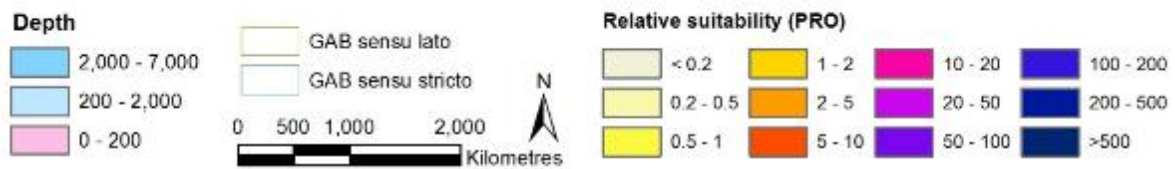
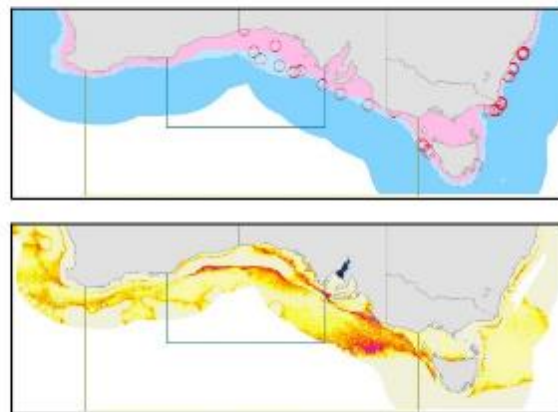


Figure 10.6. Maps of presences and model results for Mollusca: *Veprichlamys perillustris*, *Bathytoma agnata*, *Sassia kampyla*, *Fissidentalium ponderi*; and Echinodermata: *Psilaster acuminatus* and *Zoroaster macracantha*. Presences (red circles) are shown in the top panel and model results in the lower panel for each species.

Zoroaster macracantha (Asteroidea: Forcipulatida: Zoroasteridae)

Sea stars of the genus *Zoroaster* are known from waters 50 to >5,000 m deep (ALA, 2017). Waters of Spencer Gulf appear to be highly suitable for *Zoroaster macracantha*, but this is likely to be an artefact of extrapolation to high values of salinity seasonal range. Aside from that, there is high predicted suitability for this species along the GAB continental slope, especially in depths 400-1,000 m to the west of Kangaroo Island, and in areas off the south-east of South Australia (Figure 10.6), but model performance was relatively poor (low FVA and training AUC, Table 10.3).

Variables used: TEMPav (D1), K490av (D0.5), SSTmax (D0.5,D2,L), Slope (D2,M), SiO2sr (D0.5,M), Crbnt (D0.5,D1,L), NPPav (D0.5,D1), SALsr (D0.5,D2,M).

Echinus multidentatus (Echinoidea: Camarodonta: Echinidae)

Echinus multidentatus is a sea urchin recorded from depths of >300 m (ALA, 2017). Waters of Spencer Gulf appear to be highly suitable for this species, but this is likely to be an artefact of extrapolation to high values of salinity seasonal range. Greatest predicted suitability aside from that is in depths >2,000 m and particularly in >5,000 m, in areas with high sediment carbonate and gravel content (Figure 10.7). FVA of this model was relatively low, but model performance, as measured by AUC, was still good.

Variables used: PO4sr (D0.5), TEMPav (D0.5,D2), Gravel (D0.5), O2av (D0.5,L), SiO2sr (D0.5,L,M), Crbnt (D0.5,L,M), SALsr (D0.5,D1), SSTmax (D1,D2,M).

Laetmogone violacea (Holothuroidea: Elasipodida: Laetmogonidae)

Laetmogone violacea is a sea cucumber recorded from depths >450 m (ALA, 2017). Highest predicted suitability for this species was on slope (especially in >700 m) and deeper areas to ~5,000 m near the eastern end of the GAB sensu lato (Figure 10.7).

Variables used: K490av (D1,M), SALsr (D1,M), NPPsr (D2,M), Crbnt (D0.5,L), TEMPav (D1,L), Slope (D0.5,D2,M), SSTmax (D0.5,D1,D2), Ngrad (D0.5,D2), O2av (D0.5,D1,L), Gravel (D0.5,M), SiO2sr (D0.5,D2).

Asteronyx loveni (Ophiuroidea: Euryalida: Asteronychidae)

Brittle stars of the genus *Asteronyx* are known from depths of 80 to >4,000 m (ALA, 2017). Greatest predicted suitability for *Asteronyx loveni* was in depths >2,000 m, and especially in 4,000-5,000 m, along the east coast and from west of Tasmania toward the eastern edge of the GAB sensu stricto (Figure 10.7).

Variables used: K490av (D0.5,M), EPOCav (D1), TEMPav (D0.5,D1,D2,L), Ngrad (D2), NPPav (D0.5,D1), PO4sr (D2,M), NPPsr (D0.5,M), Crbnt (D0.5,D1), O2av (D0.5,D1,M), SALsr (D2,M).

Ophiomusium lymani (Ophiuroidea: Ophiurida: Ophiolepididae)

Ophiomusium lymani is a brittle star with a global distribution (excluding polar regions), recorded at depths of 130 to 4,000 m (ALA, 2017). The continental slope regions of the GAB and south-western Australia, particularly in 1,300-1,900 m, were predicted to be highly suitable for this species (Figure 10.7).

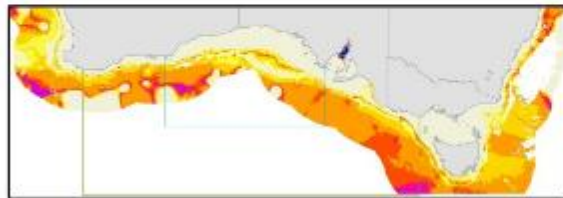
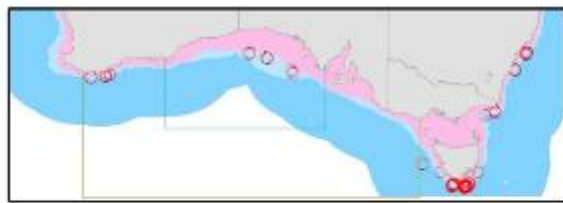
Variables used: SiO2sr (M), Sand (D0.5,M), TEMPav (D0.5,D1), SSTmax (D0.5,D2,L), Slope (D0.5,D2), Crbnt (D0.5,L,M), PO4sr (D0.5,D2), Gravel (D0.5,M), SALsr (D0.5,L).

Ophiecten hastatum (Ophiuroidea: Ophiurida: Ophiuridae)

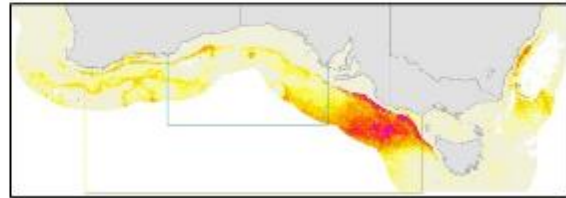
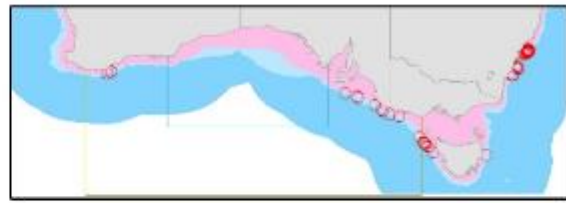
Ophiecten hastatum is a cosmopolitan brittle star known from depths of 3,000-5,000 m (Gage et al., 2004). The deeper continental slope regions (1,800-2,400 m) of the GAB and south-western Australia were predicted to be highly suitable for this species (Figure 10.7).

Variables used: SiO2sr (D0.5), TEMPav (D0.5,D1), O2av (D1,D2), Ngrad (D0.5,L), SSTmax (D0.5,D1,M), SALsr (D0.5,M).

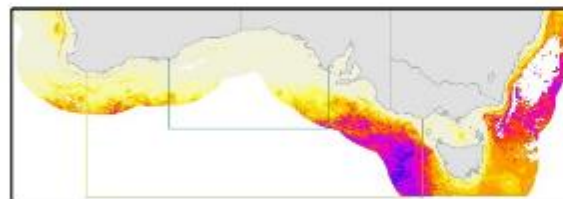
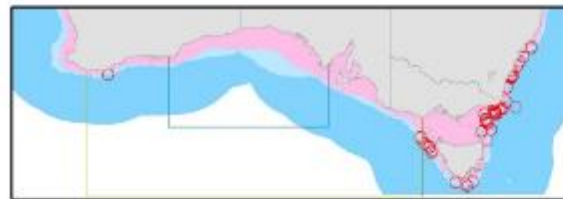
Echinus multidentatus



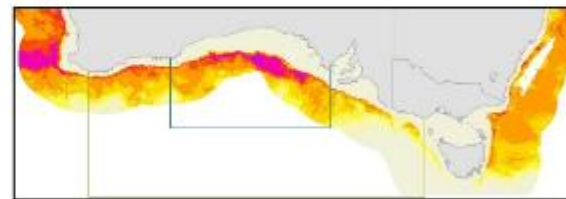
Laetmogone violacea



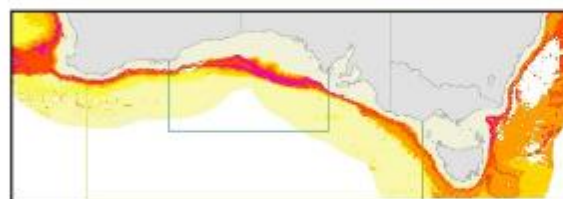
Asteronyx loveni



Ophiomusium lymani



Ophiocten hastatum



Rexea solandri

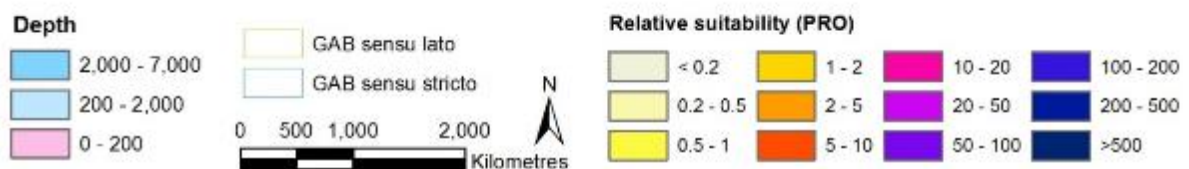
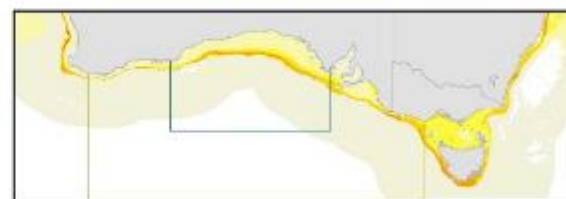
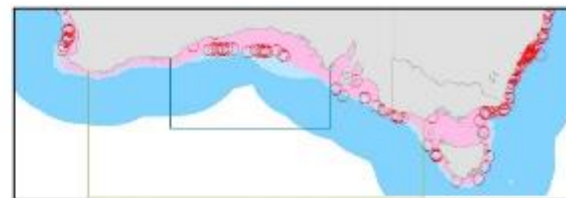


Figure 10.7. Maps of presences and model results for Echinodermata: *Echinus multidentatus*, *Laetmogone violacea*, *Asteronyx loveni*, *Ophiomusium lymani* and *Ophiocten hastatum*; and Chordata: *Rexea solandri*. Presences (red circles) are shown in the top panel and model results in the lower panel for each species.

Chordata

Rexea solandri (Actinopterygii: Perciformes: Gempylidae)

Rexea solandri, known as gemfish, is a predatory fish known from depths of 100-800 m around Australia (Australian Museum, 2017). Areas along the edge of the continental shelf (300-900 m) around temperate Australia were predicted to be suitable for this species (Figure 10.7), but model performance was relatively poor (low FVA and AUC, Table 10.3).

Variables used: TEMPav (D1), EPOCav (D0.5), SSTmax (D0.5), O2av (D0.5,D1,M), NPPav (D0.5,D1), PO4sr (D2,L).

Halosauropsis macrochir (Actinopterygii: Notacanthiformes: Halosauridae)

Halosauridae are eel-like fishes typically found at depths >2,000 m (ALA, 2017). Most of the deeper GAB region was predicted to be very highly suitable for *Halosauropsis macrochir* with an area of very high suitability at 1,300-1,800 m (Figure 10.8).

Variables used: NPPav (D0.5,M), TEMPav (D0.5,L), SSTmax (D0.5,D2,L), SiO2sr (D1,D2,M), SALsr (D0.5,M), Ngrad (D2), O2av (D0.5,L), PO4sr (D0.5,L), NPPsr (D0.5,L), Sand (D0.5,D1,D2,L).

Antimora rostrata (Actinopterygii: Gadiformes: Moridae)

Antimora rostrata, or violet cod, is a globally distributed deepwater species (Iwamoto, 1975). The GAB continental slope region (especially 1,200-1,800 m) was predicted to have very high suitability for this species (Figure 10.8).

Variables used: O2av (D1), K490av (M), TEMPav (D1,L), NPPav (D0.5,D2,L), Ngrad (D0.5), Egrad (D0.5), PO4sr (D0.5,D2), SiO2sr (D0.5,D2,M), Sand (D0.5,D2,L), Slope (D1,L,M).

Apristurus australis (Elasmobranchii: Carcharhiniformes: Pentanchidae)

Apristurus australis, known as Pinocchio catshark, is widely distributed along the Australian continental slope at depths of 600-1,000 m (ALA, 2017). Predicted suitability for this species was greatest along the continental slope of eastern Australia at 500-1,000m deep (Figure 10.8).

Variables used: NPPsr (D0.5), TEMPav (D1,L), Gravel (D0.5), Crbnt (D1,M), Ngrad (D2,L), SSTmax (D0.5,M), Egrad (D0.5,D2,L), O2av (D0.5,D2,L), SALsr (D0.5,D2,M).

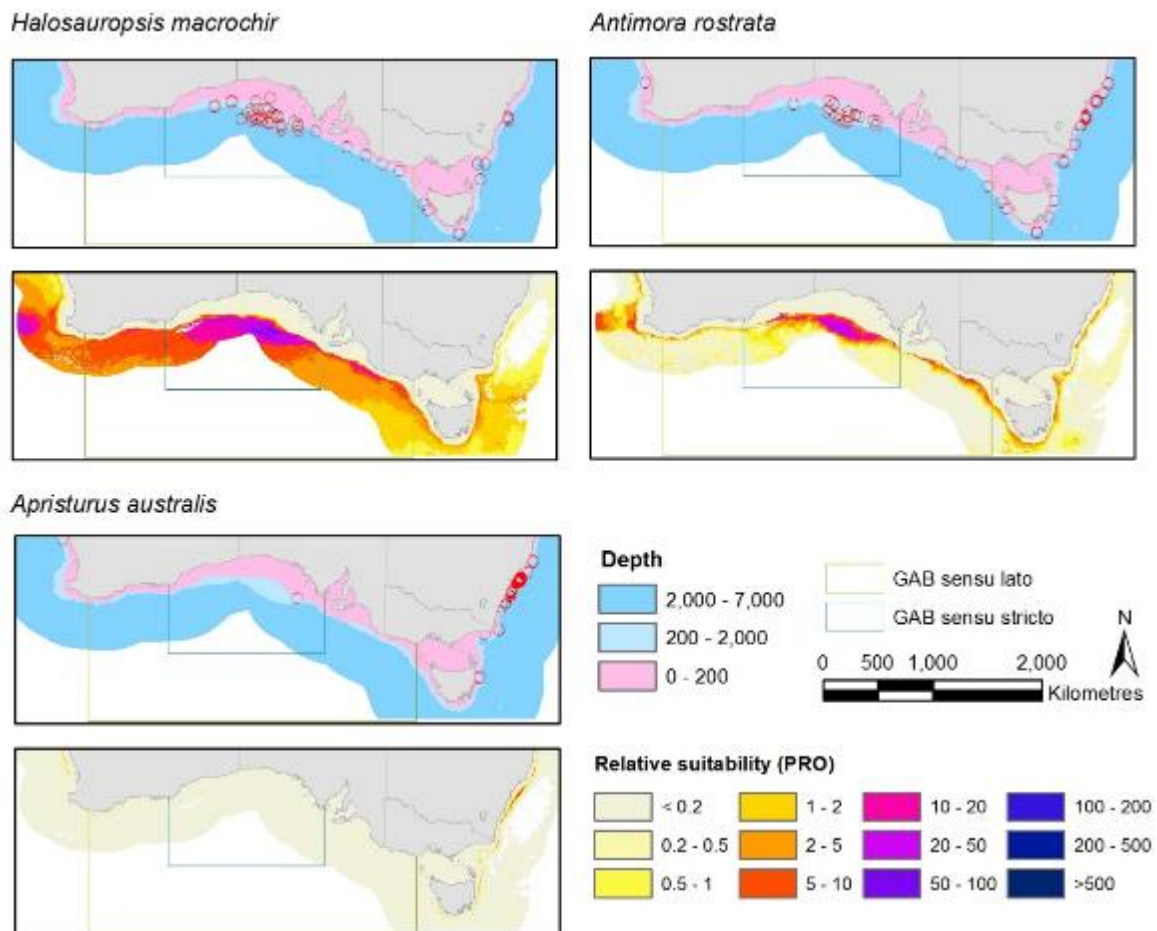


Figure 10.8. Maps of presences and model results for Chordata: *Halosauropsis macrochir*, *Antimora rostrata* and *Apristurus australis*. Presences (red circles) are shown in the top panel and model results in the lower panel for each species.

10.4.2 Combined suitability across models

The taxa chosen for modelling were a subset of those recorded at >200 m, and so it is unsurprising that average suitability class across these species was generally low on the continental shelf, greatest on the continental slope (200-2,000 m) and moderately high at greater depths (Figure 10.9 and Figure 10.10). There is a narrow band of high overall suitability near the top of the continental slope, especially around southern and eastern Australia. The extracted values per depth band show that highest combined suitability class scores occurred in the depth range 600-800 m (Figure 10.9).

Average suitability classes across phyla illustrate different patterns in the areas of greatest suitability. The top of the continental slope shows greatest overall suitability for Cnidaria (Figure 10.10) and Mollusca (Figure 10.11), especially the former, while all areas >200 m deep, are broadly suitable for the modelled Echinodermata and Chordata (Figure 10.11). Echinodermata show greatest suitability in deeper regions around south-eastern Australia, while the GAB continental slope has

greatest suitability for Chordata and Arthropoda (Figure 10.10). Several deeper areas around southern Australia also show high suitability across the modelled Arthropoda.

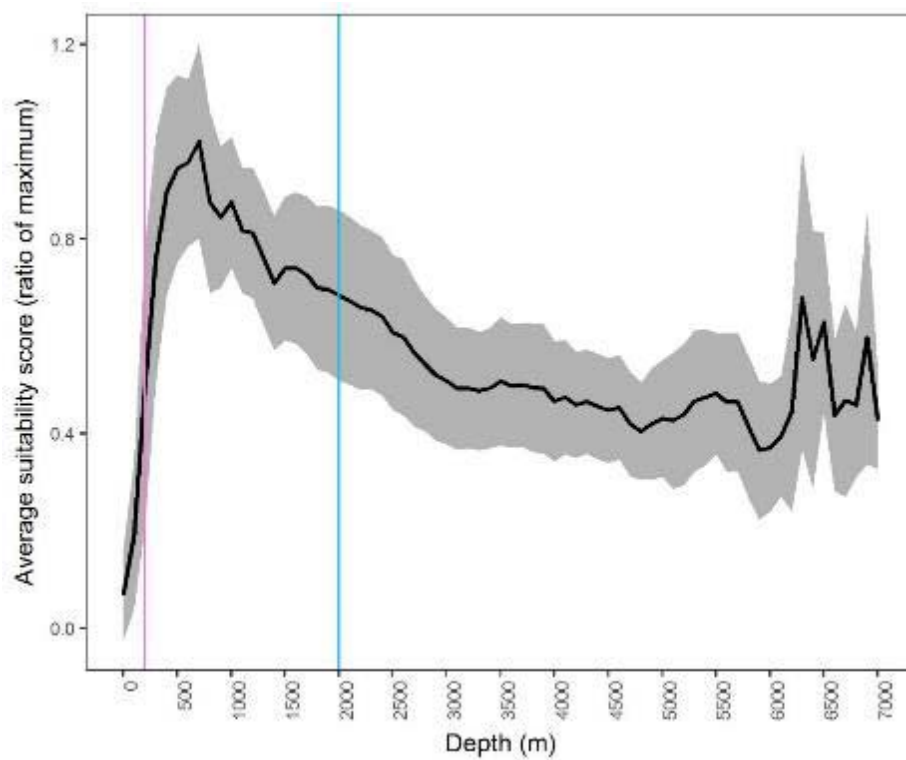


Figure 10.9. Relative average suitability class by depth (100 m categories). Grey shading shows ± 1 standard deviation of scores for each depth band. Depth 200 m is indicated by the pink line and 2,000 m by the blue line.

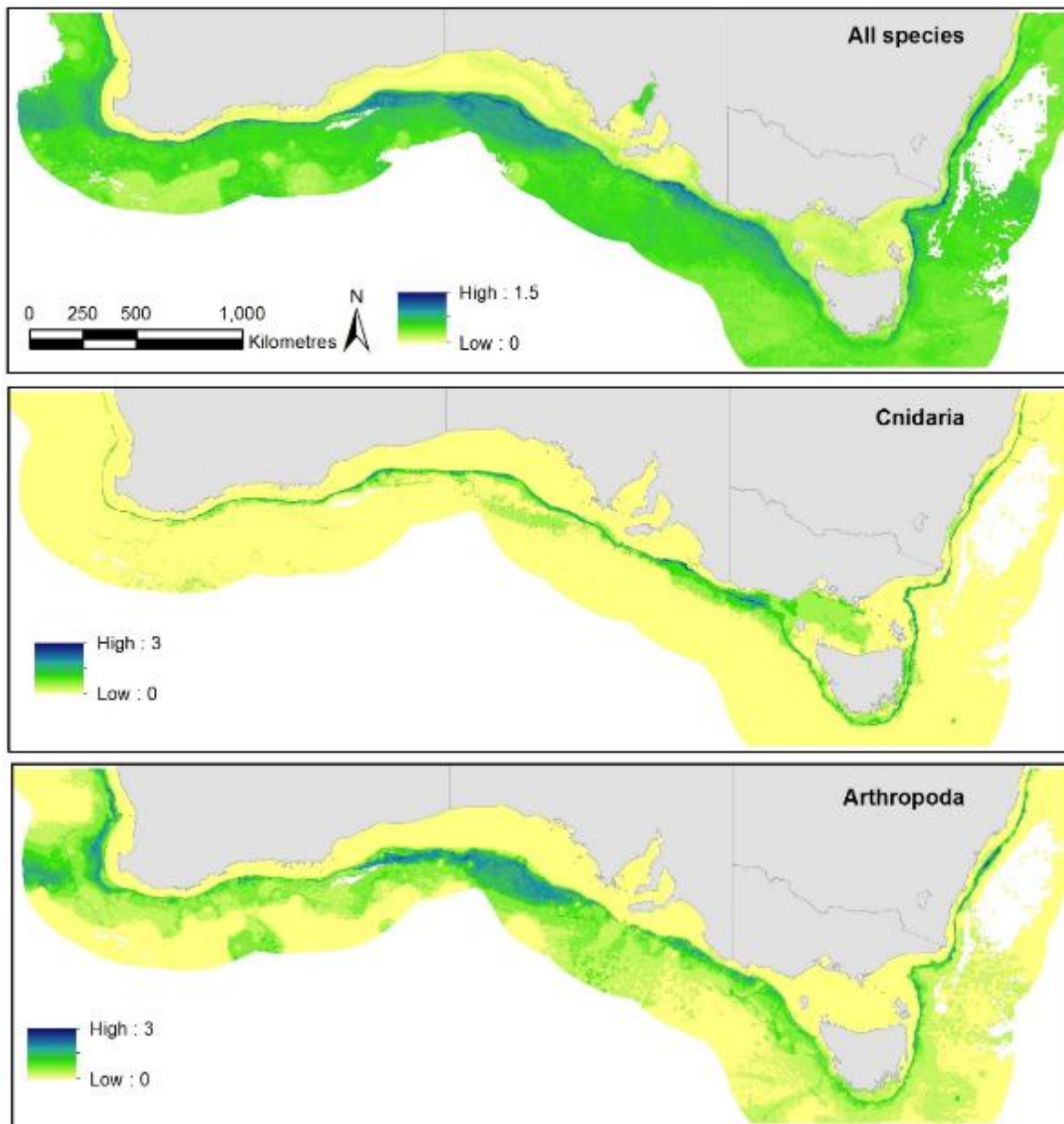


Figure 10.10. Maps of average suitability class across all 21 modelled species (top) and for phyla Cnidaria (2 species, middle), and Arthropoda (3 species, bottom). Note different scale for map of all species.

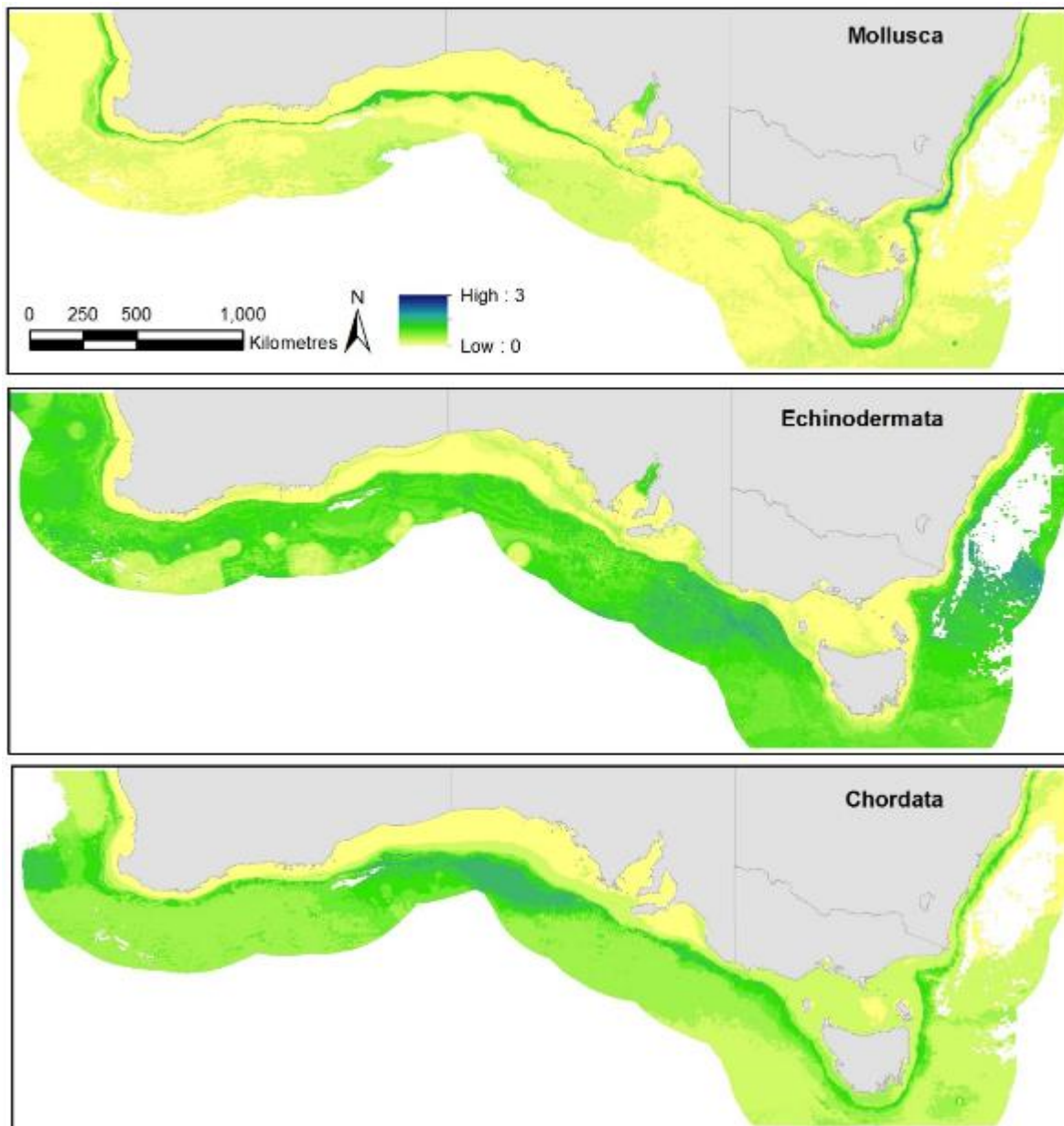


Figure 10.11. Maps of average suitability class for Mollusca (5 species, top), Echinodermata (7 species, middle), and Chordata (4 species, bottom).

10.4.3 Importance of predictor variables

Our initial variable selection process identified TEMPav as the variable with greatest predictive power across all species. This variable was included in models for all 21 species, and in 18 cases was one of the first three variables selected, further demonstrating its high predictive power. On average, TEMPav explained 12.0% of total variation. It is important to note, however, that TEMPav was one of a set of highly correlated variables (Table 10.2), and so predicted species responses cannot be attributed to temperature specifically, since they could be responding to one of the other correlated variables or a combination thereof.

Other important variables across all species were O2av (used in 19 models explaining an average of 3.9% FVA), SiO2sr (16 models 3.6% FVA) and SSTmax (16 models, 1.9% FVA). Note that SSTmax was correlated with average SST and with both the average and seasonal range of benthic irradiance, so SSTmax is also acting as a proxy for these variables. Some variables were selected in fewer models but, where selected, explained a relatively high proportion of total variation, e.g. NPPav (10 models, 4.2% FVA), and K490av (9 models, 7.9% FVA). All of the 16 candidate environmental variables were selected in at least some models, with EPOCav and Gravel selected in the fewest (6 each).

There were differences in the importance of variables between phyla. Although TEMPav was the variable with greatest predictive power in all cases, it was particularly important in models for Mollusca, Arthropoda and Cnidaria, with 17.8%, 16.7% and 13.3% average FVA respectively. For Chordata and Echinodermata, average FVA of TEMPav was 9.5% and 7.0% respectively. O2av was the second most important variable for Chordata, Arthropoda and Mollusca, with average FVA of 6.8%, 6.0% and 3.5%; this variable ranked 5th for Cnidaria (1.1% FVA) and 6th for Echinodermata (2.0% FVA). EPOCav was the second most important variable for Cnidaria (5.7% FVA) and SiO2sr for Echinodermata (8.1% FVA). Other important variables were: SiO2sr and NPPsr for Cnidaria; Crbnt and SiO2sr for Arthropoda; SSTmax and Egrad for Mollusca; SSTmax and SALsr for Echinodermata; and NPPav and SSTmax for Chordata.

10.5 Discussion

We have developed SDMs for 21 representative deep water taxa from temperate Australia. These show that the GAB region is likely to be ‘generally to highly’ suitable for most of the modelled species, especially those that have been recorded along the southern coast. In particular, the continental slope region, especially between 600-800 m is likely to be ‘highly suitable’ for many of these species. Our models were developed for single species, and the method used gives a relative occurrence rate, not probability of occurrence, so combined suitability scores should be interpreted as an ordinal, not absolute, measure of relative suitability. Despite these limitations, other studies using combinations of single-species SDMs to predict overall habitat suitability have found the combined predictions to be robust even when using only a small subset of representative species (Seebens et al., 2016). Areas predicted to have greater combined suitability are therefore likely to support a more diverse assemblage of benthic epifauna, though we cannot predict actual or relative species richness without data on species prevalences. It should be noted that our focus was on deep water species, i.e., those recorded below 200 m, so the low predicted suitability of areas <200 m deep is relevant only to this suite of species, not to benthic epifauna more widely.

The combined model outputs are likely to be only relevant to the phyla and classes included. We chose these to be representative of the available data, but some important taxa could not be included due to lack of records at the appropriate taxonomic resolution. Particular taxonomic groups of interest that were not included are the phyla Porifera (sponges), Bryozoa (lace corals) and Sipuncula (peanut worms), the Arthropod class Pycnogonida (sea spiders), and within the Cnidarian class Anthozoa, the orders Alcyonacea (soft corals) and Actinaria (anemones). While there are many records for some of these groups, especially Porifera and Bryozoa, a large proportion have not been identified to species level, or otherwise not assigned to species names. For example, specimens of some groups have been identified to distinct taxonomic units, but these may not always be comparable across surveys and cannot be linked to online database species-level records to obtain sufficient data for modelling. For current work we focussed on species-specific modelling, which is the main application of MaxEnt, but the software has also been used to predict occurrence of assemblages (e.g. Anderson et al., 2016; Halvorsen et al., 2016) and higher level taxonomic groups (e.g. Yesson et al., 2016). The modelling techniques developed could be applied to additional species in future to further develop our understanding, and, where species-level identifications are lacking, models could be applied using records at a higher taxonomic level (e.g. family or order).

Using SDMs to predict habitat suitability in unsampled regions often involves extrapolation to environmental variables outside the range used for training models. For the region of interest (depth 200-7,000 m), the training data (presences and TGS points) adequately captured the range of environmental variables, with the exception of TEMPav in areas of south-western Australia >5,000 m deep. Predictions to this area may be less reliable, but involve only slight extrapolation. The training data did not adequately characterise the full range of SALsr, which was much higher in Spencer Gulf than in the training data, leading to unreliable predictions in this region. This area is, however, outside the area of interest, and predicted high suitability here should be regarded as an artefact of extrapolating well beyond the training data range. Overall performance of models was good, based on training and test AUC and FVA. Training AUC scores were all >0.8, and were >0.9 for most species, showing good to excellent discrimination of presences. Test AUC scores assess transferability of the models to different geographic space and are expected to be lower than training AUC, with a small difference showing better model transferability. Test AUC scores were also mostly >0.8 and with a difference of <0.1 between training and test AUC. The FVA for most models was >30% and for 6 models was >40%. A few models, however, had low FVA (~20% or below), which was associated with lower test AUC scores and a greater difference between training and test AUCs.

Average bottom water temperature and oxygen content were found to be the two variables with greatest predictive power in models. It is unclear, however, whether temperature itself is the major

factor driving distributions, since this was one of a suite of highly-correlated environmental variables, which also included depth, and average bottom water phosphate, nitrate, silicate, and salinity. In the models, TEMPav should be regarded as acting as a proxy for different water masses, characterised by temperature, depth and water quality. The highly correlated nature of these variables means that individual effects cannot be resolved.

11 Assemblage level modelling Gradient Forest approach

Nick Ellis¹, Alan Williams¹, Franziska Althaus¹, Jason E. Tanner² (CSIRO¹ and SARDI² project team)

11.1 Introduction

This Section details a ‘predictive’ analysis for the spatial distribution of benthic assemblages across a broad region of the GAB. The gradient forest approach (Ellis and Pitcher, 2009; Pitcher et al., 2011a; 2016) predicts (extrapolates) species distributions from geo-located biological samples using a wide suite of environmental parameters.

We have combined all suitable data from the GAB because the approach benefits from using as many sample data as possible. In order to sample the biodiversity as fully as possible, we therefore included data sets that lay partly or wholly outside the study area; the reasoning is that these data sets may sample environments that also occur within the study area. However, to make the samples more relevant, we excluded all sites shallower than 120 m. See Appendix Section 20.2.1 for the list of biological data sets with citation information.

The two best datasets are those collected during recent surveys by the *RV Investigator*: IN2015_C02 (MNF 2015a) under the GABRP (2017) termed ‘BP epibenthic’ in figure legends, and IN2015_C01 (MNF 2015) under the Great Australian Bight Deepwater Marine Program (GABDMP, 2017) termed ‘Chevron epibenthic’ in figure legends.

11.2 Methods

11.2.1 Biological data sets

The biological data sets representing the biodiversity within the GAB are listed below.

- *GABRP epibenthic* surveys (2013 and 2015). This comprised a set of standard beam trawls at 34 sites in the deep GAB along a series of parallel transects. The response variable was weight W per taxon; 935 distinct taxa were observed, over half of which were seen only at a single site. [Note Figure labels refer to ‘BP epibenthic’].
- *GABDMP epibenthic* survey. This comprised a set of standard beam trawls at 17 sites in the deep GAB. The response variable was weight W per taxon; 407 distinct taxa were observed. [Note Figure labels refer to ‘Chevron epibenthic’]
- CSIRO Western Australian Slope *Voyage of Discovery* surveys (data in Williams et al., 2010a; McEnnulty et al., 2011). These consisted of 4 m beam trawls and Sherman sled tows. As these were targeted on the continental slope, the sites do not extend to deeper waters. The full survey continued up the coast of Western Australia, but only sites south of 30°S were

used. There were 24 beam trawl and 22 sled sites used in the analysis (see Table 11.1). The two gears were analysed separately. The response variable was density, computed as $W/(AF)$, where W is the sample weight, A is the area of the tow, and F is the sub-sampling fraction (which was <1 for some sled tows). In all, 1247 species were observed of which 914 were in sled samples and 523 were in beam trawl samples (with some in both).

- *CSIRO data-trawler historic surveys*. These were surveys carried out by CSIRO mostly along the continental shelf using the vessel *Courageous* in the late 1970s and *Soela* in the late 1980s. They used two distinct types of fish-trawl gear, the 'Frank and Bryce' and the 'Engel Hi-rise', respectively, which are treated separately in this analysis. Both counts and weights were measured, and, although there was substantial proportion of 'missing data' for one or the other, there were also a large number of cases where both counts and weights were obtained. This allowed for count-weight and weight-count regression relationships to be established for many species, so that missing measurements could then be imputed from the non-missing measurements. These surveys form part of a wider set of surveys that covered much Australia's continental shelf; where regressions could not be established with the surveys local to the GAB, regressions from the wider surveys were sometimes available. It transpired that for the Frank and Bryce, gear count (C) measurements gave the best fitting models, whereas for the Engel Hi-rise gear, weights (W) were preferred. The response variable was therefore density computed as C/A or W/A respectively. A total of 211 and 158 sites were retained for this analysis, and 185 and 237 species were observed, respectively. Data were extracted from the CSIRO data trawler (CSIRO, 2017).
- *SARDI Eastern Great Australian Bight Benthic Protection Zone survey* (Currie et al., 2007). This survey consisted of mainly shallow sites on the shelf, but 10 sites extending into deeper waters were retained for the analysis. The device was a 50 kg, 1.8 m wide, epibenthic sled; the response variable was density, computed as W/A . There were a large number of species recorded but most were seen only at a single site.
- *GAB Fishery-independent survey* (Ian Knuckey et al., unpubl. Fishwell Consulting/AFMA). This comprised a series of fish trawls at 225 sites along the shallow edge of the study region where the trawl fishery occurs. The species observed were mostly fish (116 species), with each species being observed at an average of 50 sites, and half the species present at 17 sites or more.
- *Soviet trawler surveys* (Koslow et al., 1999). The Soviet fleet carried out a large number of fish trawl surveys around the 1970s, mostly on the shelf but also sometimes in deeper

waters. There were 1516 sites included in the analysis and 454 fish species. The most reliable data were counts C (many weights were missing) so the density was computed as C/A .

11.2.2 Environmental data sets

The environmental data layers collated and used for the biophysical analysis and mapping are described and mapped above (see Section 3 Table 3.1 and Figure 3.2 to Figure 3.1). Outputs of the BENTHIS bottom stress model were not available at the time of these analyses, and the model does not cover the full domain of the analysis, thus values from the CSIRO Ribbon model were used.

11.2.3 The gradient forest approach

We used the Gradient Forest method (Ellis et al., 2012; Pitcher et al., 2012) to predict the distributions of benthic assemblage types based on multiple data sets. This is an integrative approach that uses random forest models (Breiman, 2001) of biota against multiple environmental gradients to obtain relationships of compositional change or 'turnover' along those gradients. These turnover curves are used to transform the multidimensional environment space into a corresponding biological space. Places that are close in biological space are expected to be similar in composition. A region in space having similar composition is called an 'assemblage'. The method allows us to partition biological space into a convenient number of assemblages, which can be mapped.

Each survey data set undergoes a separate gradient forest analysis. Species that have high-quality random forest models in the sense of good predictive ability (high out-of-bag R^2) contribute more to the overall biological turnover. Moreover, predictors that are more influential on species distributions (in the sense of random forest accuracy importance) are associated with more biological turnover; that is, their turnover curves have a greater magnitude. Because the turnover curves all represent a common quantity (i.e. compositional turnover) they can be combined across multiple surveys. This combination is achieved by averaging across surveys using weighting that accounts for the relative quality of each survey. It is this combined turnover curve, one for each predictor, which is used to obtain the biological space as described above.

The question of how many assemblages to partition biological space into is important to interpreting the contrasts in biodiversity within each assemblage, and of practical importance to management. Too many assemblages is likely to result in relatively small differences in diversity between each, and may mean management might become unwieldy; Conversely, too few assemblages might mean each is too compositionally diverse for management at the assemblage level to be effective. The ideal is to have assemblages that are internally homogeneous but that capture important variation

in composition among assemblages. We use two strands of evidence: 1) multivariate regression tree (MRT) models of each survey to provide a minimum number of assemblages; and 2) constrained ordination of the species Bray-Curtis dissimilarity data using the proposed assemblage labelling as the explanatory variable (Legendre et al., 2011). The MRT method allows the optimal number of nodes of the regression tree to be obtained by cross-validation, so this provides an objective measure of the minimum number of assemblages that are present in each survey. Typically MRT produces 2 to 5 nodes. With the ordination approach, biological space first is partitioned into 2, 3, ..., 30 assemblages using a clustering technique (PAM—partitioning around medoids). Each partition labelling is used as a categorical explanatory variable in the ordination for each survey, and the F ratio, which is a measure of the explanatory power of the labelling, is recorded. The partitioning having the highest F ratio across all surveys (geometric mean) and that satisfies the minimum number criterion is the candidate for the preferred number of assemblages.

Having decided on the desired number of assemblages, they can be mapped geographically and also described in terms of the environments expected there.

11.2.4 Extrapolation and gap analysis

This analysis can be considered a form of prediction: we are attempting to predict the biological composition in areas (*grids*) where we have no biological information from a small number of places (*sites*) where we do have biological information. If the environments at the grids are similar to the environments at the sites, then we may have more confidence in our predictions. However, the study area is a vast region that, apart from the deep GABRP and GABDMP surveys, has only been sampled around its periphery. We therefore expect that the environments on the grids will be somewhat different to environments on the sites, and so the prediction is a kind of *extrapolation*.

The issue of extrapolation is most acute when the value of the predictor at the grid lies outside the range of the predictor on the sites. The gradient forests do not have any information on values in this range, so one must make an assumption as to how much turnover to attribute to the change. We *could* assume that the turnover changes linearly beyond the range of the predictors at the average turnover rate over the observed range. However this causes problems for this analysis, because parts of the study area have predictors (especially chlorophyll A) which are substantially outside the observed range, resulting in large areas of biological space lying outside the observed range of biological space. This exterior region is essentially unknown territory as regards biodiversity, and so it does not make sense to partition it into assemblages, which are equally unknown. The remedy we use is to attenuate the extrapolation beyond the observed range so that instead of increasing linearly, the turnover increases with the square root of the change from the mean value on the sites.

This shifts the focus of the partitioning into assemblages back to areas where we have more confidence in the prediction. However, it also somewhat masks the uncertainty, leading to overconfidence in the predictions in areas where extrapolation has occurred. We can address this by mapping the uncertainty using a 'gap analysis' (Pitcher and Ellis, 2011b). The degree of extrapolation at a grid can be quantified by the dissimilarity of the grid's species composition from any observed site. The usual measure of dissimilarity is Bray-Curtis distance. We fit a regression of Bray-Curtis distance for all pairs of sites within a survey, weighted over all surveys, where the explanatory variables are geographical distance and biological distance. This allows us to predict the Bray-Curtis distance between any grid and any site. We can then map the minimum predicted Bray-Curtis distance to all sites; areas of high Bray-Curtis distance indicate areas of greater uncertainty.

11.3 Results and Discussion

11.3.1 Predictive mapping of faunal assemblages in the GAB

Individual survey gradient forests

There were seven surveys, two of which (*Voyage of Discovery* and *Data trawler*) were split into separate gears, so in all nine gradient forests were calculated. Diagnostic figures from these analyses are presented in Appendix, Section 20.2.2, The GABRP epibenthic and Engel Hi-rise surveys provided the most biodiversity information, followed by the Frank and Bryce survey and the GABDMP survey (Table 11.1 and Section 20.2.2 Appendix Fig A). Note that only about 10% of species could be predicted to any degree by the environmental variables; this is typical for marine survey data. Both recent deep epibenthic surveys (GABRP and GABDMP) had fairly high quality models ($R^2 = 0.3$).

There was not a particularly strong pattern in the degree of influence of the predictors (Section 20.2.2 Appendix Fig B). The most important were various water-bottom properties (silicate, oxygen, salinity, phosphate), carbonate, temperature, exported particulate organic carbon (EPOC) and depth. Both deep surveys were more discriminating in selecting influential variables, and they tended to agree on this choice (silicate, oxygen, salinity, depth, EPOC, temperature). Note that seasonal range of chlorophyll A was not strongly influential. There was considerable variation in the importance across surveys for the more influential predictors.

Table 11.1 Properties of the gradient forests from each survey, showing the number of sites in each survey, how many predictors were retained, the number of species observed, the number of species with positive out-of-bag R^2 , and the mean and total R^2 .

Survey	Sites	Predictors	Available spp	Used spp	Mean R^2	Total R^2
GABRP epibenthic	34	29	1130	60	0.31	18.47
Engel Hi-Rise	158	34	237	61	0.27	16.48
Frank and Bryce	211	34	185	42	0.24	10.16
GABDPM epibenthic	17	27	407	23	0.30	6.79
VoD Beam trawl	24	34	523	22	0.21	4.57
Fishery-independent	225	34	116	30	0.12	3.68
VoD Sled	22	34	914	6	0.43	2.61
SARDI epifauna '02	10	34	568	4	0.28	1.10
Soviet trawlers	1516	34	454	20	0.03	0.57

Combining the surveys for joint species turnover curves

The individual turnover curves for selected predictors for all the informative species are shown in Appendix Section 20.2.3. To understand what they mean take a specific example. The species *Cetonurus globiceps* in the GABDPM survey shows high turnover at a silicate (mean) threshold of 62 μM . This means that in at least 1 of the 500 random forests that were fitted to bootstrap samples of this species, the value 62 μM silicate (mean) split the data (or a substantial portion of it) into two groups such that the variance in the response (sample weight) was substantially reduced. Each turnover curve is the average of all such splits/variance reductions gathered together.

The combination of these curves over all species within a survey results in the separate curves in Figure 11.1. For example, the threshold seen in silicate (mean) for *Cetonurus globiceps* results in a jump in the brown curve at 62 μM . The combined curve (black) results from combining the separate survey curves, weighting by the relative influence of each survey as quantified by total R^2 (Table 11.1).

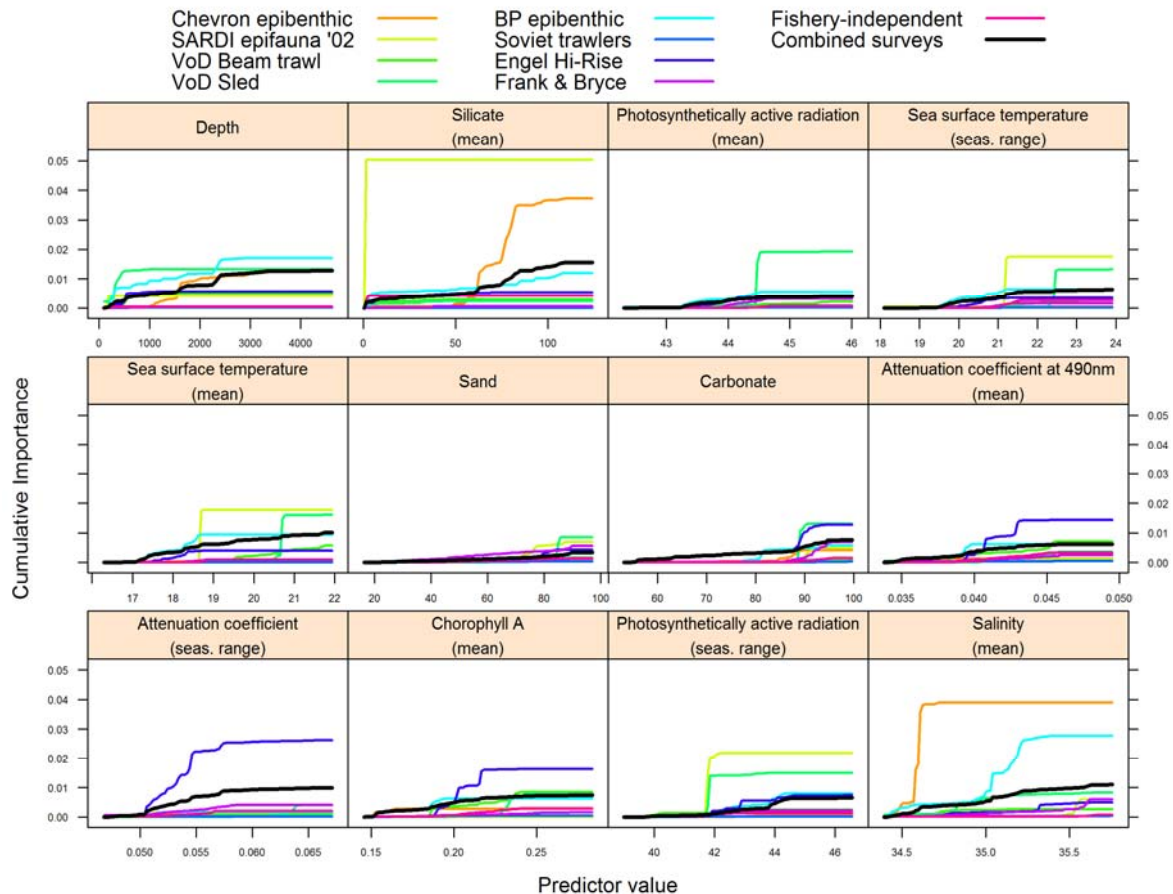


Figure 11.1 Cumulative turnover curves for each survey, and the combined turnover (black curves), for selected influential variables. The y axis is interpreted as a 'biological scale', and curves indicate the transformation from environmental space to biological space.

Defining biological space and mapping it geographically

Given the mapping from environmental to biological space as defined by the turnover curves in Figure 11.1, these mappings were applied to the environmental variables on the 0.01° prediction grid of 744,000 cells. We refer to this as *predicting* from environmental to biological space. These mappings are shown in Section 20.2.2 Appendix Fig C. We see that the seasonal range in chlorophyll A (chl_a), though not strongly influential, may have a strong influence on the resulting biological space, because its extrapolated range is 3 times wider than its observed range. Issues such as this can be readily identified from Section 20.2.2 Appendix Fig D, which is a simple diagnostic plot. Predictors lying far above the 45 degree line will be extrapolated in biological space; chl_a is the most severe example, but depth, carbonate, turbidity and EPOC are also problematic.

The resulting 744,000×29 matrix of points in biological space can be represented using principal components analysis (PCA) and plotting the first two components (Figure 11.2, bottom). The scale is arbitrary and is not shown; only the relative position of points is important. Nearby points are similar

in composition and more distant points are less similar. The main components driving predicted biological composition are given by the predictors denoted by arrows emanating from the mode of the distribution. A colour wheel is draped over the distribution of points, conformally distorted so that the centre of the wheel aligns with the mode. The colours have been rotated so that green aligns with increasing chl_a and orange with increasing temperature (T).

Applying this colour mapping of (the first two components) of biological space to the mapped region results in Figure 11.3. The wide band of the deep EEZ (blue-cyan) correspond to a relatively small region in biological space and the narrow area at the top of the slope (orange-yellow) corresponds to a larger region in biological space, suggesting more compositional variation. The red part of biological space corresponds to the sloping part in the central GAB, approximately aligned with the Ceduna and Eyre Terraces. The colour key is not ideal for showing the variation in composition in this region.

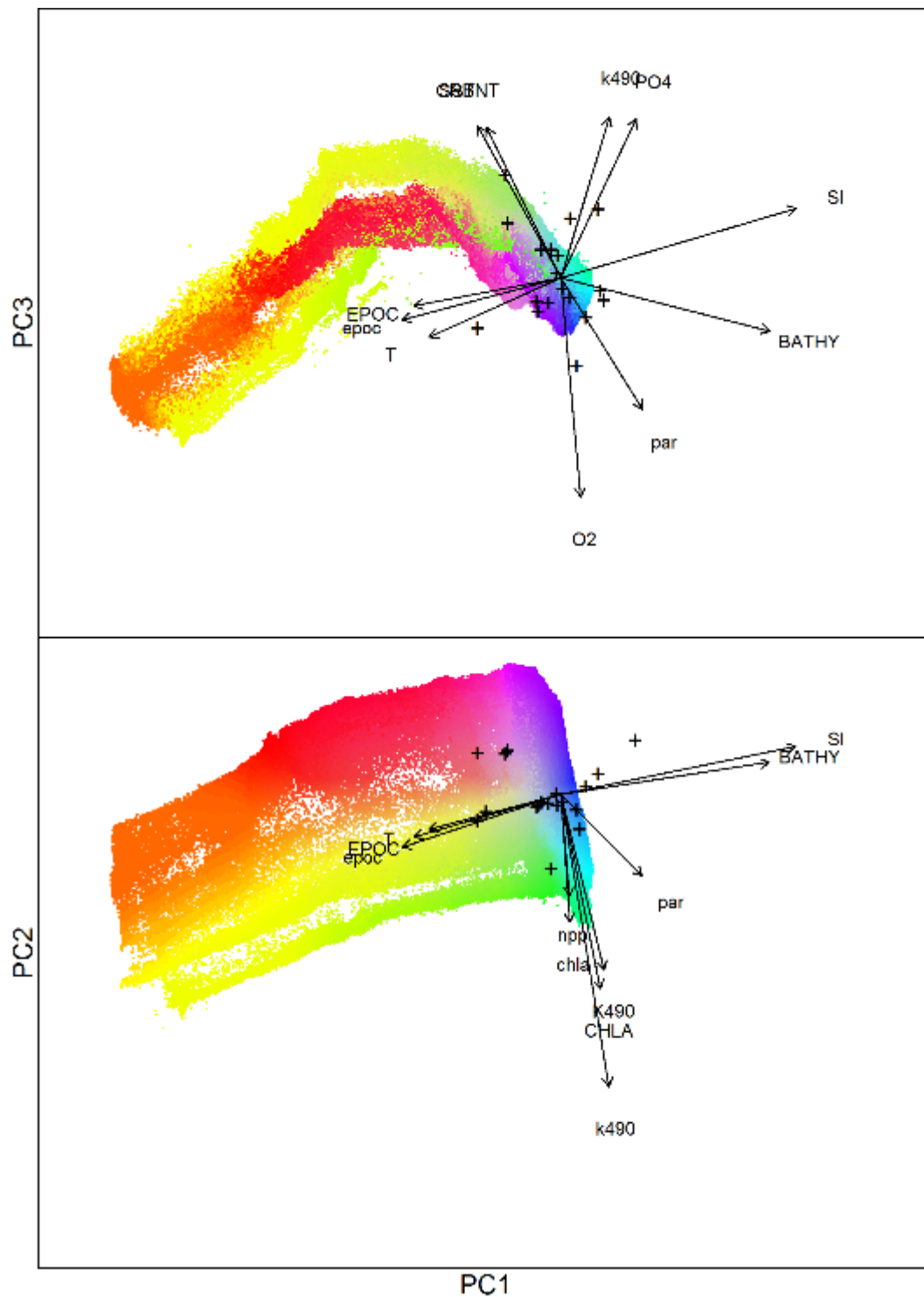


Figure 11.2 Biplots of the first three principal components of biological space, accounting for 85% of the variation over the 29 dimensions: (bottom) second vs first principal components, (top) third vs first principal components. The arrows indicate the projection of the transformed predictor axes in the relevant dimensions; crosses indicate other predictors with smaller component in the relevant dimensions. In the bottom panel, a distorted colour wheel is used with green aligning with chl a, orange with T, and grey covering the modal region. This same colour key is used in the top panel. The coincident labels in the top panel are SST and CRBNT. See Appendix 2 for the key to predictor abbreviations.

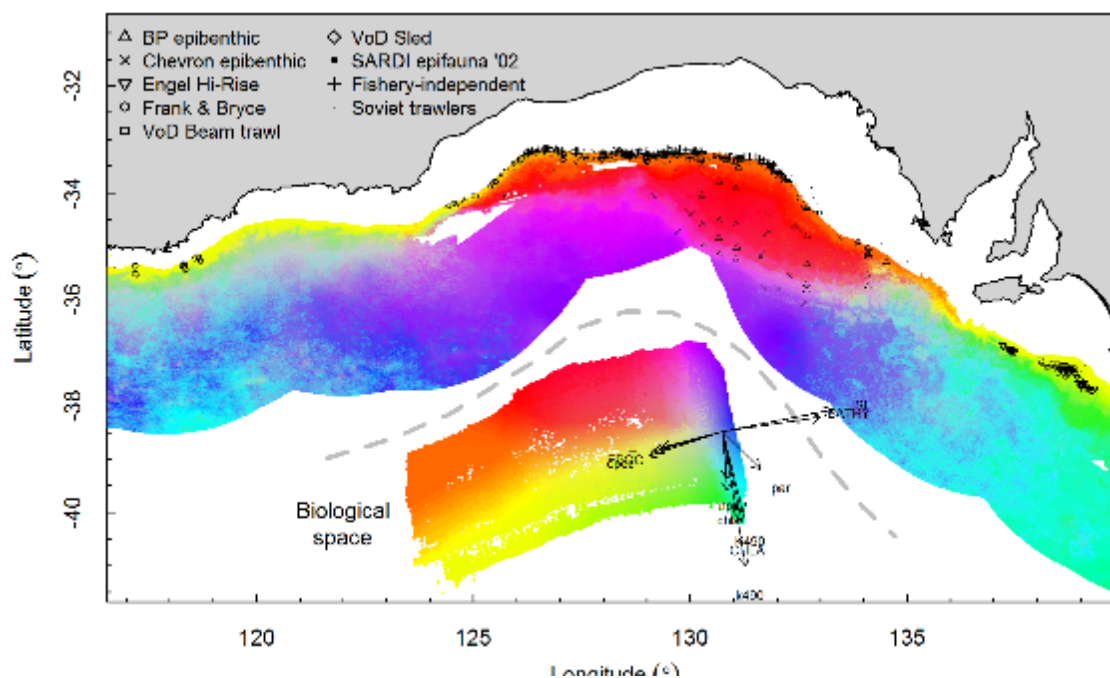


Figure 11.3 Biological space mapped geographically using the colour key from the bi-plot of Figure 11.2. The bi-plot is reproduced at the bottom (separated by the dashed line). Site locations are also indicated using symbols to represent which surveys were carried out at each site.

Partitioning biological space into assemblages

The MRT analysis (Section 20.2.2 Appendix Fig E) implies that there should be at least 4 assemblages (e.g. from the Chevron survey's MRT), and the mean F -ratio (Section 20.2.2 Appendix Fig F) suggests 10 assemblages, which seems to be a manageable number. The resulting assemblage map is shown in Figure 11.4.

Note that the partitioning is carried out in the full 29-dimensional biological space, not just the first two components. This is why some clusters in biological space do not seem very distinct. It also explains why assemblages 1 and 4 are distinct even though they appear adjacent in the bi-plot; Figure 11.2 (*top*) shows they are separated in the third component.

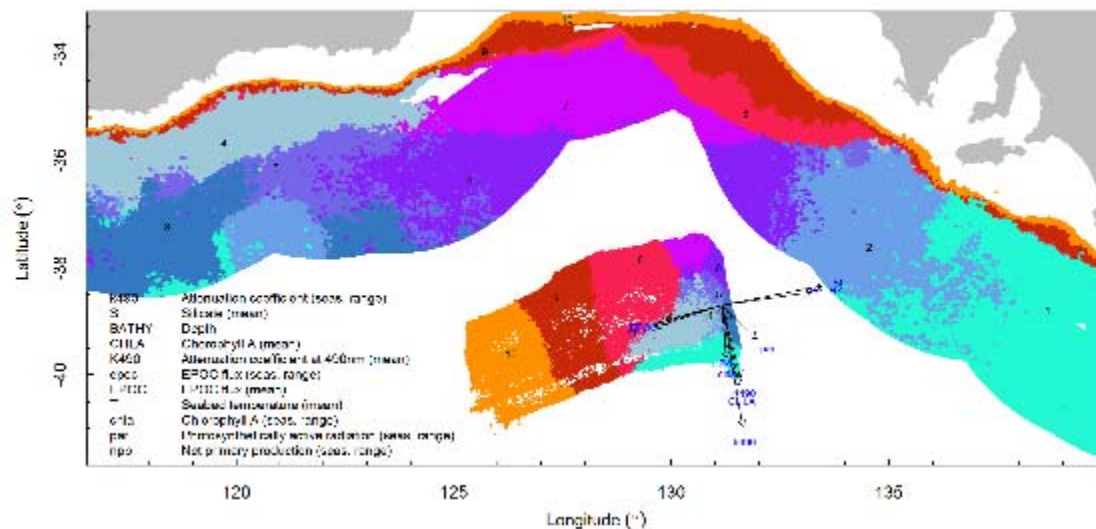


Figure 11.4 Same as Figure 11.3 but with biological space partitioned into 10 assemblages. Assemblage labels are drawn at the medoid cell (in biological space), and the colour of this cell is applied to the whole assemblage.

The analysis has partitioned the environment into 10 assemblages, among which composition is heterogeneous, and within which each composition is relatively homogeneous. The boxplots in Figure 11.5 describe the environmental make-up of each assemblage, which are summarised in descriptions below. A dagger (†) indicates the assemblage is distinct in that environment, in the sense that the interquartile range does not overlap with that of any of the other 9 assemblages.

Environmental description of the assemblages

- Assemblage 1 (170K km²): average depth (4910–5380 m), high mean turbidity (K490: 0.046–0.050 m⁻¹)†, high range of photosynthetically active radiation (par: 46.6–48.3 E m⁻²day⁻¹)†, high mean silicate (SI: 123.9–127.0 μM), low mean sea surface temperature (SST: 14.8–15.9 °C), high range of chlorophyll A (chlA: 0.310–0.354 mg m⁻³), high range of net primary production (npp: 612.3–672.7 mg C m⁻²day⁻¹), high range of turbidity (k490: 0.06–0.06 m⁻¹), high mean chlorophyll A (CHLA: 0.231–0.265 mg m⁻³).
- Assemblage 2 (132K km²): average depth (5050–5530 m), low mean sea surface temperature (SST: 15.8–16.6 °C), low mean exported particulate organic carbon (EPOC: 2.9–3.2 mg C m⁻²day⁻¹), high mean turbidity (K490: 0.041–0.044 m⁻¹).

- Assemblage 3 (87K km²): average depth (5020–5410 m), low sediment carbonate (CRBNT: 21–39 % CaCO₃)†, high mean silicate (SI: 125–126 μM), low mean water temperature at the seabed (T: 0.9–0.9 °C), high range of photosynthetically active radiation (par: 45.4–46.4 E m⁻²day⁻¹).
- Assemblage 4 (90K km²): average depth (3640–4620 m), high range of turbidity (k490: 0.05–0.06 m⁻¹).
- Assemblage 5 (69K km²): average depth (4840–5360 m), low mean water temperature at the seabed (T: 0.9–0.9 °C), low range of exported particulate organic carbon (epoc: 3.4–3.6 mg C m⁻²day⁻¹).
- Assemblage 6 (107K km²): deep (5170–5530 m), high mean phosphate (PO₄: 2.33–2.35 μM), low sediment carbonate (CRBNT: 43–67 %CaCO₃), low mean water temperature at the seabed (T: 0.9–0.9 °C), low mean exported particulate organic carbon (EPOC: 2.7–2.9 mg C m⁻²day⁻¹), low range of exported particulate organic carbon (epoc: 3.2–3.4 mg C m⁻²day⁻¹), low range of chlorophyll A (chla: 0.243–0.259 mg m⁻³), low range of turbidity (k490: 0.05–0.05 m⁻¹), high mean seabed oxygen (O₂: 4.83–4.86 mL L⁻¹).
- Assemblage 7 (96K km²): average depth (3570–4710 m), low range of chlorophyll A (chla: 0.236–0.251 mg m⁻³), low range of net primary production (npp: 464.0–480.9 mg C m⁻²day⁻¹), low range of turbidity (k490: 0.05–0.05 m⁻¹), low mean chlorophyll A (CHLA: 0.149–0.155 mg m⁻³), low mean turbidity (K490: 0.034–0.035 m⁻¹).
- Assemblage 8 (44K km²): moderately shallow (1500–1940 m)†, moderately low mean silicate (SI: 75.0–92.8 μM)†, moderately high mean water temperature at the seabed (T: 2.3–2.7 °C)†, moderately high mean exported particulate organic carbon (EPOC: 6.0–7.4 mg C m⁻²day⁻¹)†, moderately high range of exported particulate organic carbon (epoc: 6.8–8.3 mg C m⁻²day⁻¹)†, low mean seabed oxygen (O₂: 3.80–3.86 mL L⁻¹)†, high mean phosphate (PO₄: 2.33–2.47 μM), low range of net primary production (npp: 477.2–521.5 mg C m⁻²day⁻¹), low mean chlorophyll A (CHLA: 0.154–0.175 mg m⁻³), low mean turbidity (K490: 0.035–0.038 m⁻¹).
- Assemblage 9 (75K km²): shallow (790–1200 m)†, low mean silicate (SI: 21.0–62.1 μM)†, high mean water temperature at the seabed (T: 3.2–6.4 °C)†, high mean exported particulate organic carbon (EPOC: 8.9–12.8 mg C m⁻²day⁻¹)†, high range of exported particulate organic carbon (epoc: 10.0–14.9 mg C m⁻²day⁻¹)†, low mean phosphate (PO₄: 1.76–2.35 μM), high mean sea surface temperature (SST: 17.8–18.3 °C), high sediment carbonate

(CRBNT: 85–90 %CaCO₃), low mean seabed oxygen (O₂: 4.05–4.65 mL L⁻¹), low range of photosynthetically active radiation (par: 42.3–43.5 E m⁻²day⁻¹).

- Assemblage 10 (28K km²): shallow (190–400 m)†, low mean silicate (SI: 1.4–3.6 μM)†, low mean phosphate (PO₄: 0.42–0.96 μM)†, high mean water temperature at the seabed (T: 10.3–13.8 °C)†, high mean exported particulate organic carbon (EPOC: 21.8–39.9 mg C m⁻²day⁻¹)†, high range of exported particulate organic carbon (epoc: 25.5–44.8 mg C m⁻²day⁻¹)†, high mean seabed oxygen (O₂: 5.40–5.48 mL L⁻¹)†, high mean sea surface temperature (SST: 17.7–18.7 °C), high sediment carbonate (CRBNT: 87–92 %CaCO₃), high range of chlorophyll A (chla: 0.277–0.340 mg m⁻³), high range of net primary production (npp: 582.2–635.8 mg C m⁻²day⁻¹), high mean chlorophyll A (CHLA: 0.193–0.234 mg m⁻³), low range of photosynthetically active radiation (par: 41.8–44.4 E m⁻²day⁻¹).

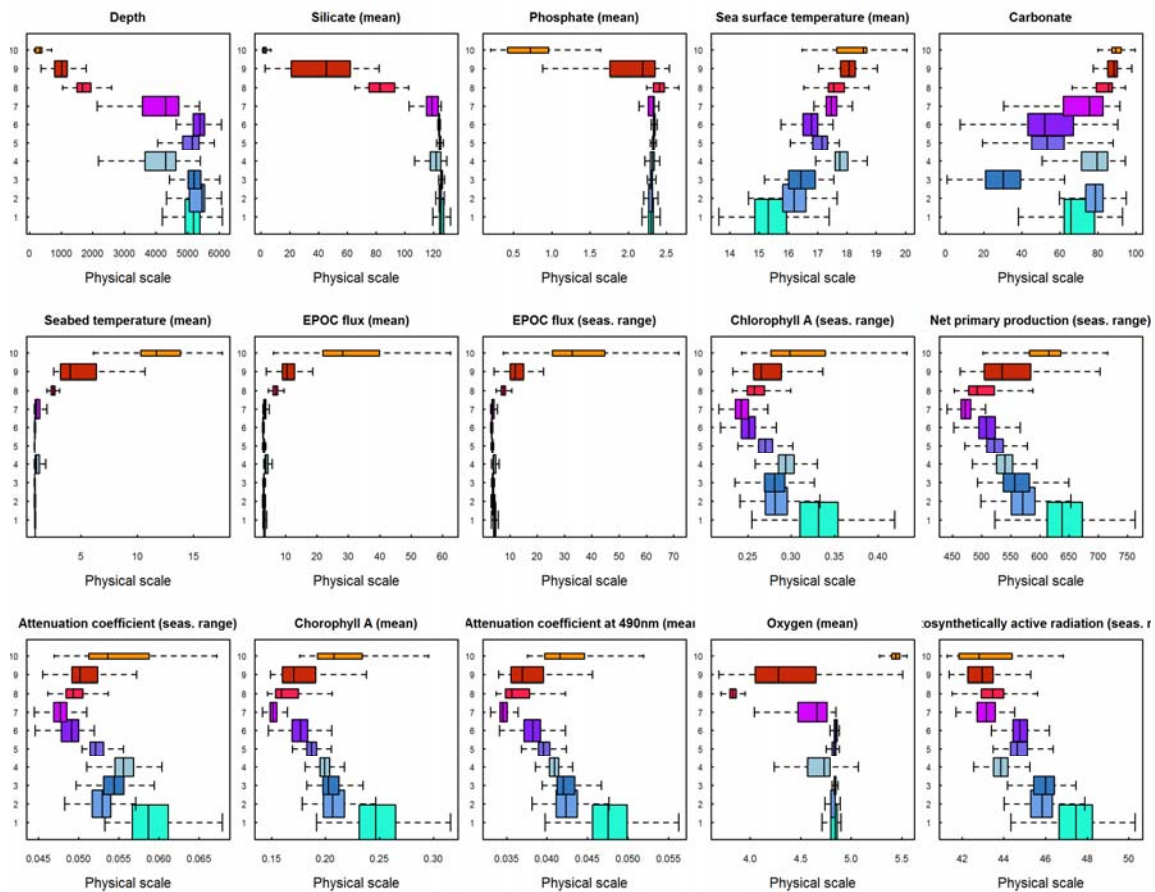


Figure 11.5 Boxplots of the most influential predictors over the 10 assemblages. The width each box is proportional to the area of the assemblage. The same colour key is used as in Figure 11.4.

Assessing the degree of extrapolation and uncertainty

A generalized linear model was fit to Bray-Curtis distance between all pairs of sites within each survey, with appropriate weighting. Both biological and geographical distance were considered as covariates, but geographical distance did not prove significant. The fitted relationship is shown in Section 20.2.2 Appendix Fig G.

Using this to predict Bray-Curtis distance to the 'nearest' site for all grids results in Figure 11.6. We see that the remotest grids are in the east, corresponding to assemblage 1 which has high chla. Areas along the shelf edge and on the central slope are the least dissimilar to observed sites.

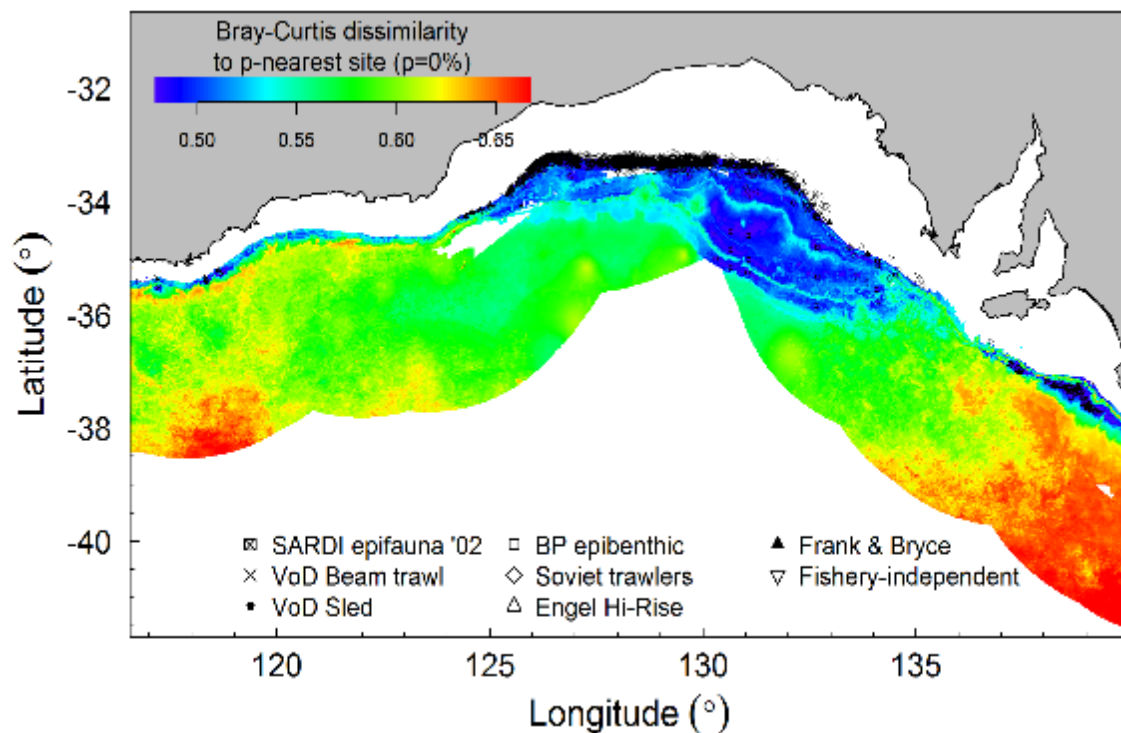


Figure 11.6 Predicted Bray-Curtis distance to the nearest site in biological space.

12 Examining metrics for benthic biological indicators in the context of ecological monitoring for oil and gas exploratory activities in the deep GAB

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12.1 Introduction

12.1.1 Scope of work

We have used our GABRP project field data in conjunction with a review of scientific and grey literature to evaluate and identify possible benthic biological indicators for future monitoring of ecological effects stemming from anthropogenic activities in the deep GAB, with a focus on oil and gas related activities. Context is provided by a summary assessment of existing management objectives for the GAB (Section 13). Our literature review focusses on studies with a broad overview of marine ecosystem monitoring, on studies with similar ecological and operational characteristics to the GAB (deep, poorly known benthic ecosystems), and on the potential impacts resulting from industry activity during exploration and early stages of development. We also consider recent Australian studies that identify indicators and essential variables for understanding the broader impacts of anthropogenic ‘pressures’ on marine ecosystems (e.g. Hayes et al., 2015).

12.1.2 Identifying indicators and variables for marine ecosystems

Scientific interest in indicators of change in marine ecosystems has increased rapidly in response to national and international policy requirements for ecologically sustainable development, and societal demands for ecosystem-health reporting (Hayes et al., 2012). For the Australian government, these imperatives create a need to assess the status of marine ecosystems at a variety of spatial and temporal scales. These include local to regional-scale assessments associated with particular anthropogenic activities, e.g. industrial development such as oil and gas extraction within individual or clusters of lease blocks, and national-scale state of the environment reporting to meet national and international obligations (Hayes et al., 2012). Australia’s planned implementation of a large network of Commonwealth Marine Reserves (CMRs) and the identification of ‘Key Ecological Features’ (KEF) in the marine environment bring both the need and opportunity to assess status and changes in the health of marine ecosystems.

Ecological indicators are a key element of monitoring for assessing and reporting environmental changes, but deciding what variables and indicators should be measured is difficult (Hayes et al., 2015). Thus, whilst there are many candidate biological variables, there is little consensus on what to use because biological and ecological characteristics are complex, temporally and spatially variable

in importance, and their interactions not well-understood (Fischer and Grimes, 2012). In response to the Australian Government's requirement to monitor marine ecosystem health, Hayes et al. (2015) recommended a process to identify biological indicators with a Driver Pressure State Impact Response (DPSIR) framework. The novel aspects of their methodology were, most notably, a focus on nationally or regionally important systems; accommodating uncertainty about what threatens these systems and how they might respond to these threats; and the emergence of essential variables as common indicators for separate systems when the process was applied at national or international scales.

Our work to identify biological indicators refers to this national-scale work to provide context for our focus on the ecosystem and activities relevant to the GABRP, i.e. pressures on deep benthic ecosystems of the GAB stemming from oil and gas industry activities.

12.1.3 Relevant characteristics of the deep GAB

Australia's deep GAB is characterised by an anticipated increase in oil and gas exploration, and a near-absence of information about the benthic ecosystems of mid- and lower continental slope depths (~1,000-3,000 m) where oil and gas exploration will be focussed (Figure 12.1). Thus, the species composition and biodiversity characteristics (e.g. richness, abundance, biogeography, and endemism) of GAB deep benthic biota (epifauna, infauna and microbial assemblages) are poorly known in all habitats, and, prior to the GABRP, virtually nothing was known about biota in any habitat below about 1,500 m depth (Rogers et al., 2013).

Exploration leases EPP 37-40 are located on the sea-ward margin of the Ceduna Terrace at depths >1,000 m, with the exception of EPP37 which reaches onto the shelf-break (Figure 12.1). The Ceduna Terrace is one of two gently sloping, marginal terraces forming the continental slope of the central GAB; they are flanked to the east and west by steep narrow slope sections, incised by numerous canyons (Rogers et al., 2013). Muddy oozes of biogenic origins dominate the sediments of the GAB continental slope and rise (Rogers et al., 2013). The physical oceanography on the GAB shelf is dominated by the eastward flowing Leeuwin Current. On the GAB slope, the westward flowing Flinders Current (strongest at ~600 m depth) and meso-scale eddies are the main oceanographic features (Rogers et al., 2013).

The importance of the first systematic surveys of benthic fauna made by the GABRP is particularly well-illustrated by two characteristics of the deep GAB. First, that oil and gas lease areas extend across and are adjacent to areas of conservation significance as determined by the location of CMRs and KEFs in the Southwest Marine Region (SWMR) (Figure 12.2). But second, that the conservation values generally attributed to shallow GAB waters (i.e. high biodiversity and high endemism), and

the stated conservation values for CMRs and KEFs (e.g. benthic invertebrate communities of the eastern GAB), are untested in deep water (Rogers et al., 2013). Anthropogenic pressures listed for the SWMR include physical habitat modification and oil spills (DSWEPaC, 2012), but until now it has not been possible to assess the implications of oil and gas exploration activities in the deep GAB.

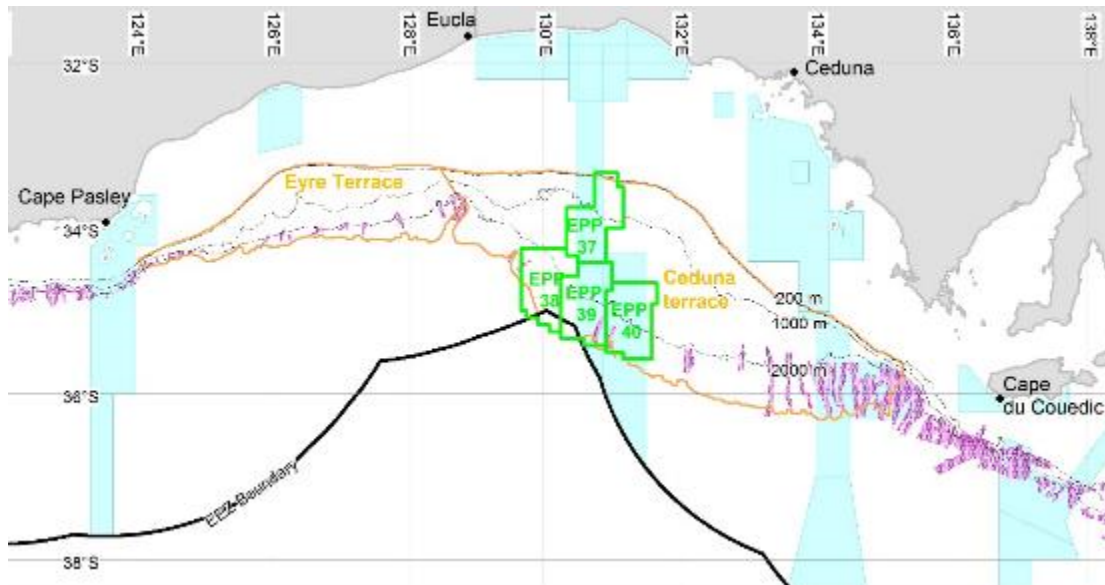


Figure 12.1 Location of the BP exploration leases (green outlines and labels) and Commonwealth Marine Reserves (blue fill) within the Great Australian Bight (GAB) showing the 200 m 1000 m and 2000 m isobaths, and the main geomorphic features: terraces (orange outline and names), and canyons (pink hashed).

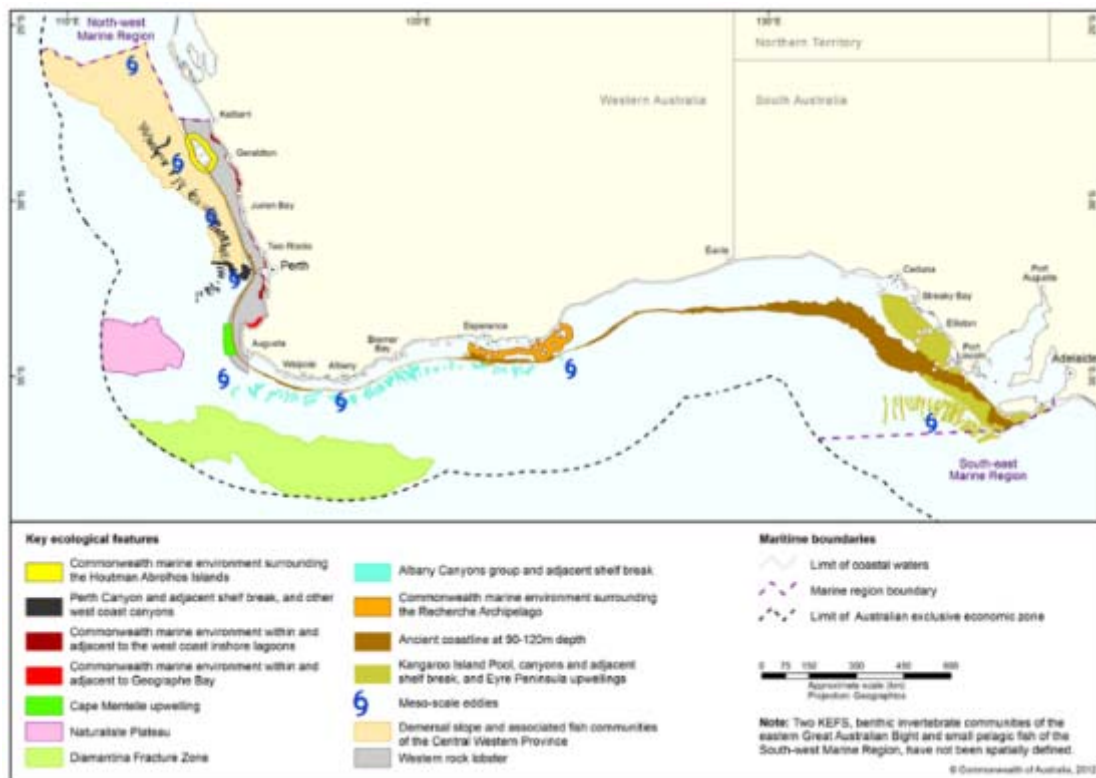


Figure 12.2 Locations of Key Ecological Features of the Southwest Marine Planning Region (DEE, 2017).

12.2 Ecological indicators and metrics

12.2.1 Review: indicators

The many published descriptions and definitions of ecological indicators were summarised by Hayes et al. (2008), from several key sources (Table 12.1). Despite the variety of definitions, Hayes et al. (2015) concluded that the three key roles of ecological indicators are to: (1) reduce the complexity of real-world systems to a small set of key characteristics that retain the information that is essential for assessing management performance; (2) track changes in the “state of the environment”; and (3) communicate outcomes to a wider audience. However, they also note that reducing the complicated dynamics of natural ecosystems to a small number of indicators remains a significant scientific challenge. Indicators should be chosen based upon defined criteria, conceptual models linking indicators to pressures and drivers, and defined strategic goals and ecological or management objectives (Boldt et al., 2014).

Identifying ecological indicators can be approached empirically and/or theoretically (Niemeijer, 2002). Empirical approaches typically rely on large and/or time series datasets, which either compare the biological and physical conditions of “pristine” reference sites to “impacted sites” or statistically identify ecosystem responses to sustained anthropogenic activity. Empirical methods typically use multivariate statistics to reduce a large set of potential indicators (ecosystem variables)

to the smallest set that best explains variations in space and time between impact sites/reference sites and ecosystem variables and human activities. Hayes et al. (2008) see their principal advantage as relying on data to 'tell the story' and not requiring detailed understanding of the ecosystem, or the cause and effect processes that link anthropogenic activity and ecosystem response. However, the clear problem with an empirical approach is the paucity of ecological data - through time and over spatial scales relevant to policy makers and managers. Hayes et al. (2008) cite other potential problems with the empirical approach as including the difficulty of identifying reference sites (Frost et al., 1992; ICES, 2005), a lack of power to detect changes within policy relevant timeframes (Nicholson and Jennings, 2004) and the inability to assign cause and effect to observed changes without substantial experimentation. It may also be difficult to compare indicators across studies that use different ordination or regression methods, or across different spatial/temporal scales without additional experimentation or mechanistic explanations for the observed changes in the system.

A top-down perspective on ecological indicators (Hayes et al., 2015) based on a literature review of system-scale indicators (excluding local-scale features such as estuaries) identified 589 indicator recommendations in 44 references (see their Appendix Table 2). They found the great majority of indicators were referenced only once or twice and concluded that the literature appears to contain very few common recommendations – although noted that use of more standardised terms would identify a greater degree of consensus. Notwithstanding, their review pointed to 10 candidate essential variables each of which were recommended on more than 5 independent occasions: five biological - (i) Fish abundance/biomass (total catch), (ii) Chlorophyll a Concentration, (iii) Harmful Algal Bloom (frequency/extent), (iv) Number of invasive species; and (v) Threatened/Endangered/Protected (number/percent species); and five physical - (vi) Area of key/important/main habitat, (vii) Area of protected habitat, (viii) Dissolved oxygen concentration, (ix) Nitrogen/Nitrate concentration, (x) Phosphorous/Phosphate concentration.

Table 12.1 Definitions of ecological indicators in the scientific literature – Table 1 of Hayes et al. (2012).

Definition	Source
A parameter, or a value derived from parameters, which points to, provides information about, or describes the state of a phenomena/environment/area, with a significance extending beyond that directly associated with a parameter value	OECD, 1993
Indicators provide information on matters of wider significance than what is actually measured or make perceptible a trend or phenomenon that is not immediately detectable	Hammond et al., 1995
Physical, chemical, biological or socio-economic measures that best represent the key elements of a complex ecosystem or environmental issue. An indicator is embedded in a well developed interpretive framework and has meaning beyond the measure that it represents	Saunders et al, 1998
A variable, pointer or index related to a criterion. Its fluctuation reveals the variations in those key elements of sustainability in the ecosystem, the fishery resource or the sector and social and economic well-being	FAO, 1999
Pointers that can be used to reveal and monitor the conditions and trends in the fishery sector	Garcia and Staples, 2000
An indicator is a sign or signal that relays a complex message, potentially from numerous sources, in a simplified manner. An ecological indicator is a measure, an index of measures or model, that characterises an ecosystem or one of its critical components. An indicator may reflect biological, chemical or physical attributes of ecological condition	Jackson et al., 2000
Two defining characteristics: 1) quantify information so its significance is more readily apparent; and 2) simplify information about complex phenomena to improve communication	Pajak, 2000
Measurable characteristics of the structure (e.g. genetic, population, habitat and landscape pattern), composition (e.g. genes, species, populations, communities and landscape types) or function (e.g. genetic, demographic/life history, ecosystem and landscape disturbance processes) of ecological systems	Niemi and McDonald, 2004
Variables, pointers or indices of a phenomena	Jennings, 2005
Indicators are quantitative/qualitative statements or measured/observed parameters that can be used to describe existing situations and measure changes or trends over time. Their three main functions are simplification, quantification and communication.	IOC, 2006
A significant physical, chemical, biological, social or economic variable which can be measured in a defined way for management purposes	CSIRO guidebook to environmental indicators ²

Hayes et al. (2015) demonstrated a process to identify ecological indicators that starts with qualitative models to identify the pathways by which known pressures impact conservation values, and identifies indicators that are predicted to react consistently despite model and pressure uncertainty. Essential variables emerged from their process as the indicators that were common to different systems (KEFs in their study) when the process was applied at national or larger scales. The process did not apply selection criteria to candidate indicators, but helps meet popular criteria (as identified in their Table 3 – see Table 12.2). In effect, they proposed that it is premature to identify

essential biological variables without first describing the location, processes and components of the essential biological systems that require measurement.

Table 12.2 Summary of popular criteria used to select indicators from a list of possible candidates. Each was recommended in ≥ 5 studies in references each cited ≥ 150 times – Table 3 of Hayes et al. (2015).

Perspective	Description
1. Scientific	1.1 Strong scientific and conceptual basis, based on well defined/validated links 1.2 Ecologically significant, reflects on a fundamental process or highly valued aspect of the ecosystem
2. Historical	2.1 Builds on existing baseline or historical records of comparative data
3. Systems	3.1 Sensitive to pressures/stresses within policy relevant time frames 3.2 Known/predictable responses to stress, discriminatory, able to disentangle the effect of other factors
4. Intrinsic	4.1 Easy to measure repeatedly 4.2 Has good statistical properties that allow unambiguous interpretation, low variability in response
5. Logistic	5.1 Feasible, cost effective, information benefits outweigh collection costs 5.2 Achievable in terms of the available resources
6. Policy	6.1 Easily understood by target audience/stakeholders 6.2 Meaningful to managers, addresses management objectives, has well established links to specific management practice or interventions 6.3 Reflects social and political interests, and target audience at hand 6.4 Predicts changes that can be averted by management action 6.5 Responsive, provides quick and reliable feedback on the effects of management intervention

At a finer scale, Zettler et al. (2013) warns against the use of static indicator species, unless species are identified that have known sensitivity or tolerance to either natural or human-induced stressors, as this does not account for possible shifts in tolerance along natural environmental gradients and between biogeographic regions.

Guidelines for post-spill monitoring of oil and gas platforms in the UK were developed after, and in response to, the Macondo incident and recommend potential indicators to be examined as bivalves, and the diversity and abundance of macrofauna (particularly amphipods and opportunistic polychaetes), and meiofauna (nematodes and copepods) (Law et al., 2011).

A post-spill monitoring program for north-west shelf platforms in the 'Wheatstone Project' in Australia has been developed by Chevron (Chevron, 2013). They list potential biological indicators as several epifaunal groups such as corals and seagrasses in shallower water, and sponges and

seawhips in deeper water. Identifications of deeper water epifauna from video would use the CATAMI classification for identifying morpho-taxa (Edwards, 2013). Infaunal community data 'is not considered to be of significant value for response actions' (Chevron, 2013).

Table 12.3 Criteria used by benthic experts to rank and categorise samples - Table 4 of Weisberg et al. (2008).

Criteria	Importance	S.D.	N
Dominance by tolerant indicator taxa	1.0	0.0	9
Presence of sensitive indicator taxa	1.2	0.4	9
Species richness (number of taxa)	1.4	0.7	9
Abundance of, or dominance by, specific higher level taxa	2.7	1.2	8
Total abundance	2.8	1.0	9
Presence of nonindigenous species	3.6	1.4	6
Diverse functional and feeding groups	3.7	1.6	4

Importance is the average importance for all experts, where: 1, very important; 2, important, but secondary; 3, marginally important; 4, useful, only to interpret the other factors; 5, not used. N is the number of experts that used the criterion.

Another, but finer grain, review of indicators from benthic macrofauna was based on expert selection (Weisberg et al., 2008; Table 12.3), testing expert 'best professional judgment' (BPJ) of environmental condition of 35 sites in California. There was strong agreement in the informative taxa chosen to determine condition of sites over a gradient of contamination exposure, and experts consistently identified polychaetes and oligochaetes as important pollution tolerant, and ophiuroids and amphipods as pollution sensitive, indicator taxa. However, a review of the effects of pollutants on polychaetes (Dean, 2008) shows that this group of animals differ greatly in responses to pollutants, and can be used as positive or negative indicators, but only within the limits of the specific sampling programs. As mentioned above, generalisations of taxon responses need to be viewed with caution (Gage, 2001; Zettler et al., 2013). Dominant species of polychaetes vary from one geographical area to another, and no single species can be used to indicate whether an environment is stressed or otherwise (Dean, 2008). In a study on the effects of shipping oil spills on shallow water benthos, polychaetes showed little change, however amphipods showed significant decreases and took four years to slowly recover (Gesteira and Dauvin, 2000). In this study, there was no proliferation of opportunistic species. Elsewhere, polychaetes have been shown to monopolise substrate in unfavourable conditions (Campbell et al., 2010). It has been suggested that a polychaete/amphipod ratio be adopted to reflect changes over time in the benthos and that a detailed knowledge of the particular benthic community is needed in order to identify effects of pollution events (Gesteira and Dauvin, 2000). A summary of particular taxa affected by human pressures in a variety of selected studies is shown in Table 12.4.

Table 12.4 Summary of selected studies that identified taxa that may be utilised as indicators for monitoring of the effects of oil and gas related pressures on marine environments.

Incident	Depth, & distance from source	Taxa	Effect / main conclusion	Reference
Macondo well blowout	290 – 2600 m deep 11 km SW of well	Epifauna – Corals (Scleractinia)	46% of corals showed impacts of >90% to colony; 3-4 months after well was capped	(White et al. 2012, Fisher et al. 2014a)
Macondo well blowout	55–75 m & 500- 1750	Epifauna – Crustacea (Decapods)	Decline in abundance and diversity and change in dominant species	(Felder et al. 2014)
Drilling (Minerva, Victoria, Australia)	60 m	Macrofauna	Sig. decrease in some fauna up to 4 months post event. Modified community up to 11 months after event.	(Currie and Isaacs 2005)
Drilling waste (Oil, water and synthetic fluids)	Various 29 m – 213 m	Macrofauna and mussels.	Impact out to 6km for up to decades (when oil used). Impact to 100 – 1000 m from drilling (when water or synthetic fluids used). Loss of filter feeders, increase in polychaetes and deposit feeders.	(Ellis et al. 2012)(review)
Drilling discharges (fluids and muds) Venuzuela	190m and 350 m	Polychaetes, bivalves, sipunculids, crustacea and nematodes	Correlation between the changed chemistry of the sediments and changes in macrobenthos. Recovery of abundance of macrofauna was uneven amongst taxa. Polychaetes responding better.	(Garcia et al. 2011)
Platform – long term production	Within 100 m of platform	Macrofauna	increase in density of polychaetes and nematodes/ decrease in harpacticoids and amphipods	(Montagna et al. 1996)
Pollution (many types, inc. oil)	Various	Polychaetes	Differ greatly in responses. Can be used as positive or negative indicators, but only within the limits of the specific sampling programs.	(Dean 2008)
Shipping oil spills (<i>Amoco Cadiz</i> and <i>Aegean Sea</i>)	Shallow (Infralittoral zone)	Macrofauna	Disappearance and slow recovery of amphipods. Little effect on polychaetes.	(Gesteira and Dauvin 2000)
Pollution studies (general)	Shallow (intratidal/ sublittoral)	Meiofauna: Ratio of nematodes to copepods	Nematode:Copepod ratios were always extremely high on polluted beaches; it has potential for monitoring organic pollution of sandy beaches.	(Raffaelli and Mason 1981, Raffaelli 1987)
Long-term monitoring (Prince William sound & Gulf of Alaska)	200-4000 m deep	Mussels & sediments	Long-term monitoring of mussels and sediments for petroleum hydrocarbons to provide benchmark for assessing the ongoing impacts of routine tanker and terminal operations.	(ACAC 2015)
Drilling waste (synthetic-based mud discharge) Brazil	890 m deep	Meiofauna and nematodes	Significant decreases in the meiofauna density and number of taxa and nematode density and richness; significant increase in relative abundances of non-selective deposit-feeding nematodes, particularly the genus <i>Sabatieria</i> one month after drilling commenced. Multivariate structure of meiofauna community still significantly different after 12 months, but univariate measures returned to background levels	(Netto et al. 2009)
Diesel Oil spill	Shallow (mangrove)	Macrofauna by type (sessile, mobile, feeding feeders)	Samples from animals with different biological requirements were collected in order to monitor polycyclic aromatic hydrocarbons concentrations. Barnacles are suggested as a sentinel species.	(Soares-Gomes et al. 2010)

Pollution impacts may also be measured based on bioaccumulation of chemicals in a variety of organisms acting as indicators. Organisms used for bioassays range from microbes (Lu et al., 2012), to crustaceans (Svendsen et al., 2007; Soares-Gomes et al., 2010), echinoderms (Schafer and Kohler, 2009), bivalves (Pereira et al., 2011), fish (van der Oost et al., 2003 ; Budzinski et al., 2004; Salamanca et al., 2008) and seabirds (Oropesa et al., 2007). In addition, Mearns et al. (2011; 2013) reviewed literature describing pollution effects on marine organisms from 2010 and 2012 respectively (and see Section 12.5 below).

Bioassays determining toxicity, uptake and bioaccumulation of contaminants may also be used as metrics for monitoring. Long-term effects of hydrocarbons in the environment are dependent on their bioavailability, which may change as they naturally degrade. Studies examining various aspects of bioavailability include: (van der Oost et al., 2003; Neff et al., 2006; Bellas et al., 2008; Springman et al., 2008; Wardlaw et al., 2008; Brack et al., 2009; Benedetti et al., 2012; Klok et al., 2012; Lindgren et al., 2014;).

12.2.2 Review: metrics

A variety of metrics are available for assessing indicators (biocriteria *sensu* Weisberg et al. 2008). Similar to indicators, metrics need to be tailored to the objectives of the monitoring project, and go hand in hand with the sampling design and methods (Peterson et al., 2001; Hammerstrom et al., 2012;). Both univariate metrics (e.g. species richness, densities or relative densities of indicator taxa, diversity indices) and multivariate metrics (comparison of community compositions) have been used for monitoring effects of human impacts (see Table 12.4).

Changes due to impacts and/or recovery are often subtle, and thus signals of change are difficult to detect at statistically robust levels. *Weight of Evidence* (WoE) approaches based on multiple *Lines of Evidence* (LoE) can be applied to boost signals of change (e.g. McDonald et al., 2007; Morales-Caselles et al., 2009; Piva et al., 2011; Benedetti et al., 2012).

Five different indices (Shannon-Wiener H' diversity, AMBI, m-AMBI, BENTIX, and BOPA) were compared for performance for assessing macrobenthic stress levels around off-shore platforms in Europe; BENTIX, H' and BOPA evaluated stress levels better than the others in the off-shore platform scenario (Spagnolo et al., 2014). Similarly, Dauvin et al. (2012) compared the results of four biotic indices: Shannon-Wiener H' diversity, AMBI and BO2A (index based on ecological groups), and ITI (index based on trophic groups), and the agreement of Best Professional Judgement (BPJ) on the assessment of ecological conditions. In addition, the use of '*sentinel species*', a particular species that by its presence or its relative abundance warns of possible imbalances in the surrounding environment or distortions in community functions, was also tested. There was little difference in

the ECOlogical Quality Status (EcoQS) assigned to sampling sites based on the objective indices, or the subjective assessment based on BPJ or sentinel species. Dauvin et al. (2012) propose that simple methods be used for diagnostic approaches. Where indices are employed, it is recommended that they be tested in, and calibrated for, the particular situation they are employed.

The abundance and proportion of tolerant and sensitive taxa are used to form benthic indices specific for geographical areas (Weisberg et al., 2008). For example, the AZTI Marine Biotic Index (AMBI) (Borja et al., 2000) was used to assess alterations in communities of soft-bottom marine benthic macrofauna caused by anthropogenic impacts in European estuarine and coastal environments, and this has been used/adapted in other places around the world (Cai et al., 2014; Muniz et al., 2005). However, reliance on indicator species alone can lead to misapplication when small numbers of individuals are present (Borja and Muxika, 2005).

Best Professional Judgement (BPJ) was put to the test by Weisberg et al. (2008). Nine experts were asked to rank sites of varying contamination exposure (Effects Range-Median quotient – ERMq) from unaffected to severely affected based on salinity, sediment texture, and species abundance information (seven parameters). Experts consistently used four parameters: dominance by tolerant taxa; presence of sensitive taxa; species richness, and total abundance. As mentioned in the previous Section, the experts consistently identified indicator species as tolerant or sensitive. Weisberg et al. (2008) found that expert assessments were quite consistent in classifying sites, and the biological parameters used most consistently correlated more highly with the expert ranking than the analytical measure of contamination exposure (ERMq).

Kropp (2004) observed that most studies of ecological communities in the sea have focused on defining community structure; however, the study of ecosystem functions, and especially the effects of anthropogenic activities on these functions, is also an important part of a benthic study. Structure is usually determined by obtaining a sample of the community and determining its constituent taxa. Measurements of function may include estimates of growth, reproduction, and development, or community processes, such as respiration and nutrient flux.

Below in Section 12.2.4 we outline examples of case studies comparing different indices, or where specific taxa and metrics were used.

12.2.3 Review: taxonomic sufficiency

Kropp (2004) observed that species-level analyses contain useful data about life-history patterns, reproductive strategies, and dispersal capabilities that can be used to anticipate impacts to communities, but more importantly, to gain insights into the potential for recovery from disturbance. Although achieving high quality and consistent taxonomic data can be difficult, it is

cautioned that restricting taxonomic identifications above a species level cannot provide the same knowledge about community structural and functional changes in response to disturbance. He cautions that when analyzing benthic samples, to use the best available taxonomy and analyze entire, discrete samples.

However, it is important to examine the effect of data aggregation on the ability to detect community changes. There was good correlation between analyses performed at taxonomic levels up to family (Vanderklift et al., 1996; Olsgard et al., 1997), but each level had a certain degree of unique information. Olsgard et al. (1997) also determined that the type of data transformation used during the analysis had more effect on the results than did the aggregation of the data, and recommended using intermediate transformations.

Gage (2001) further stressed that, with respect to studies of the deep sea, analyses done at higher taxonomic levels are premature, and that before any such approach is implemented, testing against baseline species-level data is necessary. Carney (1997) essentially agreed, arguing that to learn how important processes in the deep sea (resource partitioning, recruitment, species movements) relate at local and regional scales, the “highest quality taxonomy” must be employed. Rumohr and Karakassis (1999) stressed that the information contained in macrofaunal analyses includes more than that used in ordination analyses. Species-level analysis of faunal communities provides knowledge about community structural and functional changes in response to disturbance that is more biologically informative than that provided by higher-level analyses.

In some cases, the sample composition may determine the taxonomic level at which analyses are undertaken. Currie and Isaacs (2005) found that the species in their samples occurred at densities too low for individual analysis, and so species were pooled at higher taxonomic levels. In a review of papers on taxonomic sufficiency, Dauvin et al. (2003) conclude that: “*Cost effective and accurate littoral pollution monitoring requires only family-level identification of taxa, although in some cases it may be of interest to identify particular species whose presence or abundance is indicative of particular pollutant impacts*”. Similarly Giangrande et al. (2005) suggest that time can be saved in working at higher levels for the whole data set, but that fine levels should be used for select groups. Gesteira et al. (2003) consider that genus/family level identifications of soft-bottom macrofauna are still sufficient to detect spill effects. Similarly, Musco et al. (2011) found that family-level analysis is sufficient for routine, long-term monitoring; although, they recommend periodic analyses at a finer taxonomic level. Another consideration in determining the taxonomic level at which to undertake identification is the speed at which results can be obtained. Timely management responses require rapid turn-around of samples, whereas species level identification may take a year or more to achieve, while family level identifications tend to be much quicker. However, while acknowledging

that a lack of taxonomists is a determinate in not being able to identify samples to species, Gage (2001) warns that although ‘analysis based on taxonomic sufficiency above species level’ is done on shallower studies of stressed communities, it ‘is premature’ for deep-sea data, since not enough is known about the response of deepwater species to stress.

There is difficulty in achieving high quality and consistent taxonomic data for deep-sea faunas due to the high diversity of organisms in an underexplored marine habitat and the dearth of competent taxonomists to study it (Kropp 2004). In the study of deep-sea environments and their associated benthic communities, ensuring accurate identification of the constituent fauna is very difficult. Certainly one of the primary contributing factors is the very high diversity of the deep-sea benthos. Many species in the deep sea, especially those in relatively unexplored areas (e.g., West Africa, Brazil), are poorly known. Efforts to resolve the taxonomic uncertainties associated with the deep-sea fauna have not been well-supported, and competent taxonomists are becoming increasingly rare. Kropp (2004) provided an example from the 1980s when the U.S. Department of Interior, Minerals Management Service (MMS) sponsored a series of pioneering studies of the Atlantic Slope and Rise in advance of oil and gas exploration activities (Blake et al., 1985, 1987; Maciolek, et al., 1987a, b). These extensive studies, conducted at depths of about 255 m to 3500 m, found that about 58% of the species collected were undescribed (Grassle and Maciolek 1992; Gage 2001). Some 15 years after the last of the surveys was completed, most of the undescribed species remained so (N.J. Maciolek, personal communication, 2002).

12.2.4 Review: Case studies

Examples of biological indicators in the literature

- Macrofauna (infauna): community structure (Montagna et al., 1996; Currie and Isaacs, 2005; Santos et al., 2009; Manoukian et al., 2010; Garcia et al., 2011)
- Benthic macrofauna: correlation to change in sediment chemistry (Neff et al., 1989; Currie and Isaacs, 2005; Garcia et al., 2011)
- Meiofauna – especially nematodes and copepods: Community structure, density, number of taxa; for nematodes number of genera and trophic groups (Netto et al., 2009; Toldo and Ayup Zouain, 2009)
- Invertebrate megafaunal (Porifera/Cnidarians) density and diversity assessed in video or ROV transects (Gates and Jones, 2012; Jones et al., 2012a; 2012b)
- Infauna and bivalves (*Mytilus*): correlation to change in sediment chemistry and water quality (Gomiero et al., 2011)

Effects on benthos of drilling and platforms.

A review on effects of drilling from 72 platforms ranging 29 – 213 m in depth showed, in general, decreases in biodiversity and filter feeding communities (Ellis et al., 2012). Many effects were the result of oil being the fluid used for lubrication for the drill, this has now largely stopped, and water and synthetic fluids are used that have less negative effects on the benthos. Unanswered questions include long-term chronic effects, effects on deep-sea and hard-bottom habitats, and cumulative impacts of oil and gas activities (Ellis et al., 2012). Changes in sediment chemistry surrounding two offshore gas wells in Venezuela (Garcia et al., 2011) showed a strong correlation with changes in macrofauna (most pronounced in polychaetes and bivalves). However, these changes were no longer apparent after two years.

Infauna were examined pre and post drilling for gas at the Minerva platform (in 60 m depth) off Victoria, Australia (Currie and Isaacs, 2005). Abundances of two species, the crustacean *Apseudes* sp. 1 and polychaete *Prionospio coorilla*, decreased significantly at the well-head site immediately after drilling, but this change only lasted four months. A common bivalve, *Katlysia* sp., increased in abundance. Significant declines in the most abundant classes (Crustaceans and Polychaetes) of 45–73% were observed at all sites within a 100 m radius of the well-head following drilling, but reversed approximately four months after drilling ceased and were no longer detectable. However, there was some indication that there were modified communities at the well-head for more than 11 months following exploratory drilling.

Chronic exposure to contaminants from platforms associated with long-term production in the Gulf of Mexico showed localised effects within 100 m of the platform (Montagna et al., 1996). These were an increase in density of polychaetes and nematodes (indicating organic enrichment) and a decrease in harpacticoid copepods and amphipods (indicating toxicity) (Montagna et al., 1996).

Effects on benthos of Macondo oil rig blow out

Oil has toxic components and at low concentrations can have adverse effects on organisms (Coleman et al., 2003). A special issue on reviews of research following the rig blowout at the Macondo well site that expelled oil for 87 days in the Gulf of Mexico, was published in 2014. This includes useful reviews on deepwater corals (Fisher et al., 2014a), oceanic and sediment microbes (Joye et al., 2014), seaweeds and crustacea (Felder et al., 2014), as well as estuarine and land biology (Rabalais, 2014). Corals were found to be a good indicator of the effects of oil, with a direct effect on coral survival in situ over a two year period (White et al., 2012; Fisher et al., 2014b). Coral larval development may also have been compromised (Fisher et al., 2014a). Pre-spill studies on seaweeds and decapods at 55-80 m depth, and of decapods at 500-1750 m depth enabled comparisons with

the populations after the Macondo rig blow out. Decapods suffered a decline in abundance and diversity, and there were changes in species dominance (Felder et al., 2014). The decline in decapods may have been due to a loss of seagrass following the oil spill or possibly increases in degrading bacteria (Felder et al., 2014). There were rapid changes to microbial communities following the Macondo incident, including benthic microbes, and microbes that were responsible for the formation of flocculent 'marine snow' (Joye et al., 2014) bringing oil and dispersant to the deep-sea floor (Fisher et al., 2014a).

12.3 Ecological monitoring

12.3.1 Review: monitoring

A monitoring program gathers observations on indicators and evaluates their status and trends, particularly in relation to the predicted direction of change. This step is essential in closing the science loop and developing further understanding, and it also provides an opportunity to specify management response thresholds (Rees et al., 2008).

Indicators can be evaluated by comparison to measurements in baseline or unperturbed sites (reference-site approach) or by measuring their response along stress gradients using regression based methods (disturbance-gradient approach); in practice, elements of both approaches may be used (Hayes et al., 2015). Biocriteria (Weisberg et al., 2008) can be used to assess ecological integrity and can be developed using four approaches — comparison to historical conditions, comparison to present reference conditions, using models and consensus professional judgment.

A first and essential step in assessing ecosystem quality is to set a reference condition by which to make assessments (Borja et al., 2012). Ideally reference conditions are established based on pre-impact surveys as exemplified by '*before-after-control-impact*' (BACI) studies: e.g. (Green, 1993; Montagna et al., 1996; Currie and Isaacs, 2005; Netto et al., 2009; Santos et al., 2009; Toldo and Ayup Zouain, 2009; Manoukian et al., 2010; Gomiero et al., 2011). Where no pre-impact survey data are available, reference conditions need to be inferred based on model predictions and/or nearby unimpacted sites (e.g. Wei et al., 2012). However, Kropp (2004) cautions that all ecosystems may be subject to natural change over time or with changing conditions.

Environmental monitoring strategies depend heavily on the potential impacts of the activities that are undertaken. Initial activities in the former BP exploration leases were to include exploratory drilling for oil and/or gas, with associated shipping activities. There may be future activities related to full-scale production. The potential impacts to the natural environment associated with these activities, which obviously increase if and as production develops, include suspended sediments during drilling, accumulation of sediments and drilling muds near drill-sites, and potential changes in

sediment chemistry (Kropp, 2004). In addition, there is a potential risk of leaks and spills of hydrocarbons into the environment. The severity of such impacts is in part dependent on physical environmental factors such as local energy and current regimes (Neff et al., 1989). While many of these potential impacts are well known for shallow waters (Kropp, 2004) these may provide little basis for direct inferences into deep-sea environments. The requirements for monitoring programs can therefore be expected to differ because ecological processes in deep-sea environments (>200 m depth) are different from shallow waters (Kropp 2004), operating and recovering from anthropogenic impacts at a slower tempo (Williams et al., 2010b).

The specific design of a monitoring strategy depends on the objectives of the monitoring program – what are the management questions that need to be addressed. Kropp (2004) notes the importance of clearly stating objectives, designing a statistically relevant sampling and analysis plan that provides answers to the questions being asked, elements of structure and function, considerations of taxonomic identification of organisms, the potential use of alternative technologies, and the importance of disseminating the results to the broader community. Green (2005) discusses the characteristics of a good monitoring design and what choices must be made in view of two categories of effects from offshore oil and gas exploration that require environmental monitoring: (1) a catastrophic event like a blowout or spill, and (2) long-term chronic pollution, such as by drilling muds or leakage of hydrocarbons.

Hayes et al. (2015) envisage three possible outcomes from a monitoring program: 1. indicators behave as predicted; 2. indicators do not behave as predicted because pressures are not accurately represented in the modelling process, requiring that the model is re-run with alternative pressure scenarios; or 3. indicators do not behave as predicted because we do not currently understand the system dynamics, requiring that the model structure and/or parameterisation is re-examined. Only under the first outcome would confidence in our system understanding increase, together with the subsequent use of the indicators in assessing the performance of management actions.

We found few published guidelines for monitoring the environmental impact of oil and gas activities in general (e.g. ACAC, 2015; HELCO, 1992; OPG, 2012). On the other hand, strategies and guidelines for post-incident (post-spill) monitoring are more common in the literature (e.g. Ritchie, 1993; Toldo and Ayup Zouain, 2009; Kirby and Law, 2010; Lewis et al., 2010; Law et al., 2011; Neuparth et al., 2012; Radovic et al., 2012; Montagna et al., 2013; Chevron, 2013; Kirby et al., 2014).

A 2012 report by the International Association of Oil and Gas Producers (OPG, 2012) contains a comprehensive treatment of environmental monitoring issues relating to offshore oil and gas activities, highlighting the benefits to be gained from effective marine environmental monitoring

programs. This report outlines the data needs for various phases of offshore oil and gas projects, describes sampling methods and analyses following international standards for water and sediment samples (e.g. ISO, 2014), and outlines available models to predict effects and/or risks (OPG, 2012). The HELCO convention on the protection of the marine environment of the Baltic Sea area (HELCO, 1992) specifies that environmental assessments of the sediment composition (grain size distribution, dry matter, ignition loss, total hydrocarbon content, and Ba, Cr, Pb, Cu, Hg and Cd content), the abundance and diversity of benthic fauna, and the content of selected aliphatic and aromatic hydrocarbons be made before the operation, at annual intervals during the operation, and after the operation has been concluded. The results of such a monitoring program —the Project Environmental Monitoring of Offshore Drilling for Petroleum Exploration (MAPEM)— conducted between 2001 and 2003, in a deepwater location at Campos Basin, Brazil, are reported in a special issue of Deep-Sea Research II, introduced by Toldo and Ayup Zouain (2009). The MAPEM program was designed to assess the effects of discharge of non-aqueous fluid (NAF) impregnated drill cuttings on the environment at 900 m depth and to validate discharge models.

With regard to post-spill monitoring, Kirby et al. (2014) discuss the needs for effective monitoring of post-spill impacts in general. These authors postulate 8 principles for effective post-spill monitoring as: scientific guidance, skill and knowledge, equipment, funding, management, integration and coordination, support/buy-in by stakeholders, and practice. The *Pollution Response in Emergencies: Marine Impact Assessment and Monitoring* (PREMIAM) report by Law et al. (2011) gives detailed guidelines on survey design, sampling protocols and analytical methods for post-incidence monitoring of sub-sea oil spills in the UK. Aerial surveillance, sampling techniques for water, suspended particulates, sediments and biota are reviewed by Radovic et al. (2012), in a study focused on the dissemination of the most successful approaches to both detect and assess accidental releases using chemical as well as biological approaches for spills of either oil or Hazardous Noxious Substances (HNS) in the marine environment.

The importance of including chemical analyses of the environment alongside biological effects in monitoring impacts from human activities on marine environments is highlighted by several studies (e.g. Kropp, 2004; Lewis et al., 2010; Lyons et al., 2010; Thain et al., 2008; Radovic et al., 2012). Mearns et al. (2011; 2013) review the 2010 and 2012 released literature concerning effects of pollutants and human physical disturbances on marine and estuarine plants, animals, ecosystems and habitats, with an emphasis on oil spills. The potential use of biomarkers and bioaccumulation of chemical pollutants in environmental risk assessment (ERA) is examined by van der Oost et al. (2003); they conclude that there is little doubt that measurements of bioaccumulation and

biomarker responses in fish from contaminated sites offer great promise for providing information that can contribute to environmental monitoring programs designed for various aspects of ERA.

Skadsheim et al. (2005) developed an environmental effect and risk estimation methodology for decision-making, impact assessment, and monitoring within the Norwegian Deepwater Programme (NDP) to meet the management needs of the oil and gas industry specifically for deep-sea exploration and production.

12.3.2 Review: data needs

How can the appropriate sample size, sampling frequency, lag, and extent for a monitoring program be determined? Green (1979), among many others, strongly advocates conducting some preliminary sampling in the intended area of study. This approach will provide the information (e.g., numbers, size, and approximate distributions of the organisms comprising the community) that will allow selection of appropriate sampling parameters. If such a survey is not possible, there are two alternatives, although they are less preferable. One is to use any previously collected data from the potential study area. The other, which in practice may be more useful, is to consider that the early survey or surveys in an area are essentially preliminary surveys, and the data from them can be used to adjust the sampling design if necessary. In discussing deep water assessments of benthos in the North Sea, Gage (2001) warns against making extrapolations from shelf conditions to deepwater environments.

Including many replicates in monitoring design is especially important for the deep sea because of the relative rarity of the fauna (Gage, 2001), but Carney (2001) cautions that trying to collect enough samples to obtain adequate representation of very rare species will result in having so many samples that these species will be so rare in the data as to have no effect on the analyses.

Comprehensive sampling of large areas such as the deep-sea in the GAB is not realistically feasible within the lifetime of an exploration project. Therefore there is a need to predictively model biodiversity distributions, biomass and/or other biotic indicators, based on physical surrogate data available at broad scales, such as remotely sensed oceanographic, hydrographic or acoustic data.

In the Gulf of Mexico, Wei et al. (2010a) showed that zonal patterns of macrobenthos composition were correlated with depth and detrital particulate organic carbon (POC) export flux estimated from remotely-sensed phytoplankton pigment concentrations in the surface water. They used this correlation in Random Forest models to predict seafloor standing stocks from surface primary production, water-column integrated and export particulate organic matter (POM), seafloor relief, and bottom water properties (Wei et al., 2010b). In the North Atlantic, Johnson et al. (2007) found a

relationship between the variance in benthic standing stock (biomass and abundance of deep-sea macrobenthos) and estimated POC flux at depth (derived from SeaWiFS satellite colour imagery).

12.4 Implications for the deep GAB

12.4.1 Ecological indicators and metrics

- Need to refer to both ‘top-down’ and ‘bottom-up’ processes for indicator development. There is high value in developing indicators that have broader utility, e.g. consistent with those used for other purposes such as monitoring CMRs and KEFs.
- Options for indicators available from project data map onto those frequently used in system-level studies (e.g. catch/abundance of fish and dominant benthic invertebrate megafauna). There is good quantitative data from the GAB.
- Taxonomic resolution of our data is high, permitting the maximum versatility for indicator development, including multivariate and univariate metrics/ indices (community structure, species richness, diversity indices), and species-level metrics/ indices (sensitive/tolerant species, sentinels, endemism and biogeographic context).
- Taxonomic consistency across surveys is strong and this has been achieved by:
 - implementing a program of targeted taxonomic upgrading by experts that utilised comparative reference material and the scientific literature
 - examining the GABRP and GABDMP material side-by-side
 - critically compiling, evaluating historical collections and data
 - this has been aided by real-time documentation (e.g. web-based data sharing via ScratchPad – see GABRP website) and long-term archive (e.g. lodgement of voucher material in museum collections).
- The scope to use biomarkers for monitoring in the deep GAB is being pursued through a different project – the Chevron funded GAB Deep Marine Program. There is strong potential to use biological material from that and the GABRP to provide an excellent cross-depth and cross-habitat pre-drilling assessment of reference biomarkers.

12.4.2 Ecological monitoring for the GAB

- We have built a dataset suited to a reference-site approach. For the most part, the deep GAB can be considered to be in a pristine/minimally disturbed state, although there are some areas of bottom trawling activity in shallower areas. Data coverage in space and time is insufficient to be classed as baseline.

- A key next step is to build a conceptual model for links between indicators and measured responses, and consideration should be given to the Driver Pressure State Impact Response (DPSIR) framework of Hayes et al. (2015).
- Objectives would ideally be clearly articulated in the context of broader system-level monitoring, the anticipated change (development/expansion) of oil and gas activities, and the influence of other changes (e.g. fishing impacts, climate change).
- A review of the existing policy and management settings shows there are no pre-existing directions within the Australian jurisdiction to inform the selection of appropriate indicators and metrics for ecological monitoring of benthic ecosystems in the deep GAB.
- We note that the GAB shelf's Benthic Protection Zone was surveyed initially in 2002 (Ward et al., 2006) and resurveyed in 2006 (Currie et al., 2008). No monitoring of the shelf has taken place since 2006.

12.5 Summary

Our survey of deep-sea biodiversity at baseline (unperturbed) sites provides the basis to evaluate indicators and metrics in future comparisons – a reference-site monitoring approach (Cordes, 2016; Hayes et al., 2015). We identified several opportunities to develop indicators and metrics by considering the data at both species- and assemblage-level (Table 7.5). Many of the opportunities are underpinned by establishing a robust (consistent species-level) taxonomic foundation for the collections taken during this and other studies (Section 5). This is essential to generate robust metrics for species and assemblage level indicators, and to subsequently develop knowledge about community structural and functional changes (including recovery) in response to disturbance (Carney, 1997; Kropp, 2004). Monitoring the presence or abundance of individual species has potential to track the status of ecosystem engineers, endemics, and threatened/ endangered elements – all of which have significance for biodiversity conservation objectives. Monitoring sentinel species, those sensitive or tolerant to known stressors, may be possible but responses to either natural or human-induced stressors must be known to account for possible shifts in tolerance along natural environmental gradients and between biogeographic regions (Zettler et al., 2013). The infauna provides potential for this because amphipods (particularly ampelescids) and copepods are sensitive to oil pollution, whereas polychaetes and nematodes are less so (or can increase) (Montagna and Harper 1996; Gesteira and Dauvin 2000; Baguley et al. 2015). Both have been used in the Gulf of Mexico, including following the Macondo spill. Two key indices that may be applicable are the polychaete to amphipod and nematode to harpacticoid copepod ratios (Green and Montagna, 1996; Baguley et al., 2015). Ostracods and kinorhynchans were also lost near the Macondo

well, and echinoderms were also negatively affected by the spill (Washburn et al., 2016). In the GAB, sentinel species include cold-water corals aggregated on seamounts that were not sampled in this study, but which are known from other surveys (Williams et al., 2016).

Data resolved to species-level enable a variety of assemblage-level (composite) metrics (e.g. richness, diversity, distinctness) to be derived, and this is possible across several major taxa collected from the GAB (Table 7.5). Species-level data also permit the effect of data aggregation on the ability to detect community changes (taxonomic sufficiency) to be examined. Data aggregated at higher levels may still be informative (Vanderklift et al., 1996; Olsgard et al., 1997; Dauvin et al., 2003), however, Gage (2001) suggested that this is premature for the deep sea, and that before any such approach is implemented, testing against baseline species-level data is necessary. Nonetheless, higher level aggregation of taxa has the advantage of being rapid, needing less input from specialist taxonomists. For assemblage level analyses, the tendency is to work at the family level for macro-infauna and order (or higher) level for meiofauna, again including in deep water (e.g. Baguley et al., 2015; Washburn et al., 2016; Montagna et al., 2017). These approaches can be further explored using the data generated by this project. However, while in Section 6 we show that species, genus and family level patterns in the infaunal assemblage are broadly similar, and it is likely that this pattern will persist in response to any disturbance, we cannot be certain until such a disturbance occurs.

Robust taxonomy identified a high proportion of rarely-seen species in all groups examined in the GABRP - infauna, epifauna and fishes. This is a common observation in deep-sea fauna (e.g. Gage 2001; Williams et al., 2010a; Poore et al., 2015) and implies a need for highly replicated sampling to generate representative assemblage-level metrics. However, adequate representation of rare species in large numbers of samples will have little effect on analyses (Carney, 1997), especially when data are transformed to emphasise the ecological similarities of more abundant species (Olsgard et al., 1997).

Where reference sites should be established can only be determined once the exploration phase of industry development is further advanced because the spatial scales of potential impact are highly activity-specific (e.g. Cordes et al., 2016). However, our data for infauna, epifauna and fishes clearly show the high importance of depth to site selection. In our data, in common with other studies of megabenthos in Australian waters (Williams et al., 2010a) and more generally (Carney, 2005), assemblage composition (turnover), diversity, abundance and the proportion of endemic species are all highly correlated with depth. The GAB Commonwealth Marine Reserve has potential to provide reference sites, but it is overlain by active oil and gas lease blocks and has a history of bottom trawl

fishing in depths to about 1200 m, including on seamounts. These factors need accounting for when reference sites are considered.

Comprehensive sampling of a large poorly known area such as the deep-sea in the GAB is not realistically feasible. Therefore the use of physical surrogate data available at broad scales (remotely sensed oceanographic, hydrographic or acoustic data) is attractive for generating predictive maps of biodiversity and habitat distributions so that spatial extents and changes in them can be used as indicators. These analyses may be possible for the GAB, but the density, quality and relevance of physical covariate data available for the region is yet to be fully evaluated. Predictive modelling completed in this project (Section 11) generates an unexpectedly high number of assemblage types on the lower continental slope and continental rise. This may indicate an insufficiency of biological data density beyond the shelf break (>200 m), and influence by environmental co-variables that have limited or unknown relevance to the deep-sea fauna. Further evaluation and re-analysis of the project data will be helpful to fully understand the utility of the data available for predictive mapping. Predictive mapping is also prone to failure if environmental conditions change to the extent that they no longer fall within the range encompassed by the original conditions, as predictions then become extrapolations. This would be particularly problematic when trying to predict the consequences of a novel disturbance, such as an oil spill in the GAB system, as there are currently no data available on how the system responds to the presence of oil.

Table 12.5 Opportunities for survey collections of benthic fauna to inform ecological monitoring in the context of oil and gas development in the Great Australian Bight.

	Rationale	Indicators	Prospective taxa in GAB	Metrics	Considerations	Reference
Species						
<i>Sentinels</i>	Known or predicted response to impact/pressure	(1) Erect sessile fauna sensitive to smothering; (2) taxa responding to ambient hydrocarbon concentration	(1) Octocorals and sponges (2) Octocorals, decapods (3) Amphipod/copepods vs polychaete/ nemadode ratios; ostracods and kinorhynch	Presence/abundance (biomass and/or density)/ condition	Analyses based on traits (e.g. growth, reproduction) possible but inferential in GAB Responses likely have high spatial scale dependence	(1) Kropp (2004); Clark et al. (2015) (2) White et al. 2012; Fisher et al. 2014b; Fisher et al. 2014a; Felder et al. 2014; (3) Montagna and Harper 1996; Gesteira and Dauvin 2000; Baguley et al. 2015
<i>Ecosystem engineers</i>	Support elevated diversity and/or abundance by increasing habitat complexity	Erect sessile fauna; reef/ thicket forming taxa	(1) Octocorals and sponges; (2) stony corals		(1) Known aggregations in GAB on volcanic seamounts	(1) Williams et al. (2016)
<i>Endemics</i>	Range limited species make dis-proportionately high contribution to biogeographic structure	Potentially, species from any higher level taxon	(1) Invertebrate megafauna: the crab <i>Choniagnathus granulatus</i> and barnacle		Endemicity is difficult to identify with confidence in deep sea areas with low sampling intensity	(1) this paper (2) Williams et al (this report)
<i>Threatened, endangered</i>	High conservation value; subject to management recovery plans	Potentially, species from any higher level taxon	No invertebrate taxa presently listed	Presence/abundance/ condition	N/A	N/A
Assemblage						
<i>Composition</i>	Assemblage characterised and baseline status described by simple composite metrics	Change in composite metrics	All higher level taxa (including infauna and fishes) for which species-level taxonomy is robust: Porifera, Actinaria, Octocorallia, Scleractinia, Mollusca, Echinodermata, Arthropoda. Ratios or	Richness Diversity Evenness Distinctness Indices Ratios	(1) High confidence in taxonomy; (2) high proportions of rarely seen species indicates many replicated samples needed; and (3) need for severe data transformation to identify signals; (4) Indices need calibration to specific locations	(1) MacIntosh et al. (this issue) (2) Gage 2001 (3) Carney 2001 (4) Dauvin et al. (2012)
<i>Structure</i>	Trajectory of assemblage change based on hypothesised mechanism	Trajectories of change indicated by composite metrics	infauna highr taxa (nematode to harpacticoid and opportunistic polychaete to amphipod)	Ecological similarity of multiple species in multidimensional space (e.g. MDS)		
<i>Predicted distributions</i>	Species distribution models or habitat suitability models indicate spatial extent of species and/or assemblages	Mapped extents	Abundant individual species; whole assemblages	Change in spatial extent; areas or proportions inside protected areas or subject to impact	Data density is typically low in deep sea studies including the GAB; many environmental covariates, especially those with near sea-surface expression, have weak or unknown relevance in the deep sea; models need validation	(1) Anderson et al. (2016) (2) Ellis et al. (gradient forests, this report)

13 Summary of GAB management objectives – in the context of ‘development and testing of metrics for benthic biological indicators for ecological monitoring of oil and gas exploratory activities in the deep GAB’

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13.1 Introduction

To clarify the output for Project 3.1, we have reviewed a set of relevant documents to identify management objectives that may relate to benthic ecosystems. Our conclusions are:

1. Objectives in relevant management plans and related documents are only broadly specified and are interdependent (Figure 1). Most point back to the EPBC Act – which is detailed but does not specify indicators or metrics. We cannot identify clear and pre-existing directions “to inform the selection of appropriate indicators and metrics”.
2. The contemporary literature on indicators includes output from the National Environmental Science Programme - MarineBiodiversity Hub and output relevant to Australia, but this has mostly a ‘standard approach’ and ‘multiple-use’ focus, and little specificity for GAB-related management processes.
3. Given this, we intend to focus on a narrow set of indicators that allow measurement of potential affects by oil and gas exploration in relation to:
 - “no disturbance or minimal disturbance to the benthos inside the GAB Benthic Protection Zone”
 - “spatial and temporal variations of benthic community structure (inside vs. outside the GAB CMR)”
 - “number of known nationally listed exotic benthic species and extent of colonisation”
 - “listed threatened species and ecological communities”
4. We plan to explore indicators including single species, multi-species (composite) and biochemical measures, and do this using the approach and literature review documented in Section 12.

13.2 Sources of management objectives

13.2.1 Overview

Potential sources of management objectives to inform development of ecological indicators

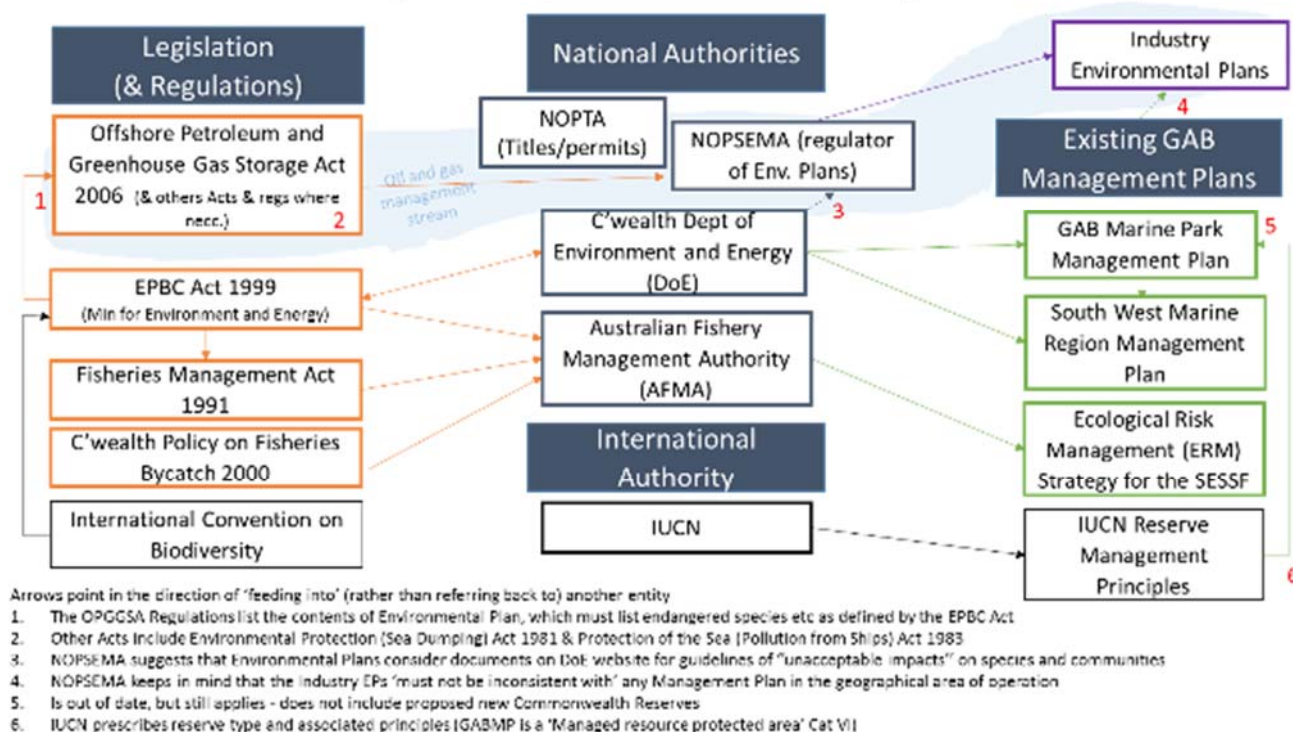


Figure 13.1 Schematic showing potential sources of management objectives to inform development of ecological indicators in Benthic 3.1.

NOPSEMA's authority is to make sure that any Environmental Plan is not inconsistent with any management plans in place.

Relevant Management Plans are:

1. GABMP Management Plan (2005-2012) which is expired, but in force.
2. SW Marine Region Bioregional Plan.
3. Ecological Risk Management (ERM) Strategy for the South East Shark and Scalefish Fishery (SESSF).

The GABMP Management Plan's Aim: To contribute towards the protection of the benthic habitat and associated ecological communities and seabed sediments characteristic of the Great Australian Bight by minimising human disturbance to the seabed in the Park.

The performance indicators for that are:

- Spatial and temporal variations of benthic community structure

- inside vs. outside the Park.
- before, during and after any operations that disturb the benthos in the region.
- Number of known nationally listed exotic benthic species and extent of colonisation.

SW Marine Region Bioregional Plan: Consistent with the objectives of the EPBC Act, and in the context of the principles for ecologically **sustainable development as defined in the Act**, the plan sets the following objectives for the region:

- conserving biodiversity and maintaining ecosystem health.
- ensuring the recovery and protection of threatened species.
- improving understanding of the region's biodiversity and ecosystems and the pressures they face.

Ecological Risk Management (ERM) Strategy for SESSF

The **objectives** of this ERM Strategy are to:

- implement management arrangements to minimise fishing impact on non-target species and habitats, with a particular focus on high risk species and habitats assessed through AFMA's Ecological Risk Assessment process
- minimise interactions with species listed under the *Environment Protection and Biodiversity Conservation Act 1999* (EPBC Act) excluding conservation dependent species.

13.2.2 National Offshore Petroleum Titles Administrator (NOPTA)

Website: <http://www.nopta.gov.au/>

NOPTA provides titles, gives advice to Minister and Authorities – alters permits – covers the same legislation and regulations as NOPSEMA - [see regulations at end of this Section]

13.2.3 National Offshore Petroleum Safety and Environmental Management Authority (NOPSEMA)

Website: <https://www.nopsema.gov.au/>

Assesses management plans

Since 2014 NOPSEMA has been ‘the sole designated assessor of petroleum and greenhouse gas activities in Commonwealth waters’ (with the Minister of Environment endorsement – see Part 10 Section 146 of EPBC Act). This means that NOPSEMA can assess impacts of matters covered by the EPBC Act – relevant here are the matters of:

- listed threatened species and ecological communities (no current listed benthic species of communities occur in the GAB).
- listed migratory species (no benthic species are currently listed).
- Commonwealth marine areas.

The relevant ‘information paper’ can be found at:

<https://www.nopsema.gov.au/assets/Information-papers/A341856.pdf>

Measurements are defined as ‘unacceptable impacts’ to TEPS, migratory species and the Commonwealth Reserve. If the activities are in a commonwealth marine park any Environmental Plan must ‘not be inconsistent’ with the plan of management for the Commonwealth Reserve.

Legislation

<https://www.nopsema.gov.au/legislation-and-regulations/environment/>

The primary legislation that NOPSEMA are in charge of is:

- *Offshore Petroleum and Greenhouse Gas Storage Act 2006*
- EPBC Act 1999

Also, must comply with

- *Environmental Protection (Sea Dumping) Act 1981*
- *Protection of the Sea (Pollution from Ships) Act 1983*

and others where relevant. The onus is on the titleholder to find out which legislations are relevant.

NOPSEMA NOTES

“is Australia’s independent regulator of safety, well integrity and environmental management for all offshore petroleum activities in Commonwealth waters.

NOPSEMA’s Environment Division is responsible for ensuring that all offshore petroleum and greenhouse gas activities in Commonwealth waters are undertaken in accordance with the Offshore Petroleum and Greenhouse Gas Storage (Environment) Regulations 2009 (Environment Regulations).

The Environment Regulations seek to ensure that every offshore petroleum activity in Commonwealth waters is carried out in a manner: consistent with the principles of ecologically sustainable development such that the environmental impacts and risks of the activity will be acceptable and reduced to as low as reasonably practicable (ALARP).”

<https://www.nopsema.gov.au/environmental-management/>

This document has a definition of impacts, <https://www.nopsema.gov.au/assets/Guidance-notes/A339814.pdf>

The ‘acceptable level’ of impact or risk for matters protected under Part 3 of the EPBC Act should be informed by having regard to information published on the DoE web site including relevant policies, guidelines, threatened species recovery plans, plans of management, management principles and other documents that are important for defining ‘acceptable levels’.

13.2.4 GAB Marine Park - Dept of Environment and Energy

GAB MP Plans (within the SW Commonwealth Marine Reserves) are in a transitional period with the old one (2005-12) expired and the new one not completed. Meanwhile the old one still applies.

GAB MP Plan 2005-2012

Website: <https://www.environment.gov.au/system/files/resources/9b53d4e7-9a12-4354-9588-163933b2cbd4/files/gab-plan.pdf>

IUCN category [see also Section below on IUCN rules in EPBC Act]

Consistent with its assignment to the World Conservation Union (IUCN) category ‘managed resource protected area’, for the next seven years the Park will be managed mainly for the sustainable use of natural ecosystems. This means that uses of the Park, including resource extraction, will be allowed if they generally:

- entail no disturbance or minimal disturbance to habitat for marine mammals inside the Marine Mammal Protection Zone and the benthos inside the Benthic Protection Zone; and

- do not threaten the ecosystems overlapping the Park, and are exempt from approval or are approved under Commonwealth laws designed to protect the environment; and
- contribute to regional and national development, and have previously occurred inside the area now covered by the Park or cannot reasonably occur outside the Park.

Objectives [called 'Aims' in this plan]

5. Natural heritage management (KRA1)

Section 5 Park's conservation values. It sets out broad strategies for improving protection for these values. Section 6 sets out specific regulations and strategies that will help to achieve these aims during the period of operation of this Management Plan while allowing people to visit and use the Park.

5.1 Species of conservation significance – only noted as Southern Right Whale and Australian Sea lion. Not currently relevant to the benthos.

5.2 Seafloor sample

Aim: To contribute towards the protection of the benthic habitat and associated ecological communities and seabed sediments characteristic of the Great Australian Bight by minimising human disturbance to the seabed in the Park

Performance indicators

- Spatial and temporal variations of benthic community structure
 - inside vs. outside the Park
 - before, during and after any operations that disturb the benthos in the region.
- Number of known nationally listed exotic benthic species and extent of colonisation.

Section 6. Park use

6.2 Fishing other than commercial fishing

Aim: To protect the Park by allowing people to carry on fishing other than commercial fishing only if it is consistent with protecting the conservation values of the Park

6.3 Commercial and scientific activities

Aim: To protect the Park by allowing people to carry on commercial and scientific activities only if they are consistent with protecting the conservation values of the Park

6.4 Commercial fishing

Aim: To protect the Park by allowing people to carry on commercial fishing only if it is consistent with protecting the conservation values of the Park

Commonwealth fisheries [those relevant to benthos]

- Gillnet Hook and Trap Fishery (part of the Southern and Eastern Scalefish and Shark Fishery)
- Small Pelagic Fishery Zone B – only operators who also hold concessions in the Great Australian Bight Trawl Fishery (part of the Southern and Eastern Scalefish and Shark Fishery)

6.5 Mining operations

Aim: To allow mining operations only if they are consistent with protecting the conservation values of the Park

Performance indicators [include]

- Benthic community composition before, during and after operations.
- Estimated total seabed area disturbed by structures.

13.2.5 International Union for Conservation of Nature (IUCN) reserve management principles.

IUCN category for GAB Marine Park

7 Managed resource protected area (category VI)

7.01A This clause sets out the management principles for a managed resource protected area (IUCN protected area management category VI).

7.01 The reserve or zone should be managed mainly for the ecologically sustainable use of natural ecosystems based on the following principles.

7.02 The biological diversity and other natural values of the reserve or zone should be protected and maintained in the long term.

7.03 Management practices should be applied to ensure ecologically sustainable use of the reserve or zone.

7.04 Management of the reserve or zone should contribute to regional and national development to the extent that this is consistent with these principles.

World Conservation Union (IUCN) protected area categories 2008

Website: <https://www.environment.gov.au/node/20957#VI>

Category VI: Protected area with sustainable use of natural resources

Protected areas are generally large, with much of the area in a more-or-less natural condition and where a proportion is under sustainable natural resource management and where low-level use of natural resources compatible with nature conservation is seen as one of the main aims of the area.

Primary objective - To protect natural ecosystems and use natural resources sustainably, when conservation and sustainable use can be mutually beneficial.

13.2.6 South-west Marine (bioregional) Plan

Plan

Website: <http://www.environment.gov.au/system/files/pages/a73fb726-8572-4d64-9e33-1d320dd6109c/files/south-west-marine-plan.pdf>

Consistent with the objectives of the EPBC Act, and in the context of the principles for ecologically sustainable development as defined in the Act, the plan sets the following objectives for the region:

- conserving biodiversity and maintaining ecosystem health
- ensuring the recovery and protection of threatened species
- improving understanding of the region's biodiversity and ecosystems and the pressures they face.

Report card

Website: <http://www.environment.gov.au/system/files/pages/a73fb726-8572-4d64-9e33-1d320dd6109c/files/south-west-report-card-commonwealth.pdf> - gives values descriptions.

Details about measures to protect components of key ecological features (e.g. protected species or protected places) under the EPBC Act can be found in the relevant species group report cards or protected places report card (www.environment.gov.au/marineplans/south-west).

13.2.7 Australian Fisheries Management Authority (AFMA)

Website: <http://www.afma.gov.au/sustainability-environment/ecological-risk-management-strategies/>

AFMA aims to minimise the impacts of commercial fisheries on all aspects of the marine environment. This is achieved through the assessment of risks and the development of appropriate ecological risk management strategies.

AFMA's adoption of ecosystem based fisheries management considers the impacts of fishing on five components of the marine environment:

- target species
- byproduct species
- bycatch/discard species
- threatened, endangered and protected species
- habitats and communities.

Through data collection and management arrangements, AFMA aims to reduce the number of species at risk by mitigating the impact of fishing. The objectives of the strategies are to:

- reduce the number of high risk species assessed through the ecological risk assessment process
- minimise interactions with species listed under the EPBCAct 1999
- reduce discarding of target and non-target species to as close to zero as practically possible
- minimise overall bycatch in the fishery over the long-term.

Ecological Risk Management (ERM) strategy for the southern and eastern scalefish and shark fishery <http://www.afma.gov.au/wp-content/uploads/2014/11/SESSF-ERM-Strategy-2015.pdf> lists species at risk in trawl fisheries etc. The ERM Strategy sets out the management actions necessary to support the objectives of the **Fisheries Management Act 1991** and **Commonwealth Policy on Fisheries Bycatch 2000**, in particular:

ensuring that the exploitation of fisheries resources and the carrying on of any related activities are conducted in a manner consistent with the principles of ecologically sustainable development (which include the exercise of the precautionary principle), in particular the need to have regard to the impact of fishing activities on non-target species and the long term sustainability of the marine environment.

To pursue this, the **objectives** of this ERM Strategy are to:

- implement management arrangements to minimise fishing impact on non-target species and habitats, with a particular focus on high risk species and habitats assessed through AFMA's Ecological Risk Assessment process
- minimise interactions with species listed under the EPBC Act, excluding conservation dependent species.

13.2.8 Industry – BP's Environment Plan

Website: http://www.bp.com/content/dam/bp-country/en_au/about-us/what-we-do/exploring-great-australian-bight/environment-plan-overview.pdf

Will provide an environmental plan to NOPSEMA in accordance with their regulations. "The Program [NOPSEMA'S environmental management authorisation process] has objectives which include ensuring activities undertaken in the offshore area are conducted in a manner consistent with the principles of ecologically sustainable development and will not result in unacceptable impacts to matters of national environmental significance (MNES) protected under Part 3 of the EPBC Act."

Risk assessment for benthos covers mainly 'Smothering and alteration of benthic habitat.'

13.2.9 EPBC Act

Environment Protection and Biodiversity Conservation Act 1999 (EPBC Act)

Environment Protection and Biodiversity Conservation Regulations 2000

Website: <https://www.legislation.gov.au/Details/C2016C00777>

Object of Act

- (1) The objects of this Act are:
- (a) to provide for the protection of the environment, especially those aspects of the environment that are matters of national environmental significance; and
 - (b) to promote ecologically sustainable development through the conservation and ecologically sustainable use [defined in 3A] of natural resources; and
 - (c) to promote the conservation of biodiversity; and
 - (c-a) to provide for the protection and conservation of heritage; and
 - (d) to promote a co-operative approach to the protection and management of the environment involving governments, the community, land-holders and indigenous peoples; and
 - (e) to assist in the co-operative implementation of Australia's international environmental responsibilities;

13.2.10 3A Principles of ecologically sustainable development

The following are the principles of ecologically sustainable development:

- (a) decision-making processes should effectively integrate both long-term and short-term economic, environmental, social and equitable considerations;
- (b) if there are threats of serious or irreversible environmental damage, lack of full scientific certainty should not be used as a reason for postponing measures to prevent environmental degradation;
- (c) the principle of inter-generational equity—that the present generation should ensure that the health, diversity and productivity of the environment is maintained or enhanced for the benefit of future generations;
- (d) the conservation of biological diversity and ecological integrity should be a fundamental consideration in decision-making;
- (e) improved valuation, pricing and incentive mechanisms should be promoted.

13.3 Other relevant documents

13.3.1 NERP report on 'Collating existing survey data for Commonwealth marine waters'

Website: <http://nerpmarinebiodiversity2015.report/collating-existing-survey-data-for-commonwealth-marine-waters/>

13.3.2 Australia's Biodiversity Conservation Strategy 2010-2030

Website: <https://www.environment.gov.au/biodiversity/publications/australias-biodiversity-conservation-strategy>

Includes Ecosystem services and resilience –

Ecosystem resilience is the capacity of an ecosystem to respond to changes and disturbances, yet retain its basic functions and structures. The resilience of ecosystems in Australia is currently being reduced by a number of threats, including:

- habitat loss, degradation and fragmentation
- invasive species
- unsustainable use and management of natural resources

- changes to the aquatic environment and water flows
- changing fire regimes
- climate change.

13.3.3 State of the marine environment report

Website: <https://www.environment.gov.au/science/soe/2011-report/6-marine/contents>

13.3.4 Limits of unacceptable Change

Website: <http://www.environment.gov.au/system/files/resources/4b6b222f-bb51-4f1e-893a-c49ffc82f346/files/acceptable-change-factsheet.pdf>

Eg Wetlands

Limits of acceptable change are defined as the variation that is considered acceptable in a particular component or process of the ecological character of the wetland, without indicating change in ecological character that may lead to a reduction or loss of the criteria for which the site was Ramsar listed (modified from definition adopted by Phillips 2006).

Stankey GH, Cole DN, Lucas RC, Petersen ME, Frissell SS. The limits of acceptable change (LAC) system for wilderness planning. General technical report no. INT-176. Ogden: United States Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station, 1985.

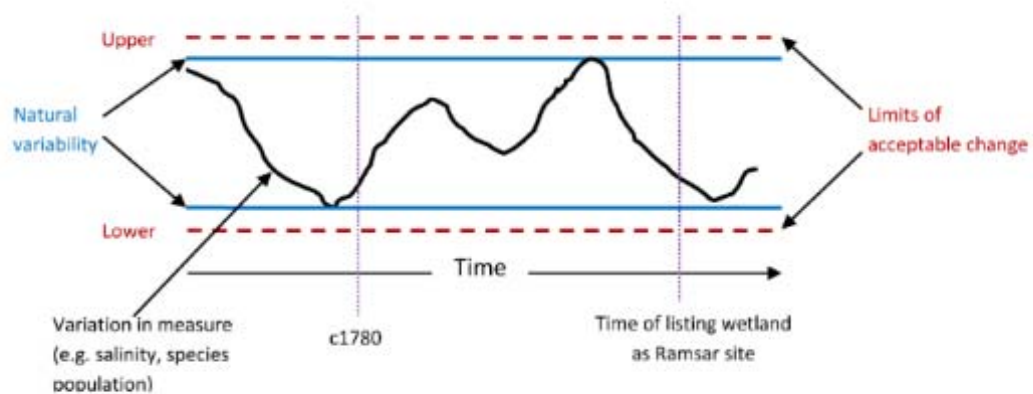


Figure 1 Comparison of natural variability and limits of acceptable change (Source: adapted from Phillips (2006).

13.3.5 Offshore Petroleum and Greenhouse Gas Storage (Environment) Regulations 2009

ENVIRONMENT REGULATIONS

The Environment Regulations state that the titleholders must clarify to stakeholders whether their activities will affect them - at all stages Exploration, Production and Decommissioning.

In force - Offshore Petroleum and Greenhouse Gas Storage (Environment) Regulations 2009 –

includes requirements, acceptance and contents of environmental plans

<https://www.legislation.gov.au/Details/F2015C00069>

Contents of an environment plan

An environment plan for an activity must include the matters set out in regulations 13, 14, 15 and 16.

13 Environmental assessment

Description of the activity

(1) The environment plan must contain a comprehensive description of the activity including the following:

- (a) the location or locations of the activity;
- (b) general details of the construction and layout of any facility;
- (c) an outline of the operational details of the activity (for example, seismic surveys, exploration drilling or production) and proposed timetables;
- (d) any additional information relevant to consideration of environmental impacts and risks of the activity.

Note: An environment plan will not be capable of being accepted by the Regulator if an activity or part of the activity, other than arrangements for environmental monitoring or for responding to an emergency, will be undertaken in any part of a declared World Heritage property—see regulation 10A.

Description of the environment

- (2) The environment plan must:
- (a) describe the existing environment that may be affected by the activity; and
 - (b) include details of the particular relevant values and sensitivities (if any) of that environment.

Note: The definition of environment in regulation 4 includes its social, economic and cultural features.

(3) Without limiting paragraph (2)(b), particular relevant values and sensitivities may include any of the following:

- (a) the world heritage values of a declared World Heritage property within the meaning of the EPBC Act;
- (b) the national heritage values of a National Heritage place within the meaning of that Act;
- (c) the ecological character of a declared Ramsar wetland within the meaning of that Act;
- (d) the presence of a listed threatened species or listed threatened ecological community within the meaning of that Act;
- (e) the presence of a listed migratory species within the meaning of that Act;
- (f) any values and sensitivities that exist in, or in relation to, part or all of:
 - (i) a Commonwealth marine area within the meaning of that Act; or
 - (ii) Commonwealth land within the meaning of that Act.

Requirements

(4) The environment plan must:

- (a) describe the requirements, including legislative requirements, that apply to the activity and are relevant to the environmental management of the activity; and
- (b) demonstrate how those requirements will be met.

Evaluation of environmental impacts and risks

(5) The environment plan must include:

- (a) details of the environmental impacts and risks for the activity; and
- (b) an evaluation of all the impacts and risks, appropriate to the nature and scale of each impact or risk; and
- (c) details of the control measures that will be used to reduce the impacts and risks of the activity to as low as reasonably practicable and an acceptable level.

(6) To avoid doubt, the evaluation mentioned in paragraph (5)(b) must evaluate all the environmental impacts and risks arising directly or indirectly from:

- (a) all operations of the activity; and
- (b) potential emergency conditions, whether resulting from accident or any other reason.

Environmental performance outcomes and standards

(7) The environment plan must:

- (a) set environmental performance standards for the control measures identified under paragraph (5)(c); and
- (b) set out the environmental performance outcomes against which the performance of the titleholder in protecting the environment is to be measured; and
- (c) include measurement criteria that the titleholder will use to determine whether each environmental performance outcome and environmental performance standard is being met.

14 Implementation strategy for the environment plan

(1) The environment plan must contain an implementation strategy for the activity in accordance with this regulation.

(2) The implementation strategy must:

- (a) state when the titleholder will report to the Regulator in relation to the titleholder's environmental performance for the activity; and
- (b) provide that the interval between reports will not be more than 1 year.

Note: Regulation 26C requires a titleholder to report on environmental performance in accordance with the timetable set out in the environment plan.

(3) The implementation strategy must contain a description of the environmental management system for the activity, including specific measures to be used to ensure that, for the duration of the activity:

- (a) the environmental impacts and risks of the activity continue to be identified and reduced to a level that is as low as reasonably practicable; and
- (b) control measures detailed in the environment plan are effective in reducing the environmental impacts and risks of the activity to as low as reasonably practicable and an acceptable level; and
- (c) environmental performance outcomes and standards set out in the environment plan are being met.

(4) The implementation strategy must establish a clear chain of command, setting out the roles and responsibilities of personnel in relation to the implementation, management and review of the environment plan, including during emergencies or potential emergencies.

(5) The implementation strategy must include measures to ensure that each employee or contractor working on, or in connection with, the activity is aware of his or her responsibilities in relation to the environment plan, including during emergencies or potential emergencies, and has the appropriate competencies and training.

(6) The implementation strategy must provide for sufficient monitoring, recording, audit, management of nonconformance and review of the titleholder's environmental performance and the implementation strategy to ensure that the environmental performance outcomes and standards in the environment plan are being met.

(7) The implementation strategy must provide for sufficient monitoring of, and maintaining a quantitative record of, emissions and discharges (whether occurring during normal operations or otherwise), such that the record can be used to assess whether the environmental performance outcomes and standards in the environment plan are being met.

(8) The implementation strategy must contain an oil pollution emergency plan and provide for the updating of the plan.

(8AA) The oil pollution emergency plan must include adequate arrangements for responding to and monitoring oil pollution, including the following:

(a) the control measures necessary for timely response to an emergency that results or may result in oil pollution;

(b) the arrangements and capability that will be in place, for the duration of the activity, to ensure timely implementation of the control measures, including arrangements for ongoing maintenance of response capability;

(c) the arrangements and capability that will be in place for monitoring the effectiveness of the control measures and ensuring that the environmental performance standards for the control measures are met;

(d) the arrangements and capability in place for monitoring oil pollution to inform response activities.

(8A) The implementation strategy must include arrangements for testing the response arrangements in the oil pollution emergency plan that are appropriate to the response arrangements and to the nature and scale of the risk of oil pollution for the activity.

(8B) The arrangements for testing the response arrangements must include:

(a) a statement of the objectives of testing; and

(b) a proposed schedule of tests; and

(c) mechanisms to examine the effectiveness of response arrangements against the objectives of testing; and

(d) mechanisms to address recommendations arising from tests.

(8C) The proposed schedule of tests must provide for the following:

(a) testing the response arrangements when they are introduced;

(b) testing the response arrangements when they are significantly amended;

(c) testing the response arrangements not later than 12 months after the most recent test;

(d) if a new location for the activity is added to the environment plan after the response arrangements have been tested, and before the next test is conducted—testing the response arrangements in relation to the new location as soon as practicable after it is added to the plan;

(e) if a facility becomes operational after the response arrangements have been tested and before the next test is conducted—testing the response arrangements in relation to the facility when it becomes operational.

(8D) The implementation strategy must provide for monitoring of impacts to the environment from oil pollution and response activities that:

(a) is appropriate to the nature and scale of the risk of environmental impacts for the activity; and

(b) is sufficient to inform any remediation activities.

(8E) The implementation strategy must include information demonstrating that the response arrangements in the oil pollution emergency plan are consistent with the national system for oil pollution preparedness and response.

(9) The implementation strategy must provide for appropriate consultation with:

(a) relevant authorities of the Commonwealth, a State or Territory; and

(b) other relevant interested persons or organisations.

(10) The implementation strategy must comply with the Act, the regulations and any other environmental legislation applying to the activity.

14 GENERAL DISCUSSION

The Benthic Biodiversity Theme, Project 3.1 in the Great Australian Bight Research Program (GABRP), has undertaken the first detailed study of benthic biodiversity in the deep (200-3000 m) waters of the Great Australian Bight. Data were generated during two large-scale surveys that, to date, are the deepest systematic surveys for benthic biodiversity undertaken in Australia's marine jurisdiction.

The extensive biological collections were systematically distributed to museums for analysis by specialist taxonomists. Upgrading of the fauna included identification to the species level, as well as adding notable taxonomic and occurrence data that included whether species were new to science or previously recorded from Australia. The result is a high quality taxonomic dataset that enables analytical results to be placed into a biogeographical context. All specimens are now stored in Australian museums and other research institutes where they are accessible to researchers conducting taxonomic revisions, describing new species, and other studies, ensuring this benthic data set will continue to contribute to knowledge and understanding of the deep sea fauna in local, regional and global contexts.

The 200 multi-corer samples yielded 1303 individual infauna specimens. These represented at least 258 species, and with some taxa only identified to class or phylum, probably many more. While no patterns in infaunal assemblage structure were found in the analysis of individual samples, the expected depth related patterns appeared when samples at each site were aggregated. This result suggests that an individual core is too small to provide a representative sample of the assemblage, but that a group of 3 cores is sufficient. Any future studies on infauna in this region should take this into consideration, and preferably use either a single cast of a multicorer as 1 sample, or utilize a sampler that collects a larger sample. There were several stations at which multiple casts were undertaken. In all cases, when samples were aggregated, the casts appeared adjacent to each other in the ordination when taken in the same year, but not when taken in different years (2013 vs 2015), indicating substantial temporal variability in the assemblage. This gives added confidence that a single cast provides a good representation of the infaunal assemblage at a site, and that the sampling gear used is not playing a large role in determining what is sampled. Individual samples from a single cast, however, were often separated in the ordination, again indicating that a single core provides an inadequate sample for infaunal analysis. There did not appear to be any unique co-occurring groups of taxa in the sampled region. Taxa accumulation curves suggest that less than 25% of infaunal species present in the region were sampled. This figure increased as taxa were aggregated into higher levels, and reached 100% at the phylum level. Thus, any additional sampling is still likely to produce a high proportion of new species.

The beam trawl samples yielded more than 600 species of invertebrate epifauna; ~ 25% were undescribed and 77 identified species were new records for Australian waters. The families and genera present were all known to occur in the deep-sea and many species had been previously recorded in Australia and worldwide; faunal composition was broadly typical for temperate deep-sea regions. The highest diversities (>80 OTUs) were recorded within the Demospongiae, Decapoda, Gastropoda and the combined Echinodermata. Multispecies analyses showed clear changes in the assemblage structure with depth; sponges and echinoderms dominated the overall biomass and density, with the former being more prominent in shallower depths. The assemblage structure is consistent with a single provincial-scale bioregion, with no longitudinal pattern in assemblage,

biomass or density distribution. Approximately 70% of species that could be assigned biogeographic data were previously recorded from Australia, with less than half (146 species, 39%) previously known from the GAB. Endemism was low however, with two species, the crab *Choniognathus granulatus* and barnacle *Arcoscalpellum inum* known only from the GAB. Results show a clear eastwards biogeographic affinity, suggesting that the deep GAB is not an equal mixing zone between western and eastern fauna; there were over twice as many species previously recorded from the southern Pacific (149) as from the Indian Ocean (64). This pattern was more dramatic when considering species that occur in only one adjacent region, with 90 species (24%) found in the southern Pacific but not the Indian Ocean, and only 6 species (<2%) from the Indian Ocean but unknown from the Pacific.

The project also compiled historical benthic biodiversity data from the GAB from a comprehensive inventory of museum records. There was a clear concordance between the historical museum data and the newly collected beam trawl survey data, with the latter grouping with geographic segments within which they were contained in both the ordinations and the cluster analyses at the species, genus and family levels. The biogeographic patterns documented are concordant with previous southern Australian deep-sea biogeographies established using fish and ophiuroids. This analysis highlighted the paucity of data from the entire southern Australian margin, which accounted for ~10% of the museum records available. GABRP data now makes up almost half of the records available from southern Australia.

The beam trawl samples also collected 108 species of fish from 49 families in 200-3000 m depths. The great majority of species were previously recorded from Australian waters (90%), and from the GAB (75%), but a markedly lower proportion of recorded species occurred at greater depths (1700-3000 m) where there had been virtually no previous sampling: 74% in Australian waters, and 30% in GAB waters. The fauna is dominated by families that typify the deep ocean: rat-tails (Macrouridae), cut-throat eels (Synphobranchidae), morid cods (Moridae), Oreosomatidae (oreo dories), slickheads (Alepocephalidae), Ophidiidae (cusk eels) and halosaurs (Halosauridae). The Macrouridae was most diverse, occurred most frequently, was abundant (density) in 400 m and all deeper strata, and top ranked by biomass and density in standardised data for all samples, and transect samples. The predominant patterns of biogeographical affinities were strongly modified by depth. Endemic species were most prevalent in shelf break and upper to mid-slope depths (both 52%), and declined with increasing depth (upper to mid-slope species 25%; lower slope/ rise 4%), consistent with a general pattern in the Australian ichthyofauna. Fish biomass (gm^{-2}) was significantly related to depth, relatively very low ($\sim 0.5 \text{ gm}^{-2}$) at 200 m depth, highest at 400 m ($\sim 3.4 \text{ gm}^{-2}$), then steadily declining with increasing depth to about 0.4 gm^{-2} at 3000 m depth. Depth was the main factor explaining assemblage structure although the lower slope and continental rise (>1500 m depths), that had not previously been sampled in Australian waters, showed relatively little difference to the mid-slope sites (<1500 m depths). There was no clear distinction of sites close to structured habitats, and no longitudinal pattern across a gradient of productivity (higher in the east due to summertime upwelling).

Comprehensive sampling of a large poorly known area such as the deep-sea in the GAB is not realistically feasible. Therefore the use of physical surrogate (covariate) data available at broad scales (remotely sensed oceanographic, hydrographic or acoustic data) will be necessary to generate predictive maps of biodiversity and habitat distributions so that spatial extents and changes in them

can be used as indicators of ecosystem status. Our project acquired regional-scale data on 46 covariates and applied leading-edge methods of predictive species distribution modelling and gradient forest assemblage mapping. These analyses demonstrate what is presently possible with data available for the GAB. The density, quality and relevance of physical covariate data available for the region is yet to be fully evaluated, and further analysis of the project data will be helpful to fully understand the utility of the data sets currently available for predictive mapping.

The GAB is presently being considered as a site for oil and gas exploration in areas extending from the shelf break (200 m) to beyond 4000 m depths. The current data set has the potential to inform biodiversity management in the GAB, including the design of an ecological monitoring program prior to oil and gas exploration, because it includes samples from within and immediately adjacent to the Great Australian Bight Commonwealth Marine Reserve and six active lease blocks. It can do this by providing quality assured inventories of fishes, mapping species distributions and associations with habitats in the area of interest, and identifying potential sites of impact and suitable control sites inside and outside reserves. Our data on fauna at baseline (unperturbed) sites provides the basis to evaluate indicators and metrics using a reference-site monitoring approach. A robust (consistent species-level) taxonomic foundation will enable a variety of assemblage-level (composite) metrics (e.g. richness, diversity, distinctness) to be derived, and this is possible across several major taxa including Porifera, Cnidaria, Mollusca, Echinodermata and Crustacea. Species-level data also permit structural and functional changes (including recovery) to be assessed in response to disturbance. Where reference sites should be established can only be determined once the exploration phase of industry development is further advanced because the spatial scales of potential impact are highly activity-specific. However, our data show the high importance of depth to site selection because faunal assemblage composition (turnover), diversity, abundance and the proportion of endemic species are all highly correlated with depth.

The project data provided selected summaries of benthic biodiversity information to ecosystem models for the GAB being developed by Theme 7 within the GABRP.

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15.5 Section 6: Tanner et al. - Macrofauna

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16 APPENDIX 1: DATA MANAGEMENT

Franziska Althaus, Pamela Brodie, Christine Trefrey, Alan Williams (CSIRO)

The GABRP surveys collected data for multiple themes and projects of the GABRP. The data sets and data flows described here are limited to the data collected for the GABRP Benthic theme Project 3.1.

The data management for the Project proceeded in accord with the 2014 BP GAB Benthic Data Management Plan outlined in Project 3.1 - Milestone 2 and presented by the Project team at the GABRP Symposium, August 2015.

16.1 Raw Datasets Created

The CESRE Integrated Survey System (ISS) database was adapted to log samples and operations for the surveys.

Alterations were made to the input forms, data variables and the printed label format to better reflect the type of samples to be collected. A process of entering sample information in bulk was developed so that sample data entry could be done in anticipation of completion of each operation and prior to the printing of barcode labels. In addition the system was adapted for separate entry of biological catch composition data at sea. The system worked effectively for the variety of sampling undertaken during the GABRP voyages.

A snapshot of all operational and sample data in the database entered at sea, was archived together with additional information derived from various sensors including the Marine National Facility standard data sets (denoted with *) at the end of each survey in the MNF End of Voyage Raw Data Archive. Sensor data can be linked to these samples using the UTC time stamps.

Raw ship-board data for Benthic 3.1:

- Gear deployment records
- Sample records: including sediment samples, macrofauna and meiofauna
- Biological catch composition: identifications to ship-board OTU
- Taxonomic photographs (identifications to ship-board OTU)
- Muscle tissue samples of selected specimens for future DNA analyses

Sensor data sets:

- CTD profiles*
- Hydrology data*
- Ship underway data (GPS, PDR, MET, and TSG)*
- Multibeam data*
- Integrated Coring Platform (ICP) acoustics; sensor data; video and telemetry
- Underway hydrocarbon data

The raw catch data were used for reporting to the Department of the Environment and Energy and to the Animal Ethics Committee under the collection permits (see Table 2.1).

16.2 Data Processing and Derived Datasets

16.2.1 GABRP Survey data

The sediment samples were processed at SARDI and data on sediment grainsize, composition and nutrient content were generated and data-based.

The processing of fauna samples can be complex and multi-stepped. Fig A1-1 outlines the work-flow for the biological collections of the GAB benthic biodiversity characterisation project surveys from the ship acquittal to archived specimens and processed catch data, from where the data can be published.

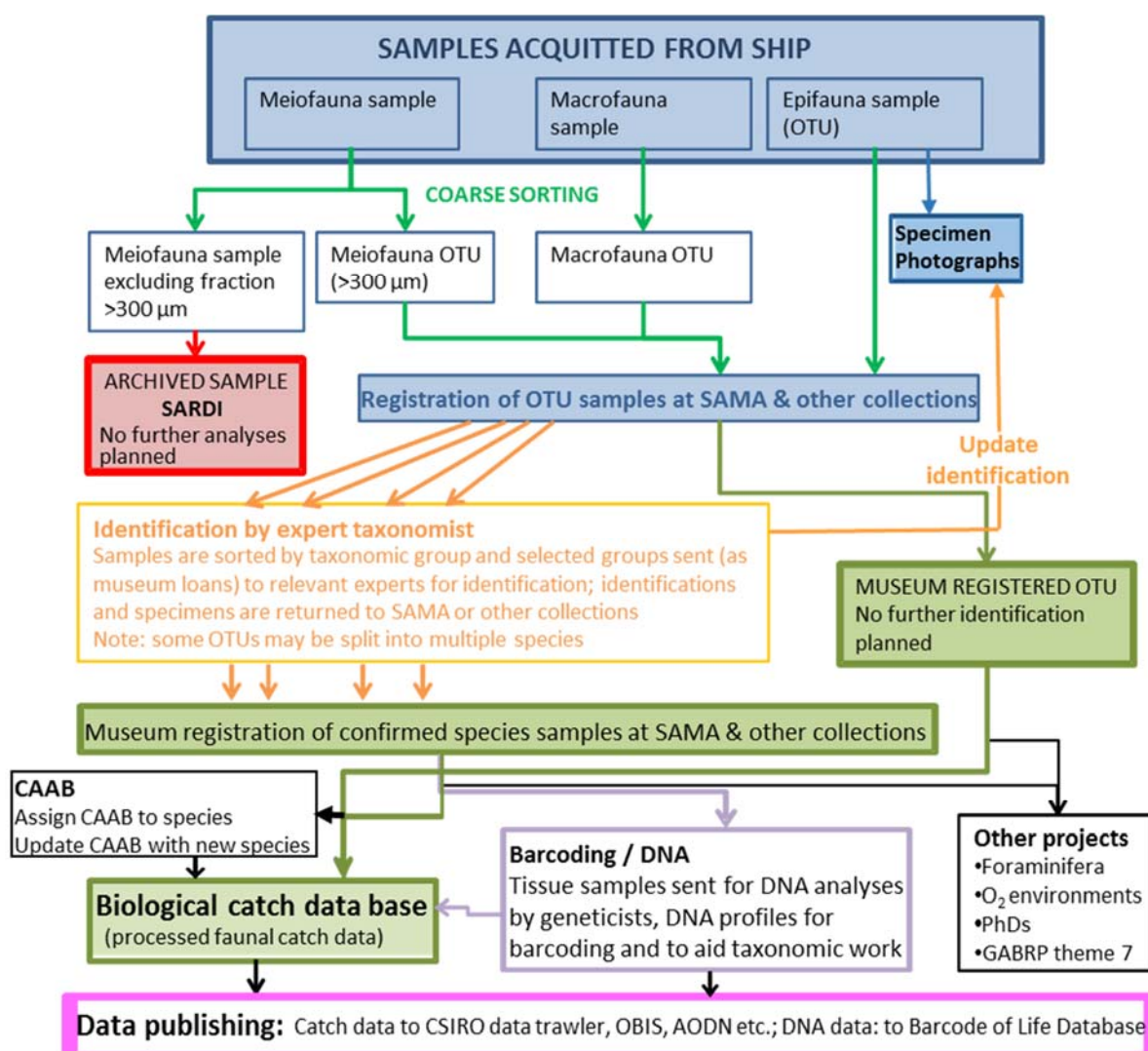


Fig A Outline of the work-flow for biological collections from the ship acquittal to archived specimens and processed catch data.

The sample processing and taxonomic work done on the biological specimen collections from the GABRP are documented in the main text. One step to draw attention to here is the assignment of a CAAB – Codes for Australian Aquatic Fauna to each taxon (Rees et al., 2017; <http://www.cmar.csiro.au/data/caab/>). As identifications are received from taxonomists the species are either assigned the relevant CAAB, if the species was previously in the catalogue, or the species is checked for its current validity status against the World Register of Marine Species (WoRMS) and if valid or confirmed by the expert as valid, included in the CAAB catalogue. As the CAAB catalogue is continuously updated with the latest information regarding taxonomy of Australian fauna, the CAAB code is a useful tool to track and standardize species names, synonyms and updates into the future. Muscle samples of the vast majority of fish species were DNA barcoded at the Cytochrome Oxidase subunit 1 gene (CO1) to provide additional support for identifications made from morphological (e.g. colour, fin placements, etc) and meristic (e.g. fin ray and scale count) observations. After careful vetting of sequences and identifications, consensus sequences for each sample will be made available through the Barcode of Life Database (<http://v4.boldsystems.org/>) (through FOAP, Fishes of Australia XVI project).

Processed data sets generated:

- Quality assured survey deployments list with calculated gear on/off bottom positions
- Sediment analyses outputs
 - grain size
 - TIC/TOC/TN
- Biological catch composition data – with updated taxonomy for selected taxa
- Infauna (Macrofauna)
- Epifauna (incl. fishes)
- DNA Barcodes for selected species

16.2.2 Data collations

In addition to survey data, existing electronic and biological specimen data were collated. These data sets are described in the main text of this report. They include:

- Environmental data sets from various web-based sources
- Historical surveys and collections: extract from the CSIRO data trawler and SARDI surveys
- Museum specimen distribution data collated from Museum data bases.

16.3 Data Curation and Archive

A representative collection of the specimens are lodged and registered mainly with the South Australian Museum (SAMA) or the Australian National Fish Collection (ANFC), additional specimens are lodged with other Australian Museums and collections including Museums Victoria (NMV) and

the Australian Museum (AMS). Tissue samples for future genetic analysis of selected species are archived by the ANFC and/or NMV. The Museums and collections ensure archiving, sample curation and accessibility for future studies. The unsorted meiofauna samples are curated and stored at SARDI.

Taxonomic photographs of specimens are archived on the CSIRO computer network. They are linked to CAAB and identifications are periodically updated as new identifications or taxonomic research is published.

The processed electronic data sets are archived in the data warehouse of the CSIRO Oanda Information and Data Centre from where they can be published to the CSIRO Data Trawler (CSIRO, 2017), the AODN, OBIS and other web-portals. Identification of catch data are periodically updated as new identifications or taxonomic research is published.

Metadata records have been created for the sediment data and the biological collection from the GAB RP surveys. As stated in the metadata, the biological collection data are 'living' data sets that will be archived by the CSIRO Oanda Information and Data Centre and will be continually updated as new taxonomic information becomes available. In addition, a metadata record for previously reported collation of museum specimens from the GAB was also created. This is a static data set compiled from museum records, the derived data set may be requested from the authors however, data IP remains with the respective institutions.

The titles of the respective MarLIN Metadata records and links are given below:

GAB Research Program: Project 3.1 – Museum specimens: data collation

<http://www.marlin.csiro.au/geonetwork/srv/eng/search#!35c51468-0632-4d71-9b37-7e9b36a15ac9>

GAB Research Program: Project 3.1 – Benthic Biodiversity Characterisation: Sediment data

<http://www.marlin.csiro.au/geonetwork/srv/eng/search#!b82bbcf3-ec2b-49e4-889d-f3629a1ded2d>

GAB Research Program: Project 3.1 – Benthic Biodiversity Characterisation: Biological collections

<http://www.marlin.csiro.au/geonetwork/srv/eng/search#!f301c328-bec4-42f9-9803-76d14eb17377>

CSIRO Oanda metadata in MarLIN conforms to the ISO 19115 metadata standard. It is harvested or otherwise made available to national systems such as: Research Data Australia (RDA); AODN and the Australian Spatial Data Directory (ASDD).

Muscle samples of the vast majority of fish species were DNA barcoded at the Cytochrome Oxidase subunit 1 gene (CO1) to provide additional support for identifications made from morphological (e.g. colour, fin placements, etc) and meristic (e.g. fin ray and scale count) observations. After careful

vetting of sequences and identifications, consensus sequences for each sample will be made available through the Barcode of Life Database (<http://www.barcodinglife.com/>) (through FOAP, Fishes of Australia XVI project).

16.4 Data Access, Use Agreements and Licensing

The biological data sets and specimens will be accessible to the public under the Creative Commons Attribution license (CC-BY 4.0) upon official release from the GABRP.

16.5 Publication of Datasets

Curated specimens and associated catch information are available to future research through loans arranged by the relevant museums and collections.

The biological catch data are groomed for inclusion into the CSIRO data trawler (<http://www.cmar.csiro.au/data/trawler/>) upon official release to the public. From there they are served to the Australian Oceans Data Portal (AODN), Atlas of Living Australia (ALA), and the Ocean Biogeographic Information System (OBIS).

Quality assured DNA barcoding data will be made available through the Barcode of Life Database (v4.boldsystems.org/) (through FOAP, Fishes of Australia XVI project).

The sediment data are released to GA for inclusion in the national marine sediments database.

17 APPENDIX 2: STUDENT PROJECTS

Student Name: Amelia Lewis

Degree Type: Doctor of Philosophy

Project Title: Uncovering the diversity of deep sea crustaceans (Isopoda and Amphipoda) from the Great Australian Bight

Institution: The University of Adelaide

17.1 Status of Student Project

17.1.1 Background

The deep-sea of the Southern Hemisphere has revealed high levels of biodiversity (e.g. Southern Ocean, surrounding New Zealand and the Pacific Ocean (Brandt et al., 2004; Brandt et al., 2007; Knox et al., 2012; Jamieson et al., 2013; Meyer-Löbbecke et al., 2014)). A dominant fauna in these studies are the crustacean taxa, specifically the peracarid groups Isopoda and Amphipoda. These taxonomic groups are considered good indicator taxa due to their longevity, habitat specialisation and possible low dispersal abilities. They can be found in all deep-sea environments, making them ideal taxa for biogeographic and biodiversity studies. These studies provide vital knowledge and increase our understanding of the deep-sea.

The Great Australian Bight (GAB) is framed by an extensive coastline with no terrestrial run off and an expansive continental shelf (Edyvane, 2000; James et al., 2001; Sorokin et al., 2007). The long isolation of southern Australia from other land masses, and the lack of glaciation, are thought to have created a unique opportunity for unparalleled diversity in the GAB (McGowran et al., 1997; Phillips, 2001). The diversity in some regions of the GAB has been examined but the deeper areas remain virtually unstudied. Preliminary reports have shown a high level of diversity present at the higher systematic levels but the finer relationships and diversity are yet to be examined (Currie et al., 2007; Sorokin et al., 2007; Currie and Sorokin, 2011). The diversity and relationships of the isopods and amphipods of the GAB are yet to be explored and based on the deep-sea literature from other regions of the world it is likely to be highly diverse. This project aims to substantially contribute to our limited knowledge of GAB biodiversity

17.1.2 Aims and significance

Aligned with the GAB Research Program's Benthic theme, the current project aims to explore the extent of the biodiversity of amphipods and isopods in the GAB. An integrative taxonomic approach will be employed to elucidate the relationships of these two diverse groups and provide a baseline

study and a comprehensive record of the isopods and amphipods from the GAB. Here the primary aims of the project are presented:

1. Develop a multigene phylogeny and test the classification of these two groups represented in the Australian deep-sea;
2. Construct a CO1 barcode library for the fauna to support future morphological identifications (and support aim 4);
3. Document the biodiversity of the isopod and amphipod fauna from the benthos of the GAB with a taxonomic checklist;
4. Examine the taxonomy and classification of *Brucerolis* isopods from the GAB;
5. Explore biogeographic patterns of peracarid taxa present in the GAB.

17.1.3 Section Progression

Broad scale multigene phylogeny of Isopods and Amphipods from the Great Australian Bight (aim 1);

A multigene phylogeny will be reconstructed with molecular data to explore the limits and composition of the isopods and amphipods from the GAB. CO1 data has been collected for the multigene phylogeny. This preliminary data will aid molecular species delineation and will complement the morphological identifications for the project (aim 2). 16S and 18S markers are currently being amplified and sequence data being produced for the multigene phylogeny. H3, 12S and 28S, will also be sequenced to provide a detailed overview of the peracarid relationships from the GAB.

Taxonomic checklist of the isopods and amphipods from the Great Australian Bight (aim 3);

The collation of a detailed taxonomic checklist for the biodiversity of isopods and amphipods in the GAB will provide the first comprehensive record of these crustacean groups in this region. The checklist will focus on all records of isopods and amphipods from the GAB collected 200m and deeper. The geographic extent and the diversity of these two major groups will be elucidated and recorded. Other information such as voucher specimen location, material examined, and any sampling details will also be included in the checklist. This checklist will be a valuable document that will provide a database of information on the GAB isopods and amphipods for future reference and identification purposes. It is likely that there will be new species elucidated from this project, therefore species descriptions for a group of diverse amphipods will be used to help document the

morphological diversity. So far there are 19 amphipod and 12 isopod families recorded from the GAB in the checklist. This document is ongoing and as the project progresses more data will be added to the checklist.

Morphological examination and taxonomy of the Serolidae isopods from the Great Australian Bight (aim 4)

The Serolidae from the GAB and the deep-sea surrounding Australia have only previously been examined morphologically and the molecular relationships are yet to be explored. *Brucerolis* and the closely related, *Acutiserolis*, are cosmopolitan in the Australian deep-sea as well as New Zealand and Antarctic waters. These genera are currently defined by a few morphological variations and the preliminary molecular results are indicative of a possible morphologically cryptic species within an existing morphospecies (*Brucerolis victoriensis*) within the GAB. Molecular and morphological examination of both genera will place GAB *Brucerolis* into taxonomic context within the serolid family by examining material from the Southern Ocean sourced from NIWA. A number of molecular markers, such as CO1, 16S, 18S and 24S, will be used to explore the relationships of these serolids. The multigene phylogeny of the serolids will incorporate all available sequence data from GenBank in order to provide taxonomic context of the *Brucerolis* and *Acutiserolis* genera.

Biogeographic and bathymetric patterns of isopods and amphipods from the Great Australian Bight (aim 5)

The sampling in the GAB covers a large region of the GAB at various depth ranges. This information, coupled with the multigene phylogeny generated from this project, will be used to explore the biogeographic and bathymetric patterns of diversity for these groups. Areas of species richness will also be explored and areas of endemism will be identified. The GAB samples are diverse but sparse, with many singletons, therefore an analysis of the species richness will be important.

Preliminary reports and studies on other organisms in the GAB have shown that there are specific regions and depths that have higher diversity levels than others (Ward et al., 2006; Sorokin et al., 2007). Comparing the diversity of other regions/organisms will help to provide a greater understanding of the diversity of the unique GAB environment. Looking at the GAB diversity as a whole and comparing it to other already studied regions such as the south east and west regions of Australian waters will provide some useful insights into the deep-sea regions of Australia.

17.1.4 References

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18 APPENDIX 3: PROJECT PUBLICATIONS

18.1 Papers

- Sherlock M, Marouchos A, and Williams A. (2014) An Instrumented Corer Platform for Seabed Sampling and Water Column Characterisation. Proceedings of the 2014 IEEE Oceans Conference, Taipei: 1-6.
- O'Hara TD, Harding C. (2014) A new species of *Sigsbeia* and additional records of ophiuroids from the Great Australian Bight. *Memoirs of Museum Victoria* 72: 131-140.
- O'Loughlin PM, and MacIntosh H. (2015) New *Prototrochus* species of sea cucumber from Australia (Echinodermata: Holothuroidea: Synaptida: Myriotrochidae). *Zootaxa* 3995, 264-670.

18.2 Presentations

AMSA:

- MacIntosh H, McCallum A, Kelly Merrin K, Tim O'Hara T, O'Loughlin M, Walker-Smith G, Williams A, Robin Wilson R, and Woolley S. (2015) New sampling highlights undescribed diversity in the deep Great Australian Bight. Australian Marine Sciences Association (AMSA) Conference, Geelong 6-9 July 2015.
- Althaus F, MacIntosh H, Williams A, Gowlett-Holmes K, Tanner JE, and Loo M. (2017) Benthic invertebrate megafauna of the deep Great Australian Bight. Australian Marine Sciences Association (AMSA) Conference, Darwin 2-6 July 2017.
- Tanner JE, Althaus F, Sorokin S and Williams A. (2017) Biogeography of southern Australian deep sea fauna. Australian Marine Sciences Association (AMSA) Conference, Darwin 2-6 July 2017.
- Williams A, Graham K, Gomom M, Bray D, McMillan P, Pogonoski J, Appleyard S, Gledhill D, Doyle S, Graham A, Osterhage D, and Althaus F. (2017) The deepest systematic collection of benthic fishes in Australian waters -continental slope and rise of the Great Australian Bight. Australian Marine Sciences Association (AMSA) Conference, Darwin 2-6 July 2017.
- Wiltshire KH, Tanner JE, Sorokin S, and Althaus F. (2017) Assessing environmental suitability of the GAB region for key deep-sea benthic taxa using species distribution modelling. Australian Marine Sciences Association (AMSA) Conference, Darwin 2-6 July 2017.

World Sponge Conference

- Sorokin S, Klautau M, Goudie L, Crowther A, Fromont J, George AM, McCormack S, and Wahab MAA. (2017) Calcareous on the shelf edge of the Great Australian Bight, Australia. 10th World Sponge Conference, Galway, 25-30 June, 2017.
- Sorokin S and Goudie L (2017) Dominance and diversity of deep-water sponges on the shelf edge and slope of the Great Australian Bight, South Australia. 10th World Sponge Conference, Galway, 25-30 June, 2017.

Systematics 2017

- Lewis A, Austin A, Guzik M, King R, Tanner JE, and Williams A. (2017) Uncovering the diversity of deep sea crustaceans (Isopoda and Amphipoda) from the Great Australian Bight. Australian Marine Sciences Association (AMSA) Conference, Darwin 2-6 July 2017.
- Tanner JE, Althaus F, MacIntosh H, Gowlett-Holmes K and Williams A. (2017) Infaunal assemblage structure in the deep Great Australian Bight. Systematics 2017, Adelaide 26-29 November 2017.

GABRP Symposia:

Williams A, Tanner JE, Sorokin S, Althaus F, Green M, Loo M, Mantilla L. (2014) Benthic projects 3.1. Great Australian Bight Research Program (GABRP) Symposium, Adelaide 5 November 2014.

Project teams (2015) Benthic biodiversity: projects 3.1 and 3.2, Presentation by the Project teams. Great Australian Bight Research Program (GABRP) Symposium, Adelaide 19 August 2015.

Project teams (2016) Benthic biodiversity: projects 3.1 and 3.2, Presentation by the Project teams. Great Australian Bight Research Program (GABRP) Symposium, Adelaide 16 August 2016.

18.3 Patents

Not applicable

18.4 Media Releases

18.4.1 New sponges species found in the Great Australian Bight

www.misa.net.au/GAB/research_results/media_releases/media_release_-_13_september_2017

The above media release was picked up by regional Eyre Peninsula newspapers and local Adelaide ABC radio who interviewed Steven Lapidge

19 APPENDIX 4: INTELLECTUAL PROPERTY

19.1 Unique discoveries

Not applicable

19.2 Action plan

Not applicable

20 APPENDIX 5: SUPPLEMENTARY DATA

20.1 Appendix – Section 5: Checklist of the GAB Invertebrate fauna

Appendix Table 1 Checklist of invertebrate species collected in 2013-2015 GAB surveys, showing total abundance, depth range and taxonomic/geographic records. Taxa for which total specimens is blank are colonial species that were broken up in the trawl, making it impossible to determine the number of colonies collected.

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
PORIFERA								
DEMOSPONGIAE								
Ancorinidae								
Ancorinidae sp. 1		1	409.85	409.85				
Asteropus sp. 1	2	1	198.85	198.85				
Psammastra sp.		1	409.85	409.85				
Stelletta sp. 1		1	388.1	388.1				
Stelletta sp. 2	49	4	189.15	425.65				
Stelletta sp. 3	17	2	382.6	409.85				
Stelletta sp. 4		1	189.15	189.15				
Stryphnus sp.		1	189.15	189.15				
Aplysiniellidae								
Suberea sp. 1	1	1	283.2	283.2				
Aplysiniidae								
Aplysina sp. 1		1	208.7	208.7				
Axinellidae								
Auletta sp.		1	409.85	409.85				
Axinella sp. 1		2	388.1	409.85				
Axinella sp. 2		1	388.1	388.1				
Axinella sp. 3		2	388.1	409.85				
Axinella sp. 4		1	221.35	221.35				
Axinella sp. 5		1	189.15	189.15				
Axinella sp. 6		1	409.85	409.85				
Axinella sp. 7		1	217.5	217.5				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Axinella</i> sp. 8	2	2	198.85	221.35				
Axinellidae sp. 1		1	221.35	221.35				
Axinellidae sp. 2		1	221.35	221.35				
Axinellidae sp. 3		2	388.1	409.85				
<i>Cymbastela</i> ? sp. 1		1	208.7	208.7				
<i>Pararhaphoxya</i> sp. 1		2	382.6	388.1				
<i>Pararhaphoxya</i> sp. 2	2	1	283.2	283.2				
<i>Phakellia</i> sp. 1		1	208.7	208.7				
<i>Phakellia</i> sp. 2		1	409.85	409.85				
<i>Phakellia</i> sp. 3		1	409.85	409.85				
Callyspongiidae								
<i>Callyspongia</i> (<i>Callyspongia</i>) sp. 1	48	6	189.15	283.2		1	1	1
<i>Callyspongia</i> (<i>Callyspongia</i>) sp. 2		1	208.7	208.7				
<i>Callyspongia</i> sp. 3	7	5	189.15	283.2				
<i>Callyspongia</i> sp. 4		1	208.7	208.7				
Chalinidae								
<i>Chalinula</i> sp. 1	1	3	189.15	221.35				
<i>Haliclona</i> (<i>Haliclona</i>) sp. 1		1	208.7	208.7				
<i>Haliclona</i> (<i>Haliclona</i>) sp. 2		1	283.2	283.2				
<i>Haliclona</i> sp.	1	1	283.2	283.2				
Chondropsidae								
<i>Chondropsis</i> sp. 1		2	208.7	217.5				
<i>Chondropsis</i> sp. 2		1	208.7	208.7				
<i>Chondropsis</i> sp. 3	1	2	221.35	283.2				
<i>Phoriospongia</i> sp. 1		1	388.1	388.1				
Coelosphaeridae								
<i>Coelosphaera</i> (<i>Coelosphaera</i>) sp. 1		1	388.1	388.1				
<i>Forcepia</i> (<i>Forcepia</i>) sp. 1		1	388.1	388.1				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Lissodendoryx (Anomodoryx) cf. dendyi</i>		1	409.85	409.85				
<i>Lissodendoryx (Lissodendoryx) sp. 2</i>	30	3	388.1	425.65				
Crellidae								
<i>Crella</i> sp.		1	409.85	409.85				
Darwinellidae								
Darwinellidae sp.		1	382.6	382.6				
Darwinellidae/Suberitidae								
Darwinellidae/Suberitidae sp. 1		2	388.1	409.85				
Dendoricellidae								
Dendoricellidae sp.		1	283.2	283.2				
<i>Fibulia</i> sp. 1		1	208.7	208.7				
Dictyodendrillidae								
<i>Dictyodendrilla</i> sp. 1		1	388.1	388.1				
Dictyonellidae								
<i>Acanthella</i> sp. 1		3	208.7	2839.5				
<i>Stylissa carteri</i>		1	208.7	208.7				
Dysideidae								
<i>cf. Euryspongia</i> sp. 1	1	1	283.2	283.2				
<i>cf. Euryspongia</i> sp. 2		2	189.15	221.35				
Halichondriidae								
<i>Ciocalypa</i> sp. 1		1	283.2	283.2				
<i>Ciocalypa</i> sp. 2		3	189.15	217.5				
<i>Halichondria</i> sp.	2	2	382.6	409.85				
Halichondriidae sp. 1		1	221.35	221.35				
Halichondriidae sp. 2		1	221.35	221.35				
Irciniidae								
<i>Irciniidae</i> sp.		1	425.65	425.65				
<i>Psammocinia</i> sp. 1		2	189.15	283.2				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Microcionidae								
<i>Clathria</i> sp.		1	217.5	217.5				
<i>Mycalidae</i>								
<i>Mycale (Mycale)</i> sp. 1	30	3	382.6	425.65				
Myxillidae								
<i>Myxilla</i> sp. 1	1	1	382.6	382.6				
Niphatidae								
<i>Amphimedon</i> sp. 1		1	409.85	409.85				
<i>Hemigellius?</i> sp. 1		1	221.35	221.35				
<i>Niphates</i> sp. 1		1	208.7	208.7				
<i>Niphates</i> sp. 2		2	189.15	217.5				
<i>Niphates</i> sp. 3		1	221.35	221.35				
Niphatidae sp. 1		2	189.15	208.7				
Niphatidae sp. 2		1	189.15	189.15				
Niphatidae sp. 3		1	198.85	198.85				
Niphatidae sp. 4		1	198.85	198.85				
Pachastrellidae								
Pachastrellidae sp. 1	5	1	4606.8	4606.8				
<i>Thenea</i> sp. 1	10380	26	411.7	2839.5				
Petrosiidae								
<i>Neopetrosia</i> sp. 1		2	208.7	221.35				
<i>Neopetrosia</i> sp. 2		1	189.15	189.15				
Phloeodictyidae								
<i>Oceanapia</i> sp.		1	221.35	221.35				
<i>Oceanapia</i> sp. 1		1	221.35	221.35				
<i>Oceanapia</i> sp. 10		2	189.15	221.35				
<i>Oceanapia</i> sp. 11		1	221.35	221.35				
<i>Oceanapia</i> sp. 12		1	283.2	283.2				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Oceanapia</i> sp. 13		1	189.15	189.15				
<i>Oceanapia</i> sp. 2		1	221.35	221.35				
<i>Oceanapia</i> sp. 3	6	2	221.35	283.2		1	1	1
<i>Oceanapia</i> sp. 4		2	221.35	283.2				
<i>Oceanapia</i> sp. 5	3	2	221.35	283.2				
<i>Oceanapia</i> sp. 6		1	221.35	221.35				
<i>Oceanapia</i> sp. 7	1	3	198.85	283.2				
<i>Oceanapia</i> sp. 8	2	1	283.2	283.2				
<i>Oceanapia</i> sp. 9	1	1	221.35	221.35				
<i>Phloeodictyidae</i> sp.		1	221.35	221.35				
Placospongiidae								
Placospongiidae sp. 1	48	6	986.6	1026.65				
Polymastiidae								
<i>Polymastia</i> sp. 1	5	2	189.15	198.85				
Raspailiidae								
<i>Aulospongius</i> sp.		1	409.85	409.85		1		
<i>Raspailia</i> (<i>Clathriodendron</i>) sp. 1		2	388.1	409.85				
<i>Raspailia</i> (<i>Parasyringella</i>) sp. 1		1	388.1	388.1				
<i>Raspailia</i> (<i>Parasyringella</i>) sp. 2		1	221.35	221.35				
<i>Raspailia</i> (<i>Raspailia</i>) sp. 1		1	388.1	388.1				
<i>Raspailia</i> (<i>Raspailia</i>) sp. 2		2	198.85	217.5				
<i>Raspailia</i> (<i>Raspailia</i>) sp. 3		1	388.1	388.1				
<i>Raspailia</i> (<i>Raspaxilla</i>) sp. 1	35	5	189.15	388.1				
Spongiidae								
<i>Hyattella</i> sp. 1		1	221.35	221.35				
<i>Leiosella</i> sp. 1		1	221.35	221.35				
<i>Leiosella</i> sp. 2		5	189.15	409.85				
<i>Leiosella</i> sp. 3	1	2	283.2	382.6				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Leiosella</i> sp. 4		2	189.15	198.85				
<i>Spongia</i> sp. 1		1	217.5	217.5				
<i>Spongia</i> sp. 2		1	189.15	189.15				
<i>Spongia</i> sp. 3		2	198.85	217.5				
Spongiidae sp. 1		1	208.7	208.7				
Spongiidae sp. 2		1	409.85	409.85				
Spongiidae sp. 3		1	388.1	388.1				
Spongiidae sp. 4		1	221.35	221.35				
Stylocordylidae								
<i>Stylocordyla</i> sp. 1	11	4	189.15	425.65				
Suberitidae								
<i>Pseudosuberites</i> sp. 1		1	221.35	221.35				
<i>Pseudosuberites</i> sp. 2		1	208.7	208.7				
<i>Rhizaxinella</i> sp. 1	31	6	189.15	1552.65				
<i>Suberites</i> sp. 1	12	10	382.6	4012.65				
<i>Suberites</i> sp. 2		1	388.1	388.1				
<i>Suberites</i> sp. 3		1	388.1	388.1				
<i>Suberites</i> sp. 4		1	409.85	409.85				
<i>Suberites</i> sp. 5		1	409.85	409.85				
Tethyidae								
<i>Tethya</i> sp. 1	16	1	198.85	198.85				
<i>Tethycometes</i> sp. 1	5	3	217.5	411.7				
Tetillidae								
Tetillidae sp. 1		1	388.1	388.1	1			
Theonellidae								
Theonellidae sp. 1		1	388.1	388.1				
Thorectidae								
<i>Aplysinopsis</i> sp. 1	5	2	198.85	221.35				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Fascaplysinopsis</i> sp. 1	2	2	189.15	198.85				
<i>Hyrtios</i> sp.	4	1	198.85	198.85				
<i>Hyrtios</i> sp. 1	2	2	198.85	208.7				
<i>Hyrtios</i> sp. 2		1	217.5	217.5				
<i>Hyrtios</i> sp. 3		1	189.15	189.15				
<i>Thorecta</i> sp. 1		1	189.15	189.15				
<i>Thorectandra</i> sp. 2		1	382.6	382.6				
Trachycladidae								
<i>Trachycladus</i> sp.		1	409.85	409.85				
Unknown								
Demospongiae sp.		2	198.85	217.5				
CALCAREA								
Amphoriscidae								
<i>Leucilla</i> sp.		1	283.2	283.2				
cf. <i>Jenkinidae</i>								
cf. <i>Jenkinidae</i> sp. 1	1	2	198.85	221.35				
Clathrinidae								
<i>Arthuria</i> sp.		1	208.7	208.7				
<i>Clathrina</i> sp.		1	283.2	283.2				
<i>Clathrinidae</i> sp. 1	7	1	283.2	283.2				
<i>Clathrinidae</i> sp. 2	2	2	189.15	198.85				
<i>Clathrinidae</i> sp. 3	3	1	283.2	283.2				
<i>Clathrinidae</i> sp. 4		1	189.15	189.15				
<i>Ernstia n.</i> sp. 1		1	208.7	208.7	1			
Grantiidae								
<i>Aphroceras</i> sp. 1		1	221.35	221.35				
Grantiidae sp.	28	6	189.15	283.2				
<i>Leucandra</i> sp.		1	189.15	189.15				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Ute</i> cf. <i>syconoides</i>	3	5	189.15	283.2				
<i>Ute</i> n. sp. 1		1	221.35	221.35	1			
Heteropiidae								
<i>Grantessa</i> sp. 1	1	4	189.15	221.35				
<i>Sycettusa</i> cf. <i>tenuis</i>		4	189.15	217.5				
Lelapiidae								
<i>Lelapia australis</i>		2	189.15	198.85				
Leucaltidae								
<i>Leucettusa lancifera</i>	15	7	189.15	1020.9				
<i>Leucettusa</i> n. sp. 1	20	6	189.15	283.2	1			
Leucascidae								
<i>Ascaltis</i> sp. 1		1	217.5	217.5				
<i>Ascaltis</i> sp. 2		1	198.85	198.85				
<i>Ascaltis</i> sp. 3	2	2	198.85	217.5				
<i>Ascoleucetta compressa</i>		4	189.15	283.2				
<i>Ascoleucetta</i> n. sp. 1	7	4	189.15	283.2	1			
<i>Ascoleucetta</i> n. sp. 2		1	189.15	189.15	1			
<i>Ascoleucetta</i> n. sp. 3	1	1	283.2	283.2	1			
<i>Ascoleucetta</i> n. sp. 4	8	2	217.5	283.2	1			
<i>Ascoleucetta</i> sp.	4	5	189.15	283.2				
Leucettidae								
<i>Leucetta</i> sp. 1		1	221.35	221.35				
<i>Leucetta</i> sp. 2	1	4	189.15	283.2				
Leucosoleniidae								
Leucosoleniidae sp. 1		2	189.15	208.7				
Leucosoleniidae sp. 2		1	198.85	198.85				
Sycettidae								
<i>Sycon</i> sp. 1	3	2	189.15	198.85				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Sycon</i> sp. 2		1	189.15	189.15				
HEXACTINELLIDA								
cf. <i>Hyalonematidae</i>								
cf. <i>Hyalonematidae</i> sp.	1	1	1020.9	1020.9				
Euplectellidae								
Euplectellidae sp. 1	5	2	1402.35	1779.1				
Euplectellidae sp. 2		1	986.6	986.6				
Euplectellidae sp. 3		1	1020.9	1020.9				
<i>Walteria flemmingi</i>	11	5	986.6	1027.2		1	1	1
Hyalonematidae								
<i>Hyalonema (Leptonema)</i> sp. 1	2	3	1026.65	2725.55				
<i>Hyalonema</i> sp. 2	1	1	1021.4	1021.4				
<i>Hyalonema</i> sp. 3		1	1020.9	1020.9				
<i>Hyalonema</i> sp. 4		1	1020.9	1020.9				
<i>Hyalonema</i> sp. 5	2	1	2014	2014				
<i>Hyalonema</i> sp. 6		1	2037.2	2037.2				
<i>Hyalonematidae</i> sp. 1	2	2	995.55	1020.9				
<i>Hyalonematidae</i> sp. 2		1	2724.9	2724.9				
<i>Hyalonematidae</i> sp. 3	1	1	1492.15	1492.15				
<i>Hyalonematidae</i> sp. 4	2	1	2014	2014				
Leucopsacidae								
Leucopsacidae sp. 1	1	1	1478.05	1478.05				
Rossellidae								
<i>Aphorme</i> sp. 1	4	1	1020.9	1020.9				
Rossellidae sp. 1	4	1	1862.95	1862.95				
Rossellidae sp. 2		1	986.6	986.6				
Rossellidae sp. 3	7	1	986.6	986.6				
Rossellidae sp. 4		1	1020.9	1020.9				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Rossellidae sp. 5	1	1	1020.9	1020.9				
Rossellidae sp. 6	1	1	1020.9	1020.9				
Unknown								
Hexactinellida sp.	1	1	3927	3927				
Hexactinosid sp. 1	33	5	1699.05	3734.55				
Hexactinosid sp. 2	2	1	1779.1	1779.1				
Hexactinosid sp. 3		1	986.6	986.6				
Lyssacinosida sp. 1	3	1	1526.6	1526.6				
CNIDARIA								
SIPHONOPHORAE								
Rhodaliidae								
<i>Dendrogramma enigmatica</i>	120	7	986.6	2725.55		1		1
OCTOCORALLIA								
ALCYONACEA								
Acanthogorgiidae								
<i>Acanthogorgia</i> sp.	1	1	986.6	986.6		1	1	1
Alcyoniidae								
<i>Anthomastus</i> n. sp. Q [NIWA TAN0803, 2014]	1	1	986.6	986.6	1	1		
<i>Anthomastus</i> sp. R [2017]	1	1	2825.55	2825.55				
<i>Eleutherobia</i> n. sp. C [2017]	1	2	189.15	198.85				
Anthothelidae								
<i>Solenocaulon</i> n. sp. B [2017]		5	189.15	1552.65	1			
<i>Trachythela</i> n. sp. A	1	1	986.6	986.6	1			
<i>Victorgorgia</i> n. sp. B	8	2	1699.05	1734.85	1			
Chrysogorgiidae								
<i>Chrysogorgia</i> sp.	3	1	1767.3	1767.3		1	1	1
<i>Radicipes</i> sp. D	4	1	2114.2	2114.2	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Clavulariidae								
<i>Clavulariidae</i> n. gen. D n. sp. C [NIWA TAN0803, 2014]	2	2	986.6	1526.6	1			
<i>Clavulariidae</i> n. gen. H n. sp. A	7	2	1701.35	1779.1	1			
Coralliidae								
<i>Hemicorallium</i> n. sp. A	1	1	1699.05	1699.05	1			
Isididae								
<i>Acanella</i> sp. A [SS200702, 2008]	5	3	986.6	1026.65	1	1		1
<i>Eknomisis</i> n. sp. A		1	989.6	989.6	1			
<i>Isididae</i> sp.	68	4	986.6	2725.55				
<i>Lepidisis</i> sp.	2	1	2014	2014				
Nephtheidae								
<i>Dendronephthya</i> cf. <i>waitei</i>	1	1	283.2	283.2		1	1	1
<i>Drifa portlandensis</i>	10	1	198.85	198.85		1	1	1
<i>Scleronephthya</i> sp. D [2017]	6	1	208.7	208.7				
Paragorgiidae								
<i>Paragorgia</i> n. sp. E	1	1	1701.35	1701.35	1			
Plexauridae								
<i>Plexauridae</i> n. gen. E n. sp. B [2017]		1	221.35	221.35	1			
<i>Swiftia</i> n. sp. C [2017]		1	995.55	995.55	1			
Primnoidae								
<i>Callogorgia flabellum</i>	5	3	986.6	1862.95		1	1	1
<i>Callogorgia</i> n. sp. B [2017]		1	995.55	995.55	1			
<i>Calyptrophora</i> cf. <i>antilla</i>	1	1	2014	2014				
<i>Narella</i> sp. H	6	1	986.6	986.6	1			
<i>Parastenella</i> n. sp. C	2	2	986.6	1699.05	1			
<i>Pseudoplumarella australis</i>		1	208.7	208.7		1	1	1
PENNATULACEA								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Anthoptilidae								
<i>Anthoptilum</i> ?cf <i>kuekenthali</i>	2	1	2003.9	2003.9		1		1
<i>Anthoptilum grandiflorum</i>	5	4	986.6	1020.9		1		
<i>Anthoptilum murrayi</i>	3	3	1020.9	1335.4				
<i>Anthoptilum</i> sp.	1	1	1020.9	1020.9				
Funiculinidae								
<i>Funiculina</i> n. sp. B [2017]	1	1	2003.9	2003.9	1			
Kophobelemnidae								
<i>Sclerobelemnnon burgeri</i>	27	3	189.15	217.5				
Pennatulidae								
<i>Pennatula</i> cf. <i>inflata</i>	1	2	995.55	1492.15				
<i>Pennatula indica</i>	1	1	1168.85	1168.85		1		
<i>Pennatula</i> sp.	3	1	425.65	425.65				
<i>Pennatula</i> sp. F [2017]	2	2	1004.65	1478.05				
Protoptilidae								
<i>Distichoptilum gracile</i>	1	1	1015.05	1015.05				
<i>Protoptilum</i> n. sp. B [GAB Mus. Rec., 2015]	302	3	2724.9	3021.4		1	1	1
<i>Protoptilum</i> sp.	3	1	1492.15	1492.15				
Umbellulidae								
<i>Umbellula</i> cf. <i>lindahli</i>	9	2	1526.6	1934.05				
<i>Umbellula</i> cf. <i>pellucida</i>	2	1	1960.9	1960.9				
<i>Umbellula lindahli</i>	4	1	2014	2014		1	1	1
<i>Umbellula pellucida</i>	94	10	1004.65	2725.55		1		1
<i>Umbellula</i> sp.	8	2	1862.95	2825.55				
ACTINIARIA								
Actinernidae								
<i>Actinernus</i> cf <i>elongatus</i>	8	2	986.6	2825.55		1	1	1
<i>Isactinernus</i> cf <i>quadrilobatus</i>	1	1	409.85	409.85				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Actiniidae								
<i>Actiniidae</i> sp.	1	1	2724.9	2724.9				
<i>Bolocera</i> sp. 1	3	2	1004.65	1492.15		1		1
Actinoscyphiidae								
<i>Actinoscyphia</i> sp. 1	2	2	995.55	2725.55	1	1	1	1
<i>Pacmanactis</i> sp. 1	6	3	382.6	411.7	1			
Actinostolidae								
<i>Actinostolidae</i> sp. 1	3	3	989.6	2725.55		1	1	1
<i>Actinostolidae</i> sp. 2	5	2	986.6	1467.65		1	1	1
<i>Sicyonis</i> sp. 1	7	3	1934.05	2037.2		1		1
<i>Stomphia</i> sp.	3	1	409.85	409.85		1		
Hormathiidae								
<i>Actinauge</i> sp. 1	5	4	1004.65	1960.9		1	1	1
<i>Amphianthus</i> sp. 1	5	5	995.55	3001.9				
<i>Amphianthus</i> sp. 2	1	1	2003.9	2003.9				
<i>Hormathia</i> sp. 1	12	4	986.6	4012.65	1	1	1	1
<i>Hormathiidae</i> sp. 1	130	5	382.6	2839.5				
<i>Hormathiidae</i> sp. 2	2	1	1526.6	1526.6				
<i>Hormathiidae</i> sp. 3	1	1	1467.65	1467.65				
<i>Hormathiidae</i> sp. 4	4	1	2839.5	2839.5				
<i>Hormathiidae</i> sp. 5	3	1	2839.5	2839.5				
<i>Hormathiidae</i> sp. 6	1	1	1467.65	1467.65				
<i>Hormathiidae</i> sp. 7	6	2	1020.9	2839.5				
<i>Hormathiidae</i> sp. 8	2	2	2724.9	2825.55				
<i>Hormathiidae</i> sp. 9	1	1	1526.6	1526.6				
<i>Monactis</i> cf <i>vestita</i>	334	10	989.6	4606.8				
<i>Paracalliactis</i> cf <i>rosea</i>	95	14	995.55	3021.4				
<i>Paracalliactis</i> sp. 1	81	12	989.6	2725.55	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Stephanauge</i> sp. 1	1	1	995.55	995.55				
<i>Stephanauge</i> sp. 2	23	2	2724.9	3021.4				
Isophelliidae								
<i>Epiphellia</i> sp. 1	32	1	1699.05	1699.05				
Unknown								
<i>Actiniaria</i> sp. 1	3	2	409.85	3001.9				
<i>Actiniaria</i> sp. 2	12	1	409.85	409.85				
<i>Actiniaria</i> sp. 3	2	1	1526.6	1526.6				
<i>Actiniaria</i> sp. 4	1	1	1526.6	1526.6				
<i>Actiniaria</i> sp. 5	1	1	411.7	411.7				
<i>Actiniaria</i> sp. 6	1	1	1934.05	1934.05				
<i>Actiniaria</i> sp. 7	1	1	411.7	411.7				
<i>Actiniaria</i> sp. 8	1	1	1552.65	1552.65				
<i>Actiniaria</i> sp. 9	1	1	425.65	425.65				
CORALLIMORPHARIA								
Corallimorphidae								
<i>Corallimorphus</i> sp. 1	8	5	2014	3021.4				
<i>Corynactis</i> sp. 1	35	2	411.7	425.65				
SCLERACTINIA								
Anthemiphylliidae								
<i>Anthemiphyllia dentata</i>	2	1	217.5	217.5		1		1
Caryophylliidae								
<i>Caryophyllia diomedae</i>	1	1	1699.05	1699.05		1		1
<i>Caryophyllia planilamellata</i>	390	9	221.35	1478.05		1	1	1
<i>Paraconotrochus zeidleri</i>	1	1	411.7	411.7		1		1
<i>Solenosmilia variabilis</i>	14	1	986.6	986.6		1	1	1
<i>Stephanocyathus platypus</i>	26	2	995.55	1020.9		1	1	1
<i>Stephanocyathus spiniger</i>	177	8	217.5	995.55		1		1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Deltocyathiidae								
<i>Deltocyathus magnificus</i>	868	5	208.7	411.7		1		1
Flabellidae								
<i>Flabellum australe</i>	18	2	382.6	409.85		1		1
<i>Flabellum hoffmeisteri</i>	170	3	388.1	425.65		1	1	1
<i>Flabellum</i> spp.	66	5	217.5	409.85				
Micrabaciidae								
<i>Letepsammia formosissima</i>	1	1	425.65	425.65		1	1	1
BRACHIOPODA								
Cancellothyrididae								
<i>Cancellothyris hedleyi</i>	155	4	208.7	411.7		1	1	1
Craniidae								
<i>Craniidae</i> sp. 1	5	1	1386.65	1386.65				
Dallinidae								
<i>Jaffaia jaffaensis</i>	184	7	198.85	986.6		1	1	1
Discinidae								
<i>Discinidae</i> sp. 1	22	3	1526.6	2240.65				
Unknown								
<i>Brachiopoda</i> sp.	7	5	189.15	986.6				
BRYOZOA								
Adeonidae								
<i>Adeonellopsis</i> sp.		1	189.15	189.15				
<i>Adeonidae</i> sp.		1	208.7	208.7				
Flustridae								
<i>Flustridae</i> sp.		1	208.7	208.7				
Lepraliellidae								
<i>Celleporaria</i> sp.	2	4	189.15	1552.65				
<i>Lepraliellidae</i> sp.		1	221.35	221.35				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Phidoloporidae								
Phidoloporidae sp.		1	208.7	208.7				
ANNELIDA								
SIPUNCULIDA								
Unknown family								
Sipuncula sp. 1	10	7	1526.6	2100.2				
Sipuncula sp. 2	429	17	1467.65	3021.4				
Sipuncula sp. 3	16	2	2724.9	2725.55				
Sipuncula sp. 4	1	1	1699.05	1699.05				
Sipuncula sp. 5	164	7	986.6	1934.05				
Sipuncula sp. 6	4	2	1349	3021.4				
Sipuncula sp. 7	38	2	388.1	1004.65				
ECHIURA								
Unknown family								
Echiura sp.	4	4	1699.05	1862.95				
POLYCHAETA								
Ampharetidae								
Ampharetidae sp.	6	4	1380.5	4068.05	1			
Ampharetidae sp. GAB1	1	1	4012.65	4012.65				
Ampharetidae sp. GAB2	6	1	1701.35	1701.35				
Ampharetidae sp. GAB3	3	2	2724.9	2825.55				
<i>Melinnopsis</i> sp. MoV 6853	1	1	1995.4	1995.4	1			
Amphinomidae								
<i>Bathychloeia sibogae</i>	13	3	1768.7	4279.15		1	1	1
<i>Chloeia inermis</i>	1	1	235.9	235.9				
<i>Chloeia</i> sp. MoV 6854	1	1	1486.2	1486.2	1			
<i>Linopherus</i> sp. MoV 6845	1	1	436.8	436.8	1			
<i>Pareurythoe</i> sp. MoV 6855	11	6	189.15	2866.8	1	1	1	1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Aphroditidae								
<i>Aphrodita goolmarris</i>	50	14	388.1	2839.5		1		1
<i>Laetmonice yarramba</i>	306	17	189.15	2079.1		1		1
Capitellidae								
<i>Notomastus</i> sp. MoV 6840	6	4	436.8	1768.7	1			
Cirratulidae								
<i>Aphelochaeta</i> sp. MoV 6842	34	21	189.3	3927	1			
<i>Aphelochaeta</i> sp. MoV 6856	8	5	378.4	2014.2	1			
<i>Aphelochaeta</i> sp. MoV 7073	1	1	1349	1349	1	1		1
<i>Aphelochaeta</i> sp. MoV 7074	3	3	2168.6	2866.8	1	1	1	1
<i>Chaetozone</i> sp. MoV 7072	10	6	1255.5	2011.9	1	1	1	1
<i>Cirratulus</i> sp.	1	1	409.85	409.85				
Cossuridae								
<i>Cossura</i> sp.	1	1	1018.1	1018.1				
<i>Cossura</i> sp. MoV 6841	1	1	1475.3	1475.3	1			
Dorvilleidae								
<i>Schistomeringos</i> sp. 1	1	1	932.4	932.4	1			
Eulepethidae								
<i>Pareulepis malayana</i>	3	2	436.8	478.2		1		1
Eunicidae								
<i>Eunice</i> sp. MoV 5794	6	2	198.85	208.7	1	1	1	1
<i>Eunice</i> sp. MoV 6033	28	5	221.35	986.6	1	1	1	1
<i>Eunice</i> sp. MoV 6036	25	4	409.85	1168.85	1	1	1	1
<i>Marphysa</i> sp.	4	1	189.15	189.15				
Fauveliopsidae								
<i>Laubieriopsis</i> sp. MoV 7075	11	5	932.4	4068.05	1			
Flabelligeridae								
<i>Brada</i> sp. MoV 7076	2	2	1349	1380.5	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Diplocirrus</i> sp. MoV 6857	2	2	932.4	1490	1			
<i>Diplocirrus</i> sp. nov GAB2016	2	2	4012.65	4115.4	1			
<i>Flabelliderma</i> sp.	1	1	1475.3	1475.3	1			
Glyceridae								
<i>Glycera lapidum</i>	16	11	212.4	1598.85		1		1
Goniadidae								
<i>Goniada antipoda</i>	1	1	2365.7	2365.7		1		1
<i>Progoniada regularis</i>	1	1	1486.2	1486.2		1		1
<i>Progoniada</i> sp. MoV 7077	8	5	932.4	4068.05	1			
Hesionidae								
<i>Hesiolyra</i> sp.	1	1	996.2	996.2		1		
<i>Leocrates chinensis</i>	8	3	986.6	1402.35				
<i>Leocrates</i> sp.	1	1	996	996				
<i>Nereimyra</i> sp.	1	1	1255.5	1255.5	1			
<i>Parahesion</i> sp. MoV 6858	7	3	203.2	235.9	1			
Lumbrineridae								
<i>Abyssoninoe</i> sp.	4	4	996.2	1607.35	1			
Magelonidae								
<i>Magelona</i> sp.	1	1	2168.6	2168.6	1			
<i>Magelona</i> sp. MoV 6859	1	1	478.2	478.2	1			
Maldanidae								
<i>Maldanella</i> sp. MoV 6860	1	1	376.3	376.3	1			
<i>Maldanidae</i> sp.	1	1	983.1	983.1				
Nephtyidae								
<i>Aglaophamus profundus</i>	1	1	3713.85	3713.85		1		1
<i>Micronephthys</i> sp. MoV 6847	5	4	204.2	1520.5	1	1	1	1
Nereididae								
<i>Neanthes bassi</i>	4	3	198.85	425.65		1		1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Neanthes</i> GAB sp. nov	9	4	3530.35	4517.55	1			
Nereididae sp.	1	1	4012.65	4012.65				
<i>Nicon</i> sp.	1	1	1380.5	1380.5	1			
Onuphidae								
<i>Anchinothria</i> sp.	12	4	989.6	1526.6	1			
<i>Anchinothria</i> sp. 1	1	1	1168.85	1168.85				
<i>Hyalinoecia</i> sp.	13	4	208.7	357.6	1			
<i>Kinbergonuphis</i> sp.	1	1	1007.15	1007.15				
<i>Nothria</i> sp.	14	7	409.85	1598.85				
<i>Paradiopatra</i> sp. MoV 6846	1	1	436.8	436.8	1			
Opheliidae								
<i>Armandia</i> sp.	5	4	983.1	1701.35				
<i>Opheliidae</i> sp. GAB1	3	2	995.9	996				
<i>Ophelina</i> sp. MoV 7078	2	2	1349	1768.7	1			
<i>Polyophthalmus</i> cf. <i>translucens</i>	13	6	378.4	4068.05	1			
Orbiniidae								
<i>Leitoscoloplos</i> sp. MoV 6848	1	1	478.2	478.2	1			
<i>Naineris</i> sp. MoV 6843	4	4	1438.2	1560.2	1			
<i>Naineris</i> sp. MoV 6844	3	3	1438.2	2014.2	1			
<i>Naineris</i> sp. MoV 7071	20	15	989.6	3734.55	1	1	1	
Orbiniidae sp. GAB 2	2	2	989.6	1268.3	1			
Paralacydoniidae								
<i>Paralacydonia</i> sp. MoV 6861	1	1	378.4	378.4	1			
Paraonidae								
<i>Aricidea</i> (Acmira) sp. 2	1	1	1380.5	1380.5	1			
<i>Aricidea</i> sp.	1	1	421.4	421.4				
<i>Aricidea</i> sp. 1	1	1	932.4	932.4	1			
<i>Paradoneis</i> sp.	4	4	421.4	2003				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Paradoneis</i> sp. 1	14	9	996	2993.7	1			
Phyllodoceidae								
<i>Phyllodoce</i> duplex	8	4	409.85	1835.95		1	1	1
<i>Phyllodoce</i> sp. 1	1	1	1607.35	1607.35	1			
<i>Pseudomystides</i> sp.	1	1	995	995		1	1	
<i>Pseudomystides</i> sp. 1	1	1	1154.1	1154.1	1			
Pilargidae								
<i>Litocorsa</i> sp. MoV 6862	1	1	204.2	204.2	1	1		
Poecilochaetidae								
<i>Poecilochaetus</i> sp. 1	7	5	996	2012.9	1			
<i>Poecilochaetus</i> sp. MoV 6595	2	2	1560.2	1995.4	1	1		1
Polycirridae								
<i>Polycirrus</i> sp.	7	1	986.6	986.6				
Polynoidae								
<i>Euphione</i> sp. MoV 6636	3	1	388.1	388.1		1		1
<i>Harmothoe</i> sp.	1	1	1168.85	1168.85				
<i>Harmothoe</i> sp. GAB1	14	4	986.6	1335.4				
<i>Harmothoe</i> sp. GAB2	5	2	1331.5	1335.4				
<i>Harmothoe</i> sp. GAB3	2	2	986.6	1835.95				
<i>Harmothoe</i> sp. GAB4	1	1	986.6	986.6				
<i>Hyperhalosydna striata</i>	2	1	208.7	208.7		1		1
<i>Lepidasthenia</i> sp. GAB1	1	1	1392.2	1392.2	1			
<i>Lepidonotinae</i> sp. GAB1	10	3	208.7	388.1	1			
<i>Lepidonotus carinulatus</i>	4	1	409.85	409.85		1		1
<i>Malmgrenia</i> sp. GAB1	2	2	1020.9	1478.05	1			
Polynoinae sp. GAB5	5	2	425.65	1026.65	1			
Sabellariidae								
<i>Gesaia</i> sp.	6	2	1335.4	1835.95	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Gesaia</i> sp. 1	1	1	932.4	932.4	1			
Sabellidae								
<i>Euchone</i> sp. 1	2	2	1255.5	1349	1			
<i>Euchone</i> sp. 2	14	3	1171.3	1380.5	1			
<i>Euchone</i> sp. MoV 6863	2	2	1013.6	1018.1	1			
<i>Potamethus</i> sp.	1	1	2839.5	2839.5				
<i>Pseudopotamilla</i> cf <i>monoculata</i>	1	1	409.85	409.85		1	1	1
Sabellidae sp.	2	2	376.3	996.2				
Sabellidae sp. 1	2	2	1177.5	1349	1			
Sabellidae sp. 2	1	1	1380.5	1380.5	1			
Sabellidae sp. 3	2	1	1380.5	1380.5	1			
Scalibregmatidae								
<i>Pseudoscalibregma</i> sp.	1	1	2760.9	2760.9	1			
<i>Travisia</i> sp. MoV 6864	1	1	376.3	376.3	1			
<i>Travisia</i> sp. MoV 763	1	1	203.2	203.2	1	1		1
Serpulidae								
<i>Apomatus</i> sp.	30	1	986.6	986.6				
<i>Apomatus</i> sp. 1	14	1	388.1	388.1				
<i>Bathyvermilia gregrousei</i>	1	1	4606.8	4606.8				
<i>Hyalopomatus</i> sp.	3	3	1386.65	4012.65				
<i>Metavermilia</i> sp.	10	1	409.85	409.85				
<i>Neovermilia sphaeropomatus</i>	30	1	986.6	986.6				
<i>Protis</i> sp.	33	5	1168.85	4606.8				
<i>Protula</i> sp.	1	1	208.7	208.7				
<i>Serpula</i> sp.	2	2	409.85	478.2				
<i>Vermiliopsis</i> sp.	12	1	411.7	411.7				
Siboglinidae								
Siboglinidae sp.	12	7	436.8	4012.65	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Sigalionidae								
<i>Fimbriosthenelais</i> sp.	1	1	217.5	217.5				
<i>Leanira</i> sp. 1	2	2	1779.1	2839.5				
<i>Sigalion</i> sp.	2	2	1168.85	2079.1				
<i>Sigalion</i> sp. MoV 6865	1	1	376.3	376.3	1			
<i>Sthenelais</i> sp. MoV 6866	3	3	983.1	1438.2	1			
Spionidae								
<i>Dipolydora</i> sp.	2	2	1015.05	2114.2				
<i>Laonice bassensis</i>	2	2	983.1	1486.2		1		1
<i>Laonice</i> sp. 1	5	3	996.2	1904.2	1	1		
<i>Laonice</i> sp. MoV 6352	1	1	212.4	212.4	1	1		1
<i>Microspio</i> sp. MoV 6851	1	1	1520.5	1520.5	1			
<i>Microspio</i> sp. MoV 6867	1	1	212.4	212.4	1			
<i>Microspio</i> sp. MoV 7079	2	2	1380.5	2365.7	1			
<i>Microspio</i> sp. MoV 7080	38	14	1005.2	3927	1			
<i>Microspio</i> sp. y	1	1	995.9	995.9	1	1		
<i>Prionospio</i> sp.	3	3	995.9	2993.7				
<i>Prionospio</i> sp. 1	1	1	1768.7	1768.7	1			
<i>Prionospio</i> sp. 2	1	1	3282.05	3282.05	1			
<i>Prionospio</i> sp. MoV 6849	3	1	378.4	378.4	1			
<i>Prionospio</i> sp. MoV 6850	1	1	2094.5	2094.5	1			
<i>Prionospio</i> sp. MoV 6852	2	2	1320.7	1560.2	1			
Spionidae GAB-2	2	2	2014.2	2018.2				
Spionidae sp. GAB 1	7	4	1486.2	1607.35				
<i>Spiophanes wigleyi</i>	3	3	204.2	436.8		1		1
Syllidae								
Eusyllinae sp. 1	1	1	421.4	421.4				
Eusyllinae sp. 2	1	1	235.9	235.9				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Exogoninae sp. 1	1	1	212.4	212.4				
Exogoninae sp. 2	1	1	204.2	204.2				
Exogoninae sp. 3	1	1	212.4	212.4				
Exogoninae sp. 4	4	3	1005.2	1904.2				
Exogoninae sp. 5	1	1	1349	1349				
Exogoninae sp. 6	1	1	932.4	932.4				
Exogoninae sp. 7	3	3	996	1255.5		1		
Exogoninae sp. 8	2	2	1349	4068.05				
Syllidae sp.	2	2	382.6	4012.65				
Syllinae sp. 1	2	2	204.2	376.3				
Syllinae sp. 2	1	1	189.3	189.3				
Syllinae sp. 3	4	3	932.4	1255.5				
Terebellidae								
Terebellidae sp.1	1	1	1380.5	1380.5				
Terebellidae sp.2	1	1	1349	1349				
Trichobranchidae								
Trichobranchidae sp.	1	1	1767.3	1767.3				
<i>Trichobranchus</i> sp.	1	1	995	995				
OLIGOCHAETA								
?Enchytraeidae								
?Enchytraeidae sp. 1	14	7	1171.7	2168.6				
?Tubificidae								
?Tubificidae sp. 1	17	7	1154.1	2229.7				
?Tubificidae sp. 2	3	1	1171.3	1171.3				
MOLLUSCA								
APLACOPHORA								
Chaetodermatidae								
<i>Falcidens</i> sp. MoV 6897	1	1	436.8	436.8	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Epimeniidae								
Epimeniidae sp. 1	5	3	382.6	411.7				
Unknown								
Aplacophora sp. 1	1	1	995.55	995.55				
Aplacophora sp. 2	16	1	189.15	189.15				
POLYPLACOPHORA								
Acanthochitonidae								
<i>Notoplax</i> sp. 1	3	3	1041.05	1041.05				
BIVALVIA								
Arcidae								
<i>Batharca perversidens</i>	2	2	2114.2	2240.65		1	1	1
<i>Bentharca asperula</i>	1	1	1526.6	1526.6		1		
Cardiidae								
<i>Pratulum thetidis</i>	1	1	283.2	283.2		1	1	1
Cuspidariidae								
<i>Cuspidaria erma</i>	1	1	388.1	388.1		1		1
<i>Cuspidaria</i> sp. 1	1	1	4606.8	4606.8				
<i>Cuspidaria</i> sp. 2	6	4	1020.9	1960.9		1		1
<i>Myonera paucistriata</i>	1	1	1862.95	1862.95				
Galeommatidae								
<i>Axinodon bornianus</i>	20	2	4517.55	4606.8				
Limidae								
<i>Lima cf benthonimbifer</i>	4	2	382.6	409.85		1	1	1
<i>Limatula</i> sp. 1	4	2	2079.1	2114.2				
Limopsidae								
<i>Limopsis</i> sp. 1	5	1	1335.4	1335.4				
<i>Limopsis</i> sp. 2	57	3	382.6	409.85				
<i>Limopsis</i> sp. 3	1245	4	2003.9	3001.9				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Lyonsiellidae								
<i>Allogramma cf oahuensis</i>	1	1	1526.6	1526.6				
<i>Policordia</i> sp. 1	1	1	1526.6	1526.6				
<i>Policordia</i> sp. 2	1	1	2839.5	2839.5				
Malletiidae								
<i>Protonucula verconis</i>	1	1	2094.5	2094.5		1	1	1
Mytilidae								
<i>Dacrydium</i> sp. 1	1	1	1255.5	1255.5				
Nuculidae								
<i>Ennucula dilecta</i>	1	1	421.4	421.4		1	1	1
<i>Nucula cf praetenta</i>	83	2	986.6	1015.05		1		1
Pectinidae								
<i>Delectopecten fosterianus</i>	20	4	986.6	1526.6		1	1	1
<i>Hyalopecten</i> sp. 1	3	3	1835.95	1960.9				
<i>Talochlamys pulleinea</i>	5	2	208.7	283.2		1	1	1
<i>Veprichlamys perillustris</i>	15	5	357.6	425.65		1	1	1
Poromyidae								
<i>Cetoconcha</i> sp. 1	1	1	388.1	388.1				
<i>Poromya</i> sp. 1	1	1	4606.8	4606.8				
<i>Poromya</i> sp. 2	1	1	1526.6	1526.6				
Propeamussiidae								
<i>Parvamussium maorium</i>	10	1	409.85	409.85				
<i>Propeamussium meridionale</i>	146	10	1835.95	4606.8				
Semelidae								
<i>Abra profundorum</i>	30	11	1767.3	4012.65		1		
Tindariidae								
<i>Tindaria</i> sp. 1	1	1	4676.5	4676.5				
<i>Tindaria</i> sp. 2	14	4	1015.05	2993.7				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Verticordiidae								
<i>Spinospella deshayesiana</i>	2	1	388.1	388.1		1	1	1
<i>Verticordia</i> sp. 1	2	2	1467.65	1526.6				
Vesicomidae								
<i>Vesicomya</i> cf <i>atlantica</i>	2	2	1171.7	3713.85				
<i>Vesicomya</i> cf <i>indica</i>	15	2	4517.55	4606.8				
SCAPHOPODA								
Dentaliidae								
Dentaliidae sp.	6	4	986.6	3877.7	1			
<i>Fissidentalium ponderi</i>	18	4	382.6	425.65		1	1	1
<i>Fissidentalium profundorum</i>	22	5	1478.05	2825.55		1		1
<i>Fissidentalium</i> sp.	115	5	409.85	1526.6	1			
<i>Graptacme</i> sp. 1	6	2	2825.55	3713.85	1			
Entalinidae								
<i>Rhomboxiphus tricarinatus</i>	21	2	1331.5	1526.6		1		1
Gadilidae								
<i>Gadila andersoni</i>	4	2	986.6	1015.05		1	1	1
Gadilidae sp.	1	1	995.9	995.9				
Laevidentaliidae								
<i>Laevidentalium leptosceles</i>	7	2	4606.8	4676.5		1	1	1
CEPHALOPODA								
Argonautidae								
<i>Argonauta nodosus</i>	1	1	1862.95	1862.95		1	1	1
Cranchiidae								
Cranchiidae sp.	2	1	189.15	189.15		1	1	1
<i>Teuthowenia pellucida</i>	1	1	1006.4	1006.4		1	1	1
Eledonidae								
<i>Eledone palari</i>	6	3	189.15	283.2		1	1	1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Enteroctopodidae								
<i>Benthoctopus</i> sp. 1	5	4	1006.4	1835.95	1	1	1	1
Joubiniteuthidae								
<i>Joubiniteuthis portieri</i>	1	1	2240.65	2240.65		1		1
Octopodidae								
<i>Octopus pallidus</i>	2	1	198.85	198.85		1	1	1
<i>Octopus</i> sp. 1	1	1	189.15	189.15	1			
<i>Octopus</i> sp. 2	1	1	388.1	388.1	1			
Ommastrephidae								
<i>Nototodarus gouldi</i>	3	3	1171.7	2165.6		1	1	1
Opisthoteuthidae								
<i>Opisthoteuthis persephone</i>	8	5	382.6	2003.9		1	1	1
<i>Opisthoteuthis pluto</i>	3	2	1004.65	1492.15		1	1	1
Pyroteuthidae								
<i>Pyroteuthis</i> cf. <i>margaritifera</i>	5	4	1021.4	1492.15		1	1	1
Sepiidae								
<i>Sepia cottoni</i>	2	2	221.35	283.2		1	1	1
<i>Sepia cultrata</i>	22	4	189.15	425.65		1	1	1
<i>Sepia hedleyi</i>	1	1	189.15	189.15		1	1	1
Sepiolidae								
<i>Austrorossia australis</i>	2	1	425.65	425.65		1	1	1
<i>Heteroteuthis</i> sp.	2	2	409.85	1004.65		1	1	1
<i>Sepiolina</i> sp. 1	8	2	388.1	425.65	1	1	1	1
Spirulidae								
<i>Spirula spirula</i>	1	1	995.55	995.55		1		
Vampyroteuthidae								
<i>Vampyroteuthis infernalis</i>	1	1	1552.65	1552.65		1	1	1

GASTROPODA

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Aglajidae								
<i>Philinopsis troubridgensis</i>	7	3	382.6	409.85		1	1	1
Arminidae								
<i>Armina</i> sp. 1	5	2	189.15	198.85				
<i>Heterodoris</i> sp. 1	3	2	986.6	1020.9	1			
<i>Heterodoris</i> sp. 2	5	1	995.55	995.55	1			
<i>Heterodoris</i> sp. 3	1	1	411.7	411.7	1			
Belomitridae								
<i>Belomitra</i> sp. 1	1	1	2725.55	2725.55	1			
<i>Belomitra</i> sp. 2	1	1	1020.9	1020.9	1			
Borsoniidae								
<i>Bathytoma agnata</i>	22	5	382.6	425.65		1	1	1
<i>Typhlomangelia</i> sp. 1	2	2	995.55	1020.9	1			
Cadlinidae								
<i>Cadlina</i> sp. 1	1	1	388.1	388.1				
Calliostomatidae								
<i>Calliostoma (Maurea)</i> sp. 1	2	1	409.85	409.85	1			
Calliotropidae								
<i>Calliotropis canaliculata</i>	62	8	986.6	1526.6		1		1
<i>Calliotropis carinata</i>	213	7	986.6	1526.6		1		1
<i>Lischkeia</i> sp. 1	1	1	4012.65	4012.65	1			
Cassidae								
<i>Oocorys sulcata</i>	6	4	986.6	1934.05		1		1
<i>Semicassis pyrum</i>	1	1	409.85	409.85		1	1	1
Cypraeidae								
<i>Umbilia armeniaca</i>	1	1	189.15	189.15		1	1	1
Discodorididae								
<i>Jorunna</i> sp. 1	2	1	411.7	411.7				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Sclerodoris</i> sp. 1	2	2	208.7	221.35				
Dorididae								
Dorididae sp. 1	4	4	986.6	1026.65				
Dorididae sp. 5	38	1	1168.85	1168.85				
Drilliidae								
<i>Splendrillia</i> sp. 1	1	1	382.6	382.6	1			
Epitoniidae								
<i>Amaea</i> sp. 1	3	1	2825.55	2825.55	1			
<i>Amaea</i> sp. B	1	1	1020.9	1020.9	1			
<i>Epitonium</i> (<i>Sodaliscala</i>) sp. 1	1	1	986.6	986.6	1			
<i>Globiscala</i> cf. <i>bonaespei</i>	1	1	1467.65	1467.65				
<i>Gregorioscala</i> sp. 1	1	1	1021.4	1021.4	1			
Eulimidae								
<i>Eulima acutissima</i>	1	1	1015.05	1015.05		1	1	1
Fasciolaridae								
<i>Chryseofusus alisonae</i>	1	1	425.65	425.65		1	1	1
<i>Fusinus pyrulatus</i>	1	1	189.15	189.15		1	1	1
<i>Granulifusus kiranus</i>	43	4	382.6	425.65		1		1
<i>Granulifusus</i> sp. 1	1	1	409.85	409.85	1			
<i>Granulifusus</i> sp. 2	2	1	388.1	388.1	1			
Fissurellidae								
<i>Emarginula superba</i>	7	2	382.6	409.85		1	1	1
<i>Puncturella</i> sp. 1	2	1	986.6	986.6	1			
<i>Rimulanax corolla</i>	237	5	382.6	425.65		1	1	1
Haminoeidae								
<i>Haminoea</i> sp.	1	1	1015.05	1015.05				
Hipponicidae								
<i>Malluvium devotum</i>	1	1	221.35	221.35		1	1	1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Marginellidae								
<i>Volvarina</i> sp. 1	1	1	1960.9	1960.9	1			
Muricidae								
<i>Emozamia licina</i>	2	1	388.1	388.1		1		1
<i>Enatimene</i> sp. 1	1	1	388.1	388.1	1			
<i>Enixotrophon carduelis</i>	57	10	411.7	1027.2		1	1	1
<i>Enixotrophon</i> cf. <i>plicilaminatus</i>	1	1	388.1	388.1	1	1		1
<i>Enixotrophon obtuseliratus</i>	1	1	1467.65	1467.65		1		1
<i>Enixotrophon plicilaminatus</i>	3	1	388.1	388.1		1		1
<i>Hirtomurex teramachii</i>	1	1	995.55	995.55		1		1
Muricidae New genus sp. 1	5	3	1467.65	1835.95	1			
Nassariidae								
<i>Tritia ephamilla</i>	18	6	986.6	1526.6		1	1	1
Naticidae								
<i>Polinices</i> sp. 1	44	12	986.6	1526.6	1			
Newtoniellidae								
<i>Ataxocerithium</i> sp. 1	1	1	388.1	388.1	1			
<i>Ataxocerithium</i> sp. 2	1	1	2079.1	2079.1				
<i>Cerithiella</i> sp. 1	1	1	1015.05	1015.05				
Pleurobranchidae								
<i>Berthella</i> sp.	1	1	409.85	409.85				
Pleurobranchidae sp.	1	1	388.1	388.1				
<i>Pleurobranchus hilli</i>	4	2	409.85	411.7		1	1	1
Pseudomelatomidae								
<i>Comitas</i> sp. 1	35	6	1020.9	1934.05	1			
<i>Inquisitor</i> sp.	1	1	388.1	388.1				
Ptychatractidae								
<i>Exilioidea</i> sp. 1	8	5	1526.6	2825.55	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Ranellidae								
<i>Monoplex exaratus</i>	3	1	221.35	221.35		1	1	1
<i>Sassia garrardi</i>	1	1	382.6	382.6		1	1	1
<i>Sassia kampyla</i>	7	1	411.7	411.7		1	1	1
Raphitomidae								
<i>Abyssosathauma</i> sp. 1	4	1	2825.55	2825.55	1			
<i>Asperdaphne</i> sp. 1	1	1	388.1	388.1	1			
<i>Bathybela</i> sp. 1	5	4	1835.95	2724.9	1			
<i>Bathybela</i> sp. 2	4	2	1526.6	1552.65	1			
<i>Gymnobela</i> sp. 1	5	2	1934.05	2724.9	1			
<i>Gymnobela</i> sp. 2	67	13	986.6	1526.6	1			
<i>Gymnobela</i> sp. 3	1	1	2839.5	2839.5	1			
<i>Gymnobela</i> sp. 4	1	1	2839.5	2839.5	1			
<i>Gymnobela</i> sp. 5	1	1	2825.55	2825.55	1			
<i>Gymnobela</i> sp. 6	6	3	2725.55	4606.8	1			
<i>Gymnobela</i> sp. 7	2	1	1335.4	1335.4	1			
<i>Neopleurotomoides</i> sp. 1	1	1	2037.2	2037.2	1			
<i>Spergo aithorrhys</i>	1	1	1552.65	1552.65				
<i>Spergo</i> sp. 1	25	8	1835.95	2839.5	1			
<i>Xanthodaphne</i> sp. 1	2	2	2825.55	4606.8	1			
Rissoidae								
<i>Benthonella</i> sp. 1	15	3	986.6	1526.6	1			
Scaphandridae								
<i>Scaphander</i> sp.	10	1	1021.4	1021.4	1			
<i>Scaphander</i> sp. 1	4	1	1335.4	1335.4	1			
<i>Scaphander</i> sp. 2	16	4	1467.65	2724.9	1			
Seguenziidae								
<i>Hadroconus diadematus</i>	6	3	1015.05	1526.6				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Halystes</i> sp.	1	1	4676.5	4676.5				
<i>Quinnia polita</i>	1	1	1015.05	1015.05		1	1	1
Seguenzioidea fam. nov.								
New genus sp. 1	107	10	986.6	1526.6	1			
Solariellidae								
<i>Archiminolia</i> sp. 1	2	1	283.2	283.2	1			
Terebridae								
<i>Hastula brazieri</i>	1	1	411.7	411.7		1	1	1
Triviidae								
<i>Trivirostra oryza</i>	1	1	189.15	189.15		1	1	1
Turbinellidae								
<i>Columbarium pagodoides</i>	12	4	382.6	425.65		1		1
Turritellidae								
<i>Colpospira curialis</i>	3	2	986.6	1015.05		1	1	1
Tylodinidae								
Tylodinidae sp.	1	1	217.5	217.5				
Velutinidae								
Velutinidae sp. 1	84	13	1478.05	2114.2	1			
Velutinidae sp. 2	3	2	198.85	221.35	1			
Velutinidae sp. 3	3	1	2037.2	2037.2	1			
Volutidae								
<i>Ericusa sericata</i>	1	1	217.5	217.5		1		1
<i>Livonia roadnightae</i>	11	6	189.15	411.7		1	1	1
ECHINODERMATA								
CRINOIDEA								
Ptilometridae								
<i>Ptilometra macronema</i>	5	2	189.15	198.85		1	1	1
ASTEROIDEA								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Asterodiscididae								
<i>Asterodiscides truncatus</i>	2	1	198.85	198.85		1	1	1
Astropectinidae								
<i>Astropecten</i> sp. 1	6	1	388.1	388.1				
<i>Astropecten</i> spp.	1	1	357.6	357.6				
Astropectinidae sp.	1	1	1402.35	1402.35				
<i>Dytaster</i> sp. 1	67	16	1478.05	4606.8				
<i>Plutonaster complexus</i>	6	2	1552.65	1960.9		1		1
<i>Plutonaster fragilis</i>	11	1	2003.9	2003.9				
<i>Plutonaster knoxi</i>	1	1	1934.05	1934.05				
<i>Proserpinaster neozelanicus</i>	3	3	382.6	425.65				
<i>Proserpinaster</i> sp. 1	4	1	411.7	411.7				
Benthopectinidae								
<i>Benthopecten</i> cf <i>munidae</i>	125	10	1020.9	2839.5		1		1
Benthopectinidae sp. 1	5	1	2037.2	2037.2				
<i>Cheiraster</i> sp. 1	2	1	388.1	388.1				
<i>Pectinaster mimicus</i>	7	3	411.7	4606.8		1		1
Brisingidae								
Brisingidae sp.	2	1	1478.05	1478.05				
<i>Hymenodiscus</i> sp. 1	12	6	1331.5	2725.55				
Echinasteridae								
<i>Henricia</i> sp.	1	1	995.55	995.55		1	1	
<i>Henricia</i> sp. 1	6	3	986.6	1020.9		1	1	
<i>Henricia</i> sp. 2	1	1	1020.9	1020.9		1	1	
<i>Henricia</i> sp. 3	2	2	1004.65	1026.65		1	1	
Goniasteridae								
<i>Ceramaster</i> sp. 1	1	1	1331.5	1331.5	1			
<i>Circeaster</i> sp. 1	1	1	1701.35	1701.35				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Goniasteridae sp.	5	2	208.7	940.1				
Goniasteridae sp. 2	15	2	1020.9	1526.6				
<i>Mediaster</i> sp. 1	8	1	986.6	986.6	1	1		
<i>Pillsburiaster</i> cf <i>aoteanus</i>	36	10	995.55	1492.15				
<i>Pillsburiaster maini</i>	1	1	1331.5	1331.5				
Luidiidae								
<i>Luidia prionota</i>	4	2	388.1	425.65		1		
Ophidiasteridae								
<i>Pseudophidiaster rhyus</i>	4	4	189.15	217.5		1	1	1
Pedicellasteridae								
<i>Hydrasterias</i> cf <i>sacculata</i>	6	2	4012.65	4606.8				
<i>Tarsaster</i> sp. 1	1	1	1767.3	1767.3				
Porcellanasteridae								
<i>Styracaster caroli</i>	4	2	995.55	4606.8				
Pseudarchasteridae								
<i>Paragonaster ridgwayi</i>	1	1	3021.4	3021.4				
<i>Perissogonaster insignis</i>	1	1	2724.9	2724.9				
<i>Pseudarchaster garricki</i>	4	2	1331.5	2037.2		1		1
<i>Pseudarchaster</i> sp. 1	1	1	1331.5	1331.5				
Pterasteridae								
<i>Calyptaster</i> sp.	145	7	409.85	3021.4	1			
<i>Diplopteraster</i> sp. 1	1	1	2003.9	2003.9	1	1	1	1
<i>Hymenaster caelatus</i>	67	6	1768.7	2839.5				
<i>Hymenaster</i> cf <i>blegvasi</i>	470	11	382.6	3021.4		1		1
<i>Hymenaster echinulatus</i>	67	4	1835.95	2240.65		1	1	1
<i>Hymenaster nobilis</i>	2	1	2724.9	2724.9				
<i>Hymenaster pullatus</i>	42	6	1478.05	2014		1		1
<i>Hymenaster</i> sp. 1	1	1	1862.95	1862.95				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Hymenaster</i> sp. 2	3	2	1934.05	1960.9				
<i>Pteraster affinis</i>	21	6	995.55	1862.95				
<i>Pteraster</i> sp.	1	1	357.6	357.6				
<i>Pteraster</i> sp. 1	4	1	3001.9	3001.9				
<i>Pteraster</i> sp. 2	2	1	411.7	411.7				
<i>Pterasteridae</i> sp.	1	1	2725.55	2725.55				
Solasteridae								
<i>Crossaster multispinus</i>	33	6	388.1	1526.6		1		1
<i>Lophaster</i> cf. <i>suluensis</i>	1	1	409.85	409.85				
Stichasteridae								
<i>Cosmasterias dyscrita</i>	1	1	986.6	986.6		1		1
<i>Smilasterias clarkailsa</i>	45	4	198.85	382.6		1		1
<i>Smilasterias triremis</i>	96	2	189.15	217.5		1		1
Zoroasteridae								
<i>Zoroaster carinatus</i>	2	2	1015.05	1020.9		1		1
<i>Zoroaster</i> cf. <i>alternicanthus</i>	3	1	995.55	995.55				
<i>Zoroaster</i> cf. <i>barathri</i>	9	5	2724.9	3021.4				
<i>Zoroaster</i> cf. <i>singletoni</i>	5	2	1015.05	1168.85				
<i>Zoroaster macracantha</i>	2	2	995.55	1021.4		1	1	1
<i>Zoroaster singletoni</i>	2	1	1331.5	1331.5				
<i>Zoroaster</i> sp.	1	1	3021.4	3021.4				
<i>Zoroaster spinulosus</i>	11	2	1168.85	1335.4		1		1
<i>Zoroasteridae</i> sp. 1	1	1	1006.4	1006.4				
OPHIUROIDEA								
Amphiuridae								
<i>Amphioplus</i> sp. MoV 2722	3	2	989.6	1699.05	1	1		1
<i>Amphiura</i> sp.	3	2	1007.15	1701.35				
<i>Amphiura</i> sp. 1	1	1	986.6	986.6				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Amphiura</i> sp. MoV 6895	2	1	204.2	204.2	1			
<i>Amphiura</i> sp. MoV 6896	1	1	436.8	436.8	1			
Asteronychidae								
<i>Astrodia tenuispina</i>	2689	5	1467.65	3021.4		1	1	1
Asteroschematidae								
<i>Ophiocreas sibogae</i>	2	2	1701.35	1767.3		1	1	1
Astrophiuridae								
<i>Ophiophycis richardi</i>	3	1	1402.35	1402.35				
Hemieuryalidae								
<i>Ophiozonella bispinosa</i>	2	2	221.35	357.6		1	1	1
Ophiacanthidae								
<i>Ophiacantha brachygnatha</i>	20	4	382.6	411.7		1	1	1
<i>Ophiacantha pacata</i>	8	3	1331.5	1492.15		1	1	1
<i>Ophiacantha rosea</i>	2	2	1699.05	1862.95	1	1		1
<i>Ophiacantha</i> sp. 1	5	1	1699.05	1699.05	1			
<i>Ophiacantha</i> sp. MoV 4533	30	3	1335.4	1862.95	1	1		1
<i>Ophiomitrella</i> sp. MoV 2779	1	1	1862.95	1862.95	1	1		1
<i>Ophiophthalmus relictus</i>	30	3	995.55	1526.6		1	1	1
<i>Ophioplinthaca plicata</i>	18	2	1699.05	1862.95		1	1	1
Ophiactidae								
<i>Ophiactis amator</i>	2	2	1862.95	2725.55		1		1
<i>Ophiactis hirta</i>	10	3	382.6	411.7		1	1	1
<i>Ophiactis resiliens</i>	1	1	208.7	208.7		1	1	1
Ophiernidae								
<i>Ophiernus vallincola</i>	28	9	986.6	1027.2		1		1
Ophiobyrssidae								
<i>Ophiobyrsa rudis</i>	1	1	388.1	388.1		1	1	1
Ophiodermatidae								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Ophiopsammus angusta</i>	6	2	382.6	409.85		1		1
Ophiophilidae								
<i>Ophiophilia</i> sp.	2	2	3713.85	4115.4				
Ophiopodidae								
<i>Ophiomastus</i> cf <i>tegulitus</i>	3	1	388.1	388.1		1	1	1
Ophiomusidae								
<i>Ophiomusa anisacanthum</i>	193	4	357.6	411.7		1	1	1
<i>Ophiomusa australe</i>	298	8	189.15	388.1		1	1	1
<i>Ophiomusa incertum</i>	60	4	221.35	1007.15		1		1
<i>Ophiomusa lymani</i>	5913	36	986.6	3021.4		1	1	1
<i>Ophiomusa scalare</i>	4176	10	189.15	995.55		1	1	1
Ophiomyxidae								
<i>Ophiomyxa australis</i>	4	4	208.7	283.2		1	1	1
<i>Ophiomyxa crinita</i>	380	8	198.85	425.65		1	1	1
Ophionereididae								
<i>Ophiodoris malignus</i>	18	1	409.85	409.85		1	1	1
<i>Ophionereis novaezelandiae</i>	2	1	221.35	221.35		1	1	1
Ophiopyrgidae								
<i>Amphiophiura bullata</i>	66	2	4517.55	4606.8		1		1
<i>Amphiophiura collecta</i>	40	9	189.15	425.65		1	1	1
<i>Amphiophiura distincta</i>	52	5	189.15	283.2		1	1	1
<i>Ophiopyrgus saccharatus</i>	10	2	986.6	1006.4		1		1
<i>Ophiura clemens</i>	175	9	986.6	1027.2		1	1	1
<i>Ophiura flagellata</i>	1	2	985.8	1020.9		1		1
<i>Ophiura irrorata</i>	2	2	932.4	989.6		1		1
<i>Ophiura irrorata concreta</i>	102	4	1835.95	1960.9		1		1
<i>Ophiura rugosa</i>	4	1	1478.05	1478.05	1	1		
<i>Ophiura</i> sp. MoV 7067	60	2	1862.95	4279.15	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Perlophiura profundissima</i>	1	1	4606.8	4606.8		1		1
Ophioscolecidae								
<i>Ophiolycus</i> sp.	1	1	989.6	989.6	1	1		1
<i>Ophioscolecidae</i> sp.	1	1	1386.65	1386.65	1			
<i>Ophioscolex</i> sp.	2	1	2724.9	2724.9				
Ophiosphalmidae								
<i>Ophiosphalma armigerum</i>	220	6	2724.9	4606.8		1	1	1
Ophiothamnidae								
<i>Ophiothamnus habrotatus</i>	4	2	221.35	235.9		1	1	1
Ophiotretidae								
<i>Ophiopristis</i> sp. MoV 5490	1	1	986.6	986.6	1	1		1
<i>Ophiotoma</i> sp cf <i>alberti</i>	1	1	1478.05	1478.05				
Ophiotrichidae								
<i>Ophiothrix aristulata</i>	61	9	198.85	425.65		1	1	1
Ophiuridae								
<i>Ophiocten australis</i>	19653	14	1467.65	4279.15		1		1
<i>Ophiura ooplax</i>	242	5	198.85	411.7		1	1	1
ECHINOIDEA								
Aspidodiadematidae								
<i>Aspidodiadema</i> sp.	1	1	4606.8	4606.8		1		1
Cidaridae								
<i>Goniocidaris sibogae</i>	8	3	198.85	1026.65		1		1
Clypeasteridae								
<i>Clypeaster</i> sp. nov. 1	295	6	189.15	283.2	1	1	1	1
Echinidae								
<i>Echinus multidentatus</i>	4	3	995.55	1402.35		1		1
Echinothuriidae								
<i>Echinothuriidae</i> sp.	15	5	1020.9	2725.55				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Hygrosoma</i> sp. 1	4	1	1862.95	1862.95				
<i>Sperosoma</i> sp.	58	8	1331.5	2825.55				
<i>Tromikosoma</i> sp.	2	2	2724.9	3001.9				
Loveniidae								
<i>Lovenia camarota</i>	2	1	388.1	388.1		1		
<i>Pseudolovenia</i> cf <i>hirsuta</i>	6	2	995.55	1020.9				
Pedinidae								
<i>Caenopedina</i> sp.	8	3	1699.05	2724.9		1		1
Phormosomatidae								
<i>Phormosoma</i> cf <i>bursarium</i>	364	3	986.6	1467.65		1		1
Phormosomatidae sp.	34	5	985.8	1026.65				
Saleniidae								
<i>Salenocidaris hastigera</i>	65	13	409.85	2839.5		1		1
Schizasteridae								
<i>Aceste ovata</i>	1	1	1007.15	1007.15		1		1
Spantagoida								
<i>Spantagoida</i> sp.	1	3	2079.1	2240.65				
Temnopleuridae								
<i>Pseudechinus notius</i>	7	3	382.6	411.7		1		1
HOLOTHUROIDEA								
Caudinidae								
<i>Paracaudina</i> sp.	1	1	4068.05	4068.05	1			
Deimatidae								
<i>Deima validum</i>	1	1	2724.9	2724.9		1		1
<i>Oneirophanta mutabilis</i>	1	1	4606.8	4606.8		1		1
Elpidiidae								
<i>Ellipinion</i> sp. nov. 1	4	3	1478.05	1552.65	1			
<i>Kolga</i> sp. 1	40	2	986.6	1335.4	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Peniagone azorica</i>	56	2	2724.9	2825.55				
<i>Peniagone</i> sp. 2	3	1	4606.8	4606.8	1			
Holothuriidae								
<i>Holothuria austrinabassa</i>	2	3	283.2	382.6		1	1	1
Laetmogonidae								
<i>Laetmogone maculata</i>	40	2	217.5	411.7		1	1	1
Mesothuriidae								
<i>Mesothuria regularia</i>	4	1	1526.6	1526.6		1		1
<i>Mesothuria</i> sp. 1	43	9	995.55	1335.4	1			
<i>Zygothuria lactea</i>	13	2	986.6	1020.9		1		1
Molpadiidae								
<i>Molpadia</i> sp. 1	1	1	3713.85	3713.85	1			
<i>Molpadia</i> sp. 2	1	1	2725.55	2725.55	1			
Myriotrochidae								
<i>Prototrochus ronae</i>	1	1	1475.3	1475.3	1	1		1
Pelagothuriidae								
<i>Enypniastes eximia</i>	911	21	986.6	2240.65		1		1
Psychropotidae								
<i>Benthodytes</i> sp. 1	23	6	2724.9	3021.4	1			
<i>Benthodytes</i> sp. 2	34	6	1004.65	4606.8	1			
<i>Psychropotes longicauda</i>	1	1	2725.55	2725.55				
<i>Psychropotes</i> sp. 1	5	3	2724.9	3021.4				
Synallactidae								
<i>Bathyplores natans</i>	45	6	217.5	3021.4		1		1
<i>Molpadiodemas involutus</i>	11	2	1960.9	2724.9		1		1
<i>Pseudostichopus hyalegerus</i>	412	6	217.5	411.7		1	1	1
<i>Pseudostichopus mollis</i>	11	2	986.6	1020.9		1		1
<i>Pseudostichopus</i> sp. 2	1	1	4606.8	4606.8				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Synallactes</i> sp.	1	1	1015.05	1015.05				
Synaptidae								
<i>Protankyra</i> sp. 1	1	1	1862.95	1862.95	1			
ARTHROPODA								
CIRRIPIEDIA								
Calanticidae								
<i>Calantica</i> sp. 1	13	3	1607.35	1734.85				
<i>Smilium acutum</i>	2	1	1699.05	1699.05		1		1
Pachylasmatidae								
<i>Eutomolasma maclaughlinae</i>	30	2	382.6	411.7		1		
Poecilasmatidae								
<i>Glyptelasma hamatum</i>	3	2	995.55	1734.85		1	1	1
Scalpellidae								
<i>Amigdoscalpellum costellatum</i>	10	4	2724.9	3021.4		1		1
<i>Amigdoscalpellum vitreum</i>	1	1	1960.9	1960.9		1		
<i>Arcoscalpellum inum</i>	22	7	409.85	1862.95		1	1	1
<i>Arcoscalpellum michelottianum</i>	1	1	1862.95	1862.95		1		
<i>Arcoscalpellum truncatum</i>	9	4	1004.65	2114.2		1		
<i>Gymnoscalpellum</i> sp. 1	1	1	2724.9	2724.9				
<i>Meroscalpellum bifurcatum</i>	1	1	4012.65	4012.65				
<i>Neoscalpellum</i> cf <i>schizoplacinum</i>	2	1	4606.8	4606.8				
<i>Neoscalpellum</i> sp. 1	1	1	4606.8	4606.8				
<i>Planoscalpellum distinctum</i>	1	1	1734.85	1734.85				
<i>Planoscalpellum planum</i>	15	5	1960.9	3021.4		1	1	1
<i>Regioscalpellum regium</i>	1	1	2724.9	2724.9		1	1	1
<i>Trianguloscalpellum</i> cf <i>uniarticulatum</i>	5	2	2825.55	2839.5				
<i>Verum australicum</i>	37	6	1835.95	3021.4		1		
<i>Verum candidum</i>	53	5	382.6	425.65		1	1	1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Verrucidae								
<i>Altiverruca</i> sp. 1	1	1	1862.95	1862.95				
<i>Gibbosaverruca</i> cf <i>nitida</i>	259	8	1699.05	2725.55				
<i>Gibbosaverruca</i> <i>navicula</i>	31	5	2003.9	2725.55		1	1	1
<i>Gibbosaverruca</i> sp. 1	24	3	1607.35	1734.85				
<i>Metaverruca</i> cf <i>recta</i>	7	1	1699.05	1699.05				
<i>Metaverruca</i> sp. 1	2	1	1699.05	1699.05	1			
TANAIDACEA								
Unknown								
Tanaidacea sp. 1	6	5	1154.1	2113.1				
Tanaidacea sp. 2	8	7	932.4	2777.8				
Tanaidacea sp. 3	11	8	996	2777.8				
Tanaidacea sp. 4	1	1	1607.35	1607.35				
Tanaidacea sp. 5	6	6	996	2168.6				
Tanaidacea sp. 6	5	2	1768.7	3734.55				
Tanaidacea sp. 7	7	5	995.9	1607.35				
Tanaidacea sp. 8	15	7	1154.1	3927				
Tanaidacea sp. 9	4	4	932.4	1560.9				
Tanaidacea sp. 10	3	3	989.6	1560.9				
Tanaidacea sp. 11	6	4	995.9	4068.05				
Tanaidacea sp. 12	1	1	995.9	995.9				
Tanaidacea sp. 13	2	2	995.9	996.2				
ISOPODA								
Aegidae								
<i>Aegapheles</i> <i>alozon</i>	1	1	357.6	357.6				
<i>Aegiochus</i> <i>beri</i>	2	2	1478.05	1526.6		1		1
<i>Aegiochus</i> cf. <i>bertrandi</i>	1	1	189.15	189.15		1		1
<i>Rocinela</i> sp. 1	1	1	382.6	382.6	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Antarcturidae								
<i>Antarcturus</i> sp. 1	1	1	3021.4	3021.4				
Bopyridae								
<i>Bathyggyge grandis</i>	2	1	2240.65	2240.65		1		1
Bopyridae sp.	5	2	217.5	409.85				
Cirolanidae								
<i>Booralana bathynella</i>	3	2	388.1	409.85		1		1
<i>Natatolana</i> cf. <i>matong</i>	7	3	189.15	409.85		1		1
<i>Natatolana</i> sp. 1	2	2	1607.35	1862.95	1			
<i>Natatolana</i> sp. MoV 6881	1	1	378.4	378.4	1			
<i>Plakolana</i> sp. MoV 6882	2	1	204.2	204.2	1			
Cymothoidae								
<i>Elthusa</i> sp. 1	1	1	382.6	382.6	1			
Dendrotonidae								
<i>Dendromunna</i> sp. 1	1	1	995.9	995.9	1			
Desmosomatidae								
<i>Chelator</i> sp. 4	2	2	995.9	2694	1			
<i>Chelator</i> sp. MoV 6868	1	1	996.2	996.2	1			
<i>Chelator</i> sp. MoV 6869	13	8	376.3	1560.2	1			
Desmosomatidae gen. nov. sp. MoV 6872	2	2	421.4	436.8	1			
Desmosomatidae New Genus A sp. 1	1	1	932.4	932.4	1			
<i>Eugerdia</i> sp. 1	1	1	996	996	1			
<i>Eugerdia</i> sp. 2	1	1	996.2	996.2	1			
Genus B sp. 1	4	2	3282.05	3927	1			
<i>Oecidiobranchus</i> sp. MoV 6871	2	2	376.3	1475.3	1			
<i>Prochelator</i> sp. 1	1	1	995	995	1			
<i>Whoia</i> sp. 1	1	1	2125.8	2125.8	1			
Gnathiidae								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Gnathia</i> sp. MoV 5729	1	1	478.2	478.2	1			
Haploniscidae								
<i>Haploniscus</i> sp. 2	1	1	2168.6	2168.6	1			
<i>Haploniscus</i> sp. 3	1	1	1560.9	1560.9	1			
<i>Haploniscus</i> sp. MoV 6874	1	1	1490	1490	1			
<i>Haploniscus</i> sp. MoV 6875	10	3	932.4	2018.2	1			
Hyssuridae								
<i>Kupellonura</i> cf. <i>currawan</i>	1	1	996	996		1		1
Ischnomesidae								
<i>Contrarimesus</i> sp. 1	1	1	2011.9	2011.9	1			
<i>Ischnomesus</i> sp. 1	1	1	932.4	932.4	1			
<i>Ischnomesus</i> sp. 2	2	2	1171.7	3282.05	1			
<i>Ischnomesus</i> sp. 3	1	1	4068.05	4068.05	1			
<i>Ischnomesus</i> sp. 4	1	1	2993.7	2993.7	1			
<i>Ischnomesus</i> sp. MoV 6876	1	1	983.1	983.1	1			
Katianiridae								
Katianiridae New genus sp. 1	1	1	995.9	995.9	1			
Leptanthuridae								
<i>Leptanthura</i> sp. 1	1	1	996.2	996.2	1			
<i>Leptanthura</i> sp. 2	1	1	995.9	995.9	1			
Macrostylidae								
Macrostylidae New Genus A sp. 1	1	1	1171.7	1171.7	1			
<i>Macrostylis</i> sp. MoV 6873	3	1	2003	2003	1			
Munnopsidae								
<i>Disconectes</i> sp. MoV 6877	1	1	1013.6	1013.6	1			
<i>Ilyarachna</i> sp. 1	2	1	995.9	995.9	1			
<i>Munneurycope</i> sp. 1	1	1	996.2	996.2	1			
<i>Nyctobadistes</i> sp. 1	5	1	995.9	995.9	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Nannoniscidae								
<i>Exilinus</i> sp. 1	1	1	996	996	1			
Paramunnidae								
<i>Pentacervation lancifera</i>	2	2	1255.5	1320.7		1	1	1
Serolidae								
<i>Brucerolis victoriensis</i>	403	16	1492.15	3021.4		1	1	1
Sphaeromatidae								
<i>Cercosphaera</i> sp. 1	1	1	189.15	189.15	1			
<i>Cilicaeopsis</i> sp. 1	3	2	189.15	198.85	1			
<i>Cilicaeopsis</i> sp. 2	1	1	409.85	409.85	1			
Thambematidae								
<i>Microthambema</i> sp. 1	2	2	932.4	3927	1			
<i>Microthambema</i> sp. MoV 6878	3	3	482.5	2003	1			
<i>Microthambema</i> sp. MoV 6879	2	2	212.4	378.4	1			
<i>Microthambema</i> sp. MoV 6880	1	1	1013.6	1013.6	1			
AMPHIPODA								
Amaryllididae								
cf. <i>Bamarooka</i> sp. 1	1	1	235.9	235.9				
Ampeliscidae								
<i>Ampelisca</i> sp. 1	1	1	212.4	212.4				
<i>Ampelisca</i> sp. MoV 6894	1	1	378.4	378.4	1			
Calliopidae								
<i>Harpinioides</i> cf. <i>drepanocheir</i>	4	1	212.4	212.4				
Caprellidae								
Caprellidae sp.	5	4	189.3	1490				
Corophiidae								
Corophiidae sp.	1	1	995.9	995.9				
Cyphocarididae								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Cyphocaris</i> sp.	1	1	1862.95	1862.95				
Cyproideidae								
<i>Austropheonoides</i> sp. 1	1	1	235.9	235.9				
Eurytheneidae								
<i>Eurythenes gryllus</i>	1	1	4606.8	4606.8				
<i>Eurythenes thurstoni</i>	1	1	1015.05	1015.05				
Eusiridae								
<i>Rhachotropis</i> sp. MoV 6884	1	1	212.4	212.4	1			
Hyperiopidae								
<i>Hyperiopis</i> sp. 1	1	1	189.3	189.3				
Ischyroceridae								
<i>Cerapus?</i> sp. 1	2	1	378.4	378.4				
Ischyroceridae sp.	1	1	996.2	996.2				
Ischyroceridae sp. 1	4	3	189.3	212.4				
<i>Ischyrocerus</i> sp. MoV 6885	5	3	189.3	235.9	1			
<i>Myersius</i> sp. MoV 6886	1	1	378.4	378.4	1			
<i>Pseudericthonius</i> sp. MoV 6887	8	5	482.5	1995.4	1			
<i>Pseudischyrocerus</i> sp. MoV 6888	2	1	235.9	235.9	1			
Kamakidae								
cf. <i>Aorcho</i> sp. 1	2	2	378.4	421.4				
Kamakidae?								
Kamakidae? sp. 1	1	1	2014.2	2014.2				
Leucothoidae								
<i>Anamixis</i> sp. 1	10	3	189.3	983.1				
Leucothoidae sp. 1	1	1	189.3	189.3				
Lysianassidae								
<i>Cheirimedon</i> sp.	1	1	4012.65	4012.65				
Lysianassoidea Unident.								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Lysianassoidea sp. 1	1	1	996.2	996.2				
Lysianassoidea sp. 2	1	1	203.2	203.2				
Lysianassoidea sp. 3	2	1	376.3	376.3				
Maeridae								
<i>Linguimaera</i> sp. 1	1	1	235.9	235.9				
Maeridae sp. 1	2	1	235.9	235.9				
Maeridae sp. 2	2	1	235.9	235.9				
Maeridae sp. 3	2	1	204.2	204.2				
Maxillipiidae?								
Maxillipiidae? sp. 1	1	1	482.5	482.5				
Oedicerotidae								
Oedicerotidae sp. 1	1	1	204.2	204.2				
Oedicerotidae sp. 2	1	1	382.9	382.9				
Phoxocephalidae								
<i>Cephalophoxoides</i> sp.	2	1	189.3	189.3				
<i>Cephalophoxoides</i> sp. MoV 6175	8	4	189.3	436.8	1	1		1
<i>Cephalophoxoides</i> sp. MoV 6889	1	1	983.1	983.1	1			
<i>Harpiniopsis</i> sp. MoV 6890	1	1	1013.6	1013.6	1			
<i>Paraphoxus?</i> sp. 1	2	1	235.9	235.9				
Phoxocephalidae sp.	2	2	212.4	996.2				
<i>Pseudharpinia</i> sp. MoV 6164	1	1	1013.6	1013.6	1	1		1
Podoceridae								
<i>Podoceridae</i> sp. 1	2	1	212.4	212.4				
Stenothoidae								
Stenothoidae sp. 1	1	1	189.3	189.3				
Synopiidae								
<i>Pseudotiron</i> sp. MoV 6891	2	2	376.3	436.8	1			
<i>Syrrhoe</i> sp. MoV 6892	1	1	376.3	376.3	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Trischizostomatidae								
<i>Trischizostoma</i> sp.	2	2	1335.4	1862.95				
Zobrachoidae								
<i>Zobracho</i> sp. MoV 6893	3	3	995.9	1995.4	1			
LOPHOGASTRIDA								
Gnathophausiidae								
<i>Gnathophausia ingens</i>	5	5	1006.4	2240.65		1	1	1
<i>Gnathophausia zoea</i>	7	4	1021.4	1862.95		1		1
DECAPODA								
AcanthePHYRIDAE								
<i>AcanthePHYRA acutifrons</i>	1	1	2724.9	2724.9		1		1
<i>AcanthePHYRA quadrispinosa</i>	7	6	995.55	3683.7		1		1
<i>AcanthePHYRA sica</i>	10	7	1526.6	4606.8		1		1
<i>AcanthePHYRA</i> sp.	2	2	1004.65	2003.9		1		1
<i>Heterogenys microphthalma</i>	1	1	2240.65	2240.65				
<i>Hymenodora gracilis</i>	1	1	2724.9	2724.9		1		1
Aristeidae								
<i>Aristeus mabahissae</i>	101	3	1015.05	1027.2		1		1
<i>Austropenaeus nitidus</i>	227	13	986.6	1552.65		1	1	1
Atelecyclidae								
<i>Trichopeltarion</i> sp. MoV 5135	6	4	357.6	411.7	1			
Axiidae								
<i>Eiconaxius</i> sp. MoV 5662	3	2	204.2	436.8	1			
Benthescymidae								
<i>Benthescymus howensis</i>	13	6	2079.1	3001.9		1		1
<i>Benthescymus investigatoris</i>	4	3	995.55	1020.9		1		1
<i>Gennadas gilchristi</i>	15	11	1004.65	3683.7		1	1	1
<i>Gennadas kempii</i>	3	3	1552.65	2079.1		1	1	1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Chirostylidae								
<i>Gastroptychus cf brevipropodus</i> nov.	6	4	189.15	221.35	1			
<i>Uroptychus flindersi</i>	2	2	409.85	411.7		1	1	1
Crangonidae								
<i>Aegaeon lacazei</i>	9	3	189.15	217.5		1	1	1
<i>Lissosabinea lynseyae</i>	2	2	198.85	388.1		1		1
<i>Parapontophilus cf difficilis</i>	84	19	388.1	2825.55	1			
Cyclodorippidae								
<i>Tymolus similis</i>	174	6	217.5	411.7		1	1	1
Cymonomidae								
<i>Cymonomus cf deforgesi</i> nov.	3	3	986.6	1020.9	1			
<i>Cymonomus cf umitake</i> nov.	1	1	388.1	388.1	1			
<i>Cymonomus delli</i>	11	3	382.6	425.65		1		1
<i>Cymonomus soela</i>	2	1	995.55	995.55		1		1
Diogenidae								
<i>Dardanus arrosor</i>	9	4	189.15	283.2		1	1	1
<i>Paguristes aciculus</i>	64	8	189.15	411.7		1	1	1
<i>Strigopagurus elongatus</i>	1	1	283.2	283.2		1	1	1
Dromiidae								
<i>Austrodromidia incisa</i>	6	2	189.15	217.5		1		1
<i>Austrodromidia insignis</i>	17	3	189.15	217.5		1	1	1
<i>Austrodromidia octodentata</i>	1	1	208.7	208.7		1	1	1
<i>Stimdromia lateralis</i>	7	4	189.15	221.35		1	1	1
Epialtidae								
<i>Rochinia mosaica</i>	4	1	189.15	189.15		1	1	1
Geryonidae								
<i>Chaceon albus</i>	4	3	1026.65	1526.6		1		1
Glyphocrangonidae								

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Glyphocrangon cf ferox</i> sp.nov.	42	4	2079.1	2725.55	1			
<i>Glyphocrangon cf fimbriata</i> sp. nov.	20	6	1492.15	2825.55	1			
<i>Glyphocrangon dimorpha</i>	15	4	1960.9	2037.2		1		
<i>Glyphocrangon elephas</i>	16	2	411.7	425.65		1	1	1
Goneplacidae								
<i>Pycnoplax meridionalis</i>	4	2	198.85	212.4		1	1	1
<i>Pycnoplax victoriensis</i>	14	5	217.5	425.65		1	1	1
Inachidae								
<i>Cyrtomaia maccullochi</i>	25	4	382.6	411.7		1	1	1
<i>Dorhynchus ramusculus</i>	109	9	189.15	1026.65		1	1	1
<i>Platymaia wyvillethomsoni</i>	42	7	189.15	425.65		1	1	1
Latreilliidae								
<i>Eplumula australiensis</i>	2	2	189.15	208.7		1	1	1
Leucosiidae								
<i>Ebalia tuberculosa</i>	89	11	189.15	425.65		1	1	1
<i>Merocryptus lambriformis</i>	7	3	198.85	283.2		1	1	1
Lithodidae								
<i>Neolithodes flindersi</i>	7	5	986.6	1331.5		1	1	1
Majidae								
<i>Choniognathus granulosus</i>	3	2	189.15	198.85		1	1	1
<i>Leptomithrax globifer</i>	5	3	189.15	208.7		1	1	1
<i>Prismatopus spatulifer</i>	9	3	189.15	217.5		1	1	1
<i>Teratomaia richardsoni</i>	1	1	425.65	425.65		1		1
Munididae								
<i>Munida cf manqingae</i> sp. nov.	1	1	1779.1	1779.1	1			
<i>Munida endeavourae</i>	4	2	989.6	1007.15		1		1
<i>Munida haswelli</i>	1	1	198.85	198.85		1	1	1
<i>Munida</i> sp. nov 5661	1	1	204.2	204.2	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
Munidopsidae								
<i>Galacantha rostrata</i>	14	7	1835.95	2825.55		1		1
<i>Munidopsis arietina</i>	4	4	1835.95	2079.1				
<i>Munidopsis cf granosa</i> sp. nov.	3	3	3713.85	4606.8	1			
<i>Munidopsis cf subsquamosa</i> sp. nov.	1	1	2725.55	2725.55	1			
<i>Munidopsis crenatirostris</i>	1	1	382.6	382.6		1		1
Nematocarcinidae								
<i>Nematocarcinus productus</i>	146	27	995.55	3021.4		1		1
<i>Nematocarcinus sigmoideus</i>	39	7	1015.05	4606.8		1		1
<i>Nematocarcinus</i> sp.	4	1	986.6	986.6				
Nephropidae								
<i>Metanephrops velutinus</i>	1	1	411.7	411.7		1	1	1
<i>Nephropsis acanthura</i>	2	2	986.6	995.55		1	1	1
<i>Nephropsis suhmi</i>	5	4	986.6	1552.65		1	1	1
Oplophoridae								
<i>Oplophorus novaezeelandiae</i>	1	1	2114.2	2114.2		1	1	1
<i>Systellaspis debilis</i>	4	4	1862.95	4606.8		1		1
Paguridae								
<i>Goreopagurus poorei</i>	1	1	1020.9	1020.9		1		1
<i>Lophopagurus nanus</i>	4	3	208.7	283.2		1	1	1
<i>Pagurodes inarmatus</i>	63	14	1331.5	2114.2		1	1	1
<i>Propagurus haigae</i>	4	2	411.7	425.65		1		1
Palicidae								
<i>Pseudopalicus macromeles</i>	31	4	189.15	283.2		1	1	1
Pandalidae								
<i>Chlorotocus novaezeelandiae</i>	50	3	189.15	217.5		1	1	1
<i>Plesionika cf macropoda</i> sp. nov.	16	1	400	400	1			
<i>Plesionika edwardsii</i>	14	2	198.85	208.7		1		1

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Plesionika martia</i>	10	1	388.1	388.1		1	1	1
<i>Plesionika semilaevis</i>	1	1	1020.9	1020.9		1		1
Parapaguridae								
<i>Oncopagurus</i> sp. nov. 1	100	7	995.55	1026.65	1			
<i>Parapagurus bouvieri</i>	10	4	409.85	2014		1	1	1
<i>Parapagurus furici</i>	61	5	1335.4	3021.4				
<i>Parapagurus latimanus</i>	350	15	986.6	3021.4		1	1	1
<i>Parapagurus richeri</i>	242	22	995.55	3021.4		1		1
Pasiphaeidae								
<i>Leptochela sydniensis</i>	1	1	212.4	212.4		1	1	1
<i>Parapasiphae sulcatifrons</i>	3	3	995.55	2014		1		1
<i>Pasiphaea barnardi</i>	4	1	1021.4	1021.4		1		1
<i>Pasiphaea</i> cf <i>longitaenia</i> sp. nov	3	2	1007.15	1027.2	1			
<i>Pasiphaea</i> cf <i>oshoroae</i> sp. nov	3	2	2037.2	2240.65	1			
<i>Pasiphaeidae</i> sp.	1	1	1027.2	1027.2				
Polychelidae								
<i>Pentacheles laevis</i>	1	1	1021.4	1021.4		1	1	1
<i>Pentacheles validus</i>	6	6	1335.4	1960.9		1	1	1
<i>Stereomastis surda</i>	1	1	1026.65	1026.65		1		1
<i>Willemoesia pacifica</i>	36	6	2724.9	4012.65		1	1	1
Scyllaridae								
<i>Antarctus mawsoni</i>	7	4	198.85	409.85		1	1	1
<i>Ibacus alticrenatus</i>	29	8	189.15	425.65		1	1	1
Sergestidae								
<i>Allosergestes sargassi</i>	2	1	2037.2	2037.2		1	1	1
<i>Deosergestes corniculum</i>	1	1	995.55	995.55		1		1
<i>Deosergestes disjunctus</i>	5	3	995.55	1478.05		1	1	1
<i>Deosergestes</i> sp.	3	3	986.6	2240.65				

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescribed	Known from Australia	Known from GAB	Temperate Australia
<i>Parasergestes armatus</i>	1	1	2240.65	2240.65		1		1
<i>Petalidium foliaceum</i>	1	1	2114.2	2114.2		1	1	1
<i>Phorcosergia potens</i>	4	3	1006.4	2079.1		1	1	1
<i>Prehensilosergia prehensilis</i>	2	2	986.6	2725.55		1	1	1
Sergestidae sp.	2	1	1862.95	1862.95				
Sicyoniidae								
<i>Sicyonia australiensis</i>	1	1	198.85	198.85		1		1
Thoridae								
<i>Eualus</i> sp. nov. 1	1	1	986.6	986.6	1			
<i>Eualus</i> sp. nov. 2	2	2	986.6	989.6	1			
<i>Lebbeus clarehannah</i>	1	1	411.7	411.7		1		1
<i>Lebbeus</i> sp. nov. 1	1	1	1015.05	1015.05	1			
STOMATOPODA								
Squillidae								
<i>Anchisquilloides mcneilli</i>	15	4	189.15	1026.65		1	1	1
PYCNOGONIDA								
Ammotheidae								
<i>Chonothoa</i> sp. nov. 1	1	1	189.15	189.15	1			
Callipallenidae								
<i>Callipallene</i> sp. MoV 6883	1	1	212.4	212.4	1			
<i>Meridionale</i> sp. nov. 1	1	1	189.15	189.15	1			
<i>Parapallene</i> sp. nov 1	1	1	189.15	189.15	1			
Colossendeidae								
<i>Colossendeis colosse</i>	1	1	1335.4	1335.4		1		1
<i>Colossendeis cucurbita</i>	55	13	1006.4	2114.2		1		1
<i>Colossendeis macerrima</i>	11	4	1835.95	2014		1	1	1
<i>Colossendeis minor</i>	42	13	1526.6	3021.4		1		1
<i>Colossendeis</i> sp. nov.	1	1	1467.65	1467.65	1			

Taxonomic Group	Total specimens	# of stations	Min depth (m)	Max depth (m)	Undescri bed	Known from Australia	Known from GAB	Temperate Australia
<i>Colossendeis spicula</i>	7	3	1934.05	2014		1		1
<i>Colossendeis tasmanica</i>	11	5	1934.05	2079.1		1		1
Pallenopsidae								
<i>Bathypallenopsis antipoda</i>	1	1	283.2	283.2				
<i>Pallenopsis gippslandiae</i>	1	1	283.2	283.2		1		1

20.2 Appendix – Section 8: Checklist of the GAB fish fauna

Appendix Table 2 Checklist of fish species collected in 2013-2015 GAB surveys, showing total abundance, depth range and taxonomic/geographic records.

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
Scyliorhinidae										
<i>Apristurus ampliceps</i>	12	1	1	1021	1021		?	?	?	East-Indo-west Pacific
Rajidae										
<i>Dipturus cerva</i>	10	1	1	199	199	No	Yes	Yes	Yes	Endemic
Chimaeridae										
<i>Hydrolagus trolli</i>	2430	1	1	1863	1863	No	No	Yes	Yes	West Pacific
Nettastomatidae										
<i>Venefica proboscoidea</i>	286	5	5	1335	2114	No	No	Yes	Yes	Circumglobal
Congridae										
<i>Bassanago bulbiceps</i>	610	5	4	358	412	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Gnathophis umbrellabius</i>	275	15	2	189	199	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Gnathophis melanocoelus</i>	71	7	2	189	199	No	Yes	Yes	Yes	Endemic
Synaphobranchidae										
<i>Diastobranchus capensis</i>	11277	19	13	1015	2079	No	Yes	Yes	Yes	Circumglobal
<i>Ilyophis cf. brunneus</i>	20	2	2	996	2037	No	Yes	Yes	Yes	Circumglobal
<i>Synaphobranchus affinis</i>	1236	7	4	940	1021	No	Yes	Yes	Yes	Circumglobal
<i>Synaphobranchus brevidorsalis</i>	16023	24	15	1005	2079	No	Yes	Yes	Yes	Circumglobal
<i>Simenchelys parasitica</i>	80	1	1	987	987	No	Yes	Yes	Yes	Atlantic-Indo-west-central Pacific
<i>Histiobranchus australis</i>	764	17	9	1006	2826	No	Yes	Yes	Yes	Atlantic-Indo-west-central Pacific
<i>Synaphobranchus</i> sp 1	3785	29	8	987	1027	?	Yes	Yes	Yes	East-Indo-west Pacific
Halosauridae										
<i>Halosauropsis macrochir</i>	12297	64	19	1015	2840	No	Yes	Yes	Yes	Circumglobal
<i>Aldrovandia phalacra</i>	447	6	5	1027	1527	No	Yes	Yes	Yes	Circumglobal
Notacanthidae										
<i>Notacanthus sexspinis</i>	512	5	3	987	1015	No	Yes	Yes	Yes	Circumglobal
<i>Polyacanthonotus challenger</i>	560	7	6	1335	2079	No	No	Yes	Yes	Antitropical
Argentinidae										
<i>Argentina australiae</i>	12	5	2	189	283	No	Yes	Yes	Yes	Endemic
Phosichthyidae										

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
<i>Polymetme illustris</i>	1	1	1	358	358	No	Yes	Yes	Yes	Endemic
Alepocephalidae										
<i>Rouleina attrita</i>	312	1	1	987	987	No	Yes	Yes	Yes	Circumglobal
<i>Alepocephalus</i> cf <i>antipodianus</i>	792	1	1	2037	2037	?	?	?	?	Circumglobal?
<i>Narcetes stomias</i>	394	1	1	1527	1527	No	No	Yes	Yes	Circumglobal
<i>Conocara murrayi</i>	151	2	2	2037	2241	No	No	Yes	Yes	Atlantic-Indo-west Pacific
<i>Alepocephalus productus</i>	776	1	1	2037	2037	?	?	?	?	Circumglobal?
<i>Leptoderma</i> sp.	1	1	1	1027	1027	?	?	?	?	?
Platytroctidae										
<i>Holtbyrnia laticauda</i>	2	1	1	1478	1478	No	Yes	Yes	Yes	Southern circumglobal
Bathysauridae										
<i>Bathysaurus ferox</i>	4505	11	7	1005	2037	No	Yes	Yes	Yes	Atlantic-Indo-west Pacific
Paraulopidae										
<i>Paraulopus nigripinnis</i>	797	34	8	199	426	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Paraulopus melanostomus</i>	23	1	1	358	358	No	Yes	Yes	Yes	ENDEMIC
Bathysauropsidae										
<i>Bathysauropsis gracilis</i>	1385	47	14	1332	2826	No	Yes	Yes	Yes	Southern circumglobal
Ipnopidae										
<i>Bathypterois filiferus</i>	150	3	1	2826	2826	No	No	Yes	Yes	Southern circumglobal?
<i>Ipnops murrayi</i>	159	23	5	1934	2840	No	No?	No?	No?	Southern circumglobal?
Brachionichthyidae										
<i>Brachionichthys</i> cf. <i>australis</i>	1	2	1	283	283	No	Yes	Yes	Yes	Endemic
Antennariidae										
<i>Kuiterichthys furcipilis</i>	8	2	1	199	199	No	Yes	Yes	Yes	Endemic
Chaunacidae										
<i>Chaunacops melanostomus</i>	5	1	1	2241	2241	No	No	Yes	Yes	East Indian
Euclichthyidae										
<i>Euclichthys polynemus</i>	2276	118	6	358	426	No	Yes	Yes	Yes	East-Indo-west Pacific
Moridae										
<i>Mora moro</i>	1840	3	2	940	1021	No	Yes	Yes	Yes	Circumglobal
<i>Pseudophycis barbata</i>	4	3	2	189	1836	No	Yes	Yes	Yes	East-Indo-west Pacific

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
<i>Tripterophycis gilchristi</i>	28	4	1	410	410	No	Yes	Yes	Yes	East Atlantic Indo-west Pacific
<i>Antimora rostrata</i>	11569	40	17	996	2114	No	Yes	Yes	Yes	Circumglobal
<i>Lepidion microcephalus</i>	966	4	3	940	1021	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Physiculus luminosa</i>	1	1	1	209	209	No	Yes	Yes	Yes	Indo-Pacific
<i>Guttigadus globiceps</i>	431	48	14	940	1468	No	Yes	Yes	Yes	Southern circumglobal
Melanonidae										
<i>Halargyreus</i> sp.	664	1	1	1005	1005	Yes	Yes	Yes	Yes	East-Indo-west Pacific
Ophidiidae										
<i>Dannevigia tusca</i>	5104	2	1	383	383	No	Yes	Yes	Yes	Endemic Atlantic-Indo-west-central Pacific
<i>Bassozetes robustus</i>	38	1	1	2826	2826	No	No	Yes	Yes	Circumglobal
<i>Spectrunculus grandis</i>	5960	1	1	3002	3002	No	No	Yes	Yes	Endemic?
<i>Dicrolene</i> sp.	417	38	12	1335	2826	No	?	?	?	
Carapidae										
<i>Echiodon rendahli</i>	10	1	1	199	199	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Pyramodon ventralis</i>	26	5	1	209	209	No	No	Yes	Yes	Indo-west Pacific
Bythitidae										
<i>Cataetx chthamalorhynchus</i>	30	1	1	940	940	No	Yes	Yes	Yes	Indo-west Pacific
<i>Cataetx</i> sp 1	84	2	2	1527	1553	Yes	No	No	No	Indian
Zoarcidae										
<i>Zoarcidae</i> sp.	18	1	1	2840	2840	No	No	No	No	Endemic?
Macrouridae										
<i>Coelorinchus mirus</i>	327	40	4	388	426	No	Yes	Yes	Yes	Endemic
<i>Lepidorhynchus denticulatus</i>	198	16	3	358	412	No	Yes	Yes	Yes	Pacific
<i>Coryphaenoides serrulatus</i>	7853	40	10	940	1027	No	Yes	Yes	Yes	Indo-west Pacific
<i>Coryphaenoides subserrulatus</i>	7	6	3	986	1021	No	Yes	Yes	Yes	Southern circumglobal
<i>Nezumia soela</i>	862	28	9	1005	1553	No	Yes	Yes	Yes	Endemic
<i>Cetonurus globiceps</i>	35191	166	11	987	1335	No	Yes	Yes	Yes	Circumglobal
<i>Idiolorhynchus andriashevi</i>	76	1	1	1492	1492	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Coryphaenoides dossenus</i>	49	8	4	987	1021	No	Yes	Yes	Yes	East Atlantic Indo-west Pacific
<i>Coelorinchus acanthiger</i>	1863	23	7	986	1492	No	Yes	Yes	Yes	Indo-west Pacific

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
<i>Coryphaenoides filicauda</i>	1098	89	19	1006	3021	No	No	Yes	Yes	Southern circumglobal
<i>Coryphaenoides murrayi</i>	658	7	4	1468	1961	No	Yes	Yes	Yes	Indo-West Pacific
<i>Coryphaenoides striaturus</i>	1048	11	7	1478	2014	No	Yes	Yes	Yes	East Atlantic Indo-west Pacific
<i>Haplomacrourus nudirostris</i>	1	1	1	986	986	?	?	?	?	
<i>Hymenocephalus longibarbis</i>	51	38	4	358	426	No	No	Yes	Yes	East-Indo-west Pacific
<i>Kuronezumia leonis</i>	315	3	3	986	1492	No	Yes	Yes	Yes	Southern circumglobal
<i>Nezumia kapala</i>	6	1	1	996	996	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Coelorinchus trachycarus</i>	2857	18	11	996	1492	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Hymenocephalus nascens</i>	8	3	2	986	987	No	No	Yes	Yes	East-Indo-west Pacific
<i>Trachonurus yiwardaus</i>	308	5	4	1005	1468	No	Yes	Yes	Yes	Endemic
<i>Coelorinchus amydrozosterus</i>	1043	137	6	358	426	No	Yes	Yes	Yes	Endemic
<i>Paracetonus</i> sp.	58	27	3	1335	2725	?	No	No	No	?
Bathygadidae										
<i>Bathygadus cottoides</i>	1511	100	10	1021	1553	No	Yes	Yes	Yes	East Atlantic Indo-west Pacific
<i>Bathygadus spongiceps</i>	560	1	1	1015	1015	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Gadomus pepperi</i>	1068	13	6	996	1027	No	Yes	Yes	Yes	Endemic
Trachichthyidae										
<i>Hoplostethus latus</i>	48	2	2	199	209	No	Yes	Yes	Yes	Endemic
<i>Hoplostethus atlanticus</i>	3390	3	2	987	1015	No	Yes	Yes	Yes	Atlantic-Indo-west Pacific
Oreosomatidae										
<i>Alloctytus verrucosus</i>	19744	41	12	987	1527	No	Yes	Yes	Yes	Antitropical
<i>Neocyttus psilorhynchus</i>	216	1	1	1863	1863	No	No	Yes	Yes	East-Indo-west Pacific
Macroramphosidae										
<i>Macroramphosus scolopax</i>	182	40	5	189	283	No	Yes	Yes	Yes	Circumglobal
Syngnathidae										
<i>Solegnathus</i> cf. <i>spinosissimus</i>	2	4	1	189	189	No	Yes	Yes	Yes	East-Indo-west-Pacific
Sebastidae										
<i>Helicolenus percoides</i>	288	13	3	189	209	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Trachyscorpia eschmeyeri</i>	440	1	1	987	987	No	Yes	Yes	Yes	Southern circumglobal

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
<i>Helicolenus barathri</i>	441	13	5	358	426	No	Yes	Yes	Yes	East-Indo-west Pacific
Scorpaenidae										
<i>Phenacoscorpius adenensis</i>	2	1	1	209	209	No	No	Yes	Yes	Indo-west Pacific
Triglidae										
<i>Lepidotrigla</i> sp. [of Gomon et al 2008]	193	9	5	189	2037	Yes	Yes	Yes	Yes	Endemic
<i>Pterygotrigla polyommata</i>	2	7	3	221	388	?	?	?	?	East-Indo-west Pacific
Platycephalidae										
<i>Platycephalus conatus</i>	402	5	4	189	410	No	Yes	Yes	Yes	Endemic
Hoplichthyidae										
<i>Hoplichthys haswelli</i>	9071	77	7	189	426	No	Yes	Yes	Yes	Endemic
Cottidae										
<i>Antipodocottus elegans</i>	1	1	1	426	426	No	No	Yes	Yes	East-Indo-west Pacific
Psychrolutidae										
<i>Psychrolutes marcidus</i>	2080	1	1	2114	2114	No	Yes	Yes	Yes	Endemic
Serranidae										
<i>Lepidoperca occidentalis</i>	6	1	1	189	189	No	Yes	Yes	Yes	Endemic
Acropomatidae										
<i>Verilus anomalus</i>	1295	162	5	189	426	No	Yes	Yes	Yes	Endemic
Serranidae										
<i>Lepidoperca filamenta</i>	60	6	1	209	209	No	Yes	Yes	Yes	Endemic
Epigonidae										
<i>Epigonus denticulatus</i>	316	27	2	388	410	No	Yes	Yes	Yes	Circumglobal
<i>Epigonus robustus</i>	13	1	1	986	986	No	Yes	Yes	Yes	Southern circumglobal
<i>Rosenblattia robusta</i>	1	1	1	2826	2826	No	Yes	Yes	Yes	Southern circumglobal
Pentacerotidae										
<i>Zanclistius elevatus</i>	1104	3	3	189	209	No	Yes	Yes	Yes	East-Indo-west Pacific
Labridae										
<i>Pseudolabrus rubicundus</i>	2	1	1	209	209	No	Yes	Yes	Yes	Endemic
Pinguipedidae										
<i>Parapercis</i> sp. 5 [of Johnson]	132	11	4	189	221	?	Yes	Yes	Yes	Endemic
Callionymidae										
<i>Foetorepus phasis</i>	1	3	2	221	358	No	Yes	Yes	Yes	East-Indo-west Pacific
<i>Foetorepus apricus</i>	221	66	5	383	426	No	Yes	Yes	Yes	Endemic
Gobiidae										

Name	Total weight (g)	Tot. no. ind.	No. Samples	Min Depth (m)	Max Depth (m)	Undescribed	Known from GAB	Known from Temp. Australia	Known from Australia	Wider distribution
<i>Nesogobius</i> sp.	1	1	1	189	189	Yes	Yes	Yes	Yes	Endemic
Pleuronectidae										
<i>Azygopus pinnifasciatus</i>	364	39	5	358	412	No	Yes	Yes	Yes	Endemic
Tetraodontidae										
<i>Omegophora armilla</i>	65	22	4	189	1027	No	Yes	Yes	Yes	Endemic

20.3 Appendix – Section 11

20.3.1 List of biological survey data sources

CSIRO Surveys:

- ‘GABRP epibenthic Survey’: GAB Research Program: Project 3.1 – Benthic Biodiversity Characterisation: Biological collections. MarLIN

<http://www.marlin.csiro.au/geonetwork/srv/eng/search#!f301c328-bec4-42f9-9803-76d14eb17377>

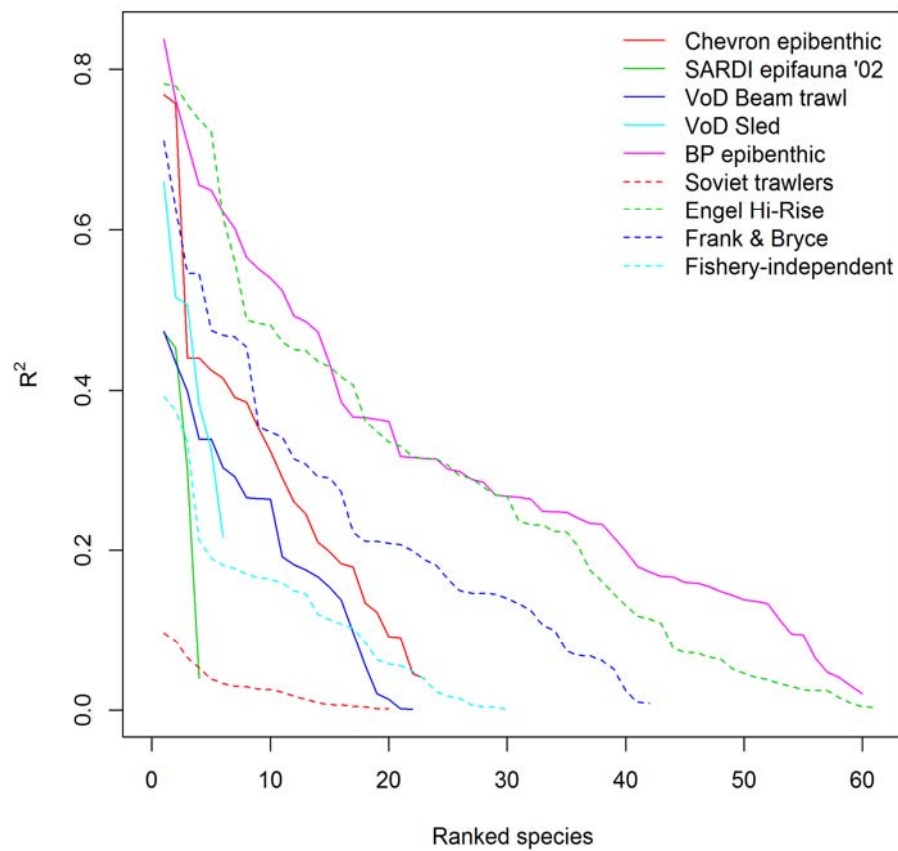
- Demersal fauna of the continental slope off Western Australia - Voyage SS 01/91 (Williams et al., 1996). MarLIN # 4951 :
http://www.marine.csiro.au/marg/edd_search.Browse_Citation?txtSession=4951
- FRV ‘Courageous’ Fish Trawl surveys, 1978–1979, CSIRO includes FRV Courageous voyages: COUR197831, COUR197832, COUR197833, COUR197834, COUR197835, COUR197945, COUR197946, COUR197947, COUR197949, COUR197950, COUR197951, COUR197952 (see individual MarLIN records for these voyages, <http://www.marine.csiro.au/marg/> search).
- FRV ‘Soela’ regional exploratory fishery surveys, 1980–1984, CSIRO. includes Soela voyages: SO198001, SO198003, SO198004, SO198005, SO198006, SO198007, SO198102, SO198102, SO198105, SO198202, SO198204, SO198401, SO198402, SO198403, SO198404, SO198405, SO198406 (see individual MarLIN records for these voyages, <http://www.marine.csiro.au/marg/> search).
- Soviet trawl surveys 1969–1977, data compilation, CSIRO (Koslow et al., 1999) includes voyages: ALBA196909, ALBA197009, ALBA197103, ALBA197310, BACA197506, BERG196503, BERG196601, BERG196705, EQUA197109, KAME197607, KOR196802, LIRA196702, LIRA196806, LIRA197304, MY-TIC197803, P-DER197210, P-DER197405, P-DER197512, PDER197701, POSE197107, POSE197704, PROM196811, PROM197002, RADU196608, RADU197206, RADU197503, SESK196601, SHAN197405, SRTM196903, SUTC196807, TICH197703, TICH197710.
- Voyage of discovery - benthic biodiversity of the deep continental shelf and slope in Western Australia South West Region, SS10/2005, (Williams et al., 2010a), MarLIN # 6937 :
http://www.marine.csiro.au/marg/edd_search.Browse_Citation?txtSession=6937

Surveys by other research agencies:

- Eastern Great Australian Bight benthic sled and grab infauna survey dataset, 2002, SARDI (Ward et al., 2003).
- Eastern Great Australian Bight benthic sled epifauna survey dataset, 2006, SARDI (Currie et al., 2008).
- Eastern Great Australian Bight grab infauna survey dataset, 2006, SARDI (Currie et al., 2007).
- SESSF GAB Fishery Independent Surveys (FIS) dataset, Fishwell Consulting/AFMA.

20.3.2 Gradient forest diagnostic figures

Note: Figure labels in this section refer to data from the GABRP epibenthic survey as 'BP epibenthic' and from the GABDMP as 'Chevron epibenthic survey epibenthic'.



ig A: Performance of the biological models in each survey. For each survey the species are ranked in descending order of R^2 . Species with null models (negative R^2) are omitted. The area under each curve is an indication of the biodiversity information content of each survey.

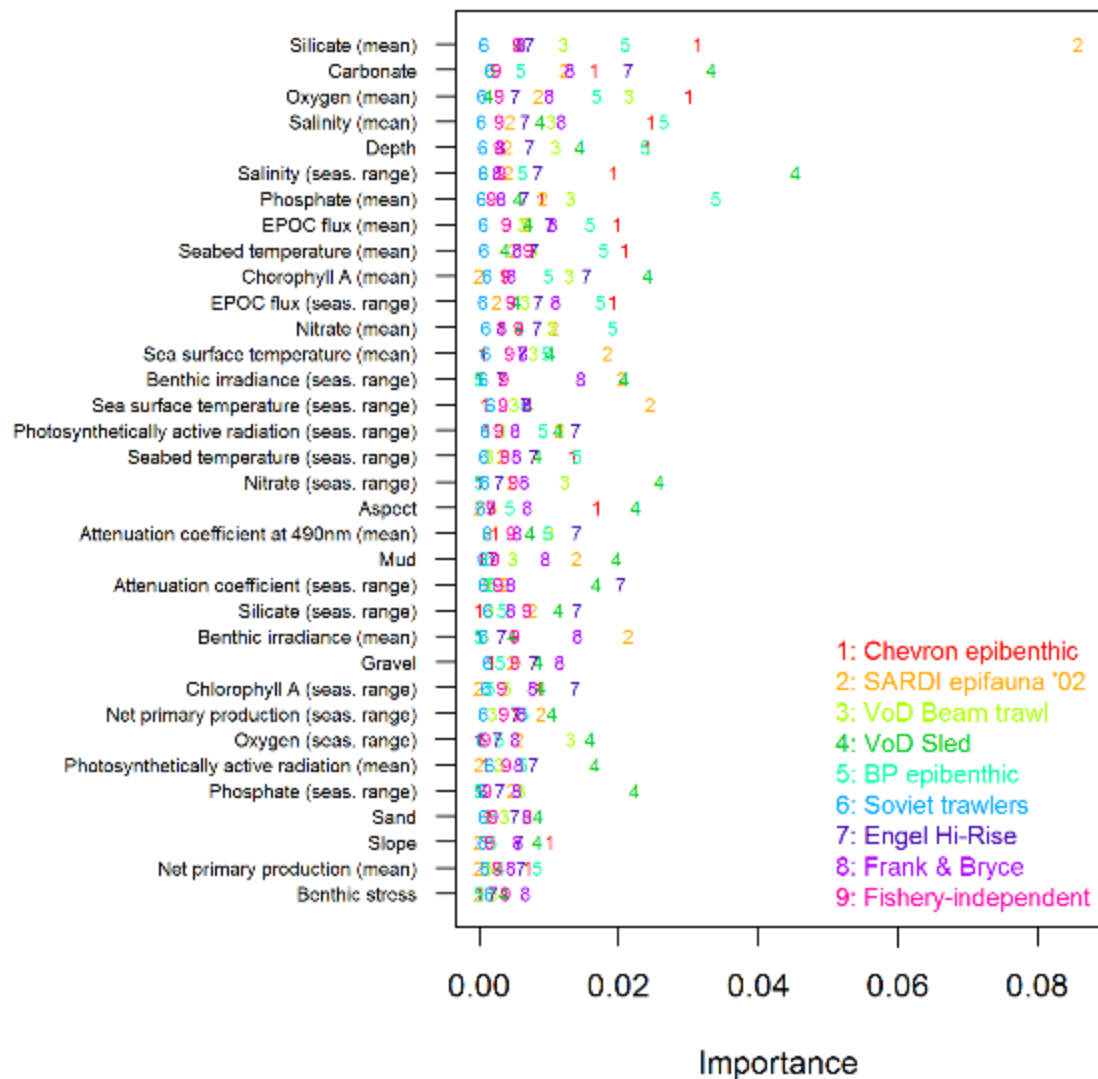


Fig B: Relative importance of each predictor in each survey, sorted by mean importance across surveys.

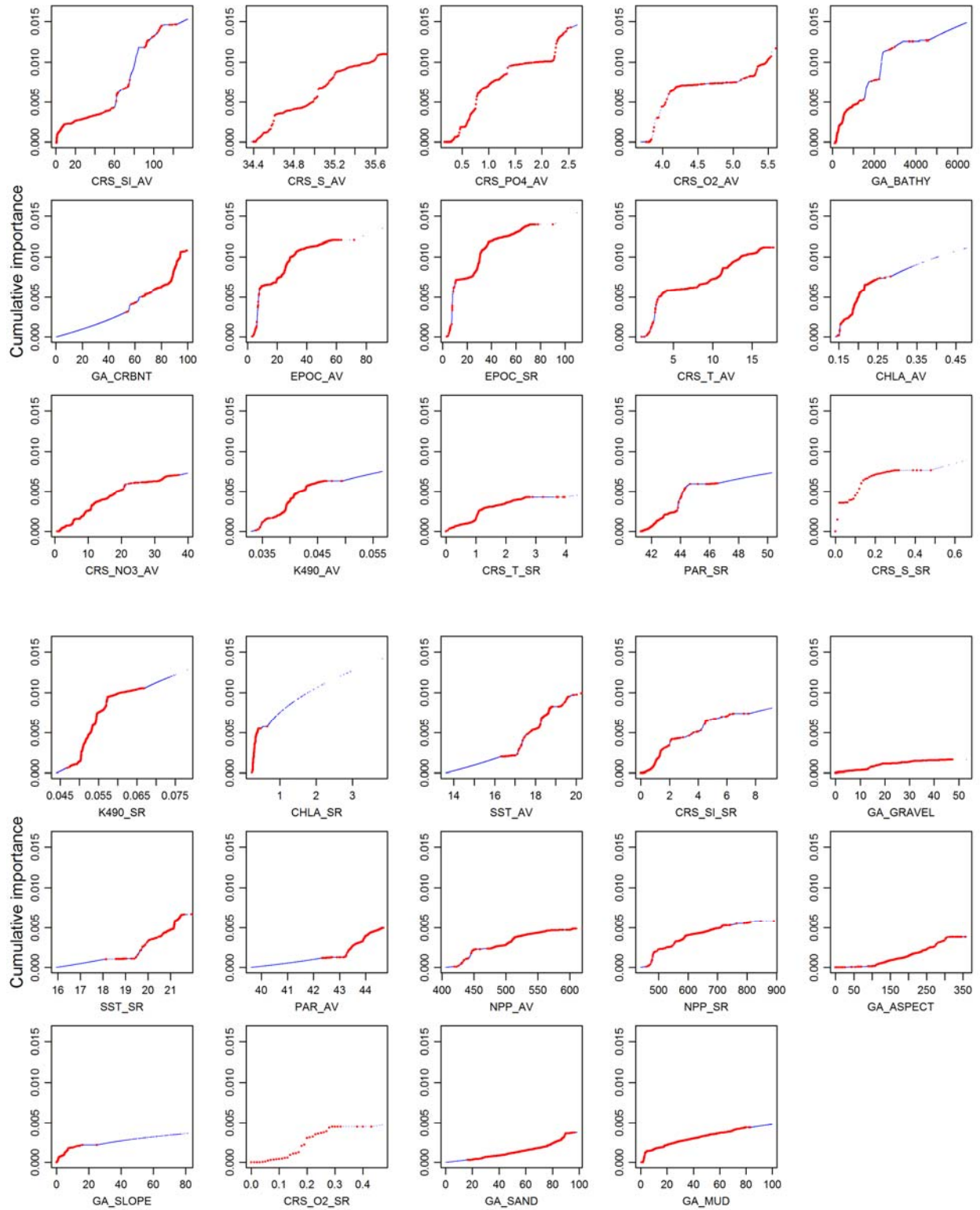


Fig C: Predicting from environmental gradient to biological (turnover) gradient. The red dots are values at the sites and blue dots are at the grids. Extrapolation beyond the range of the sites has been attenuated by a square-root power law.

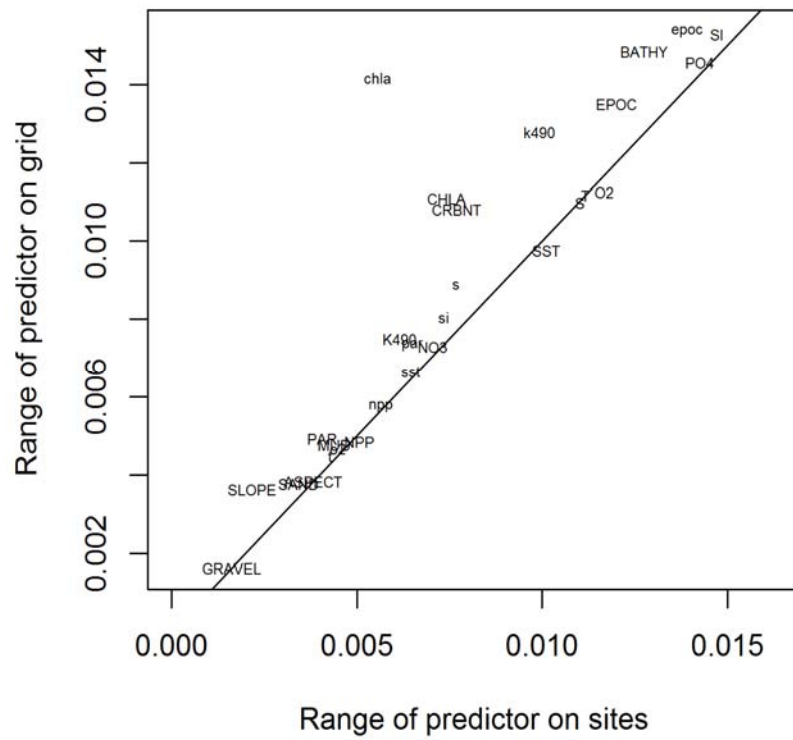




Fig E: Multivariate regression trees for each of the 9 surveys. The number of terminal nodes is determined by cross-validation.

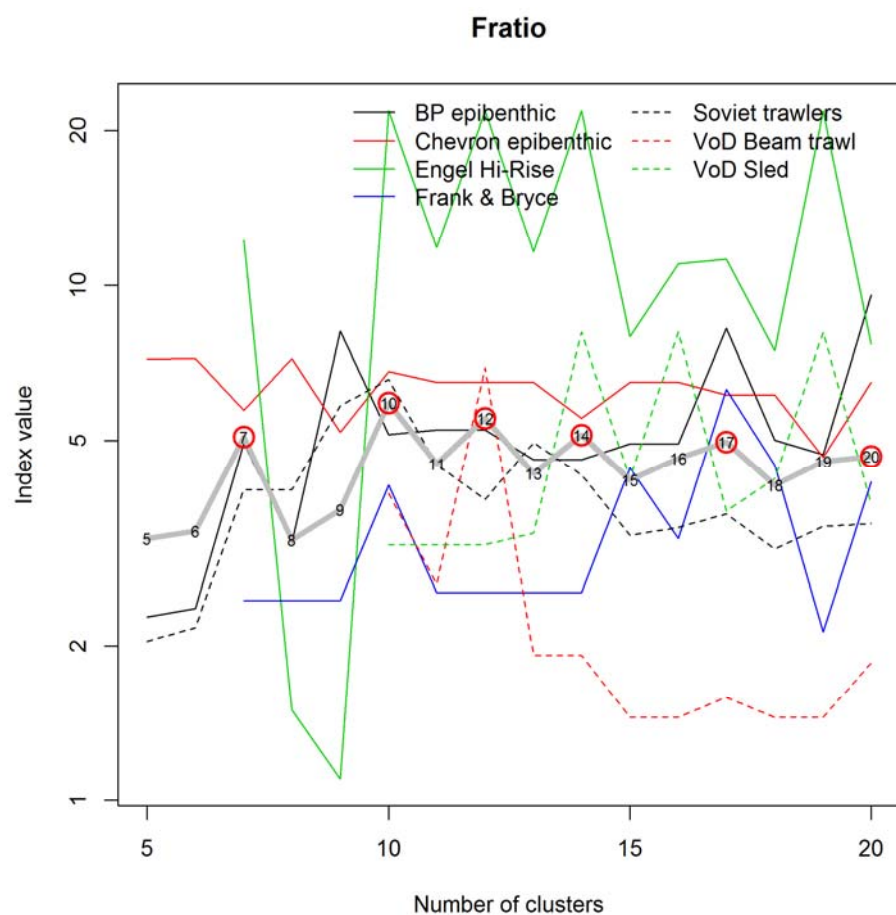


Fig F: F-ratio results of MANOVA illustrating variation in survey site data explained by a range of clusterings (5–30) of the regional biological space.

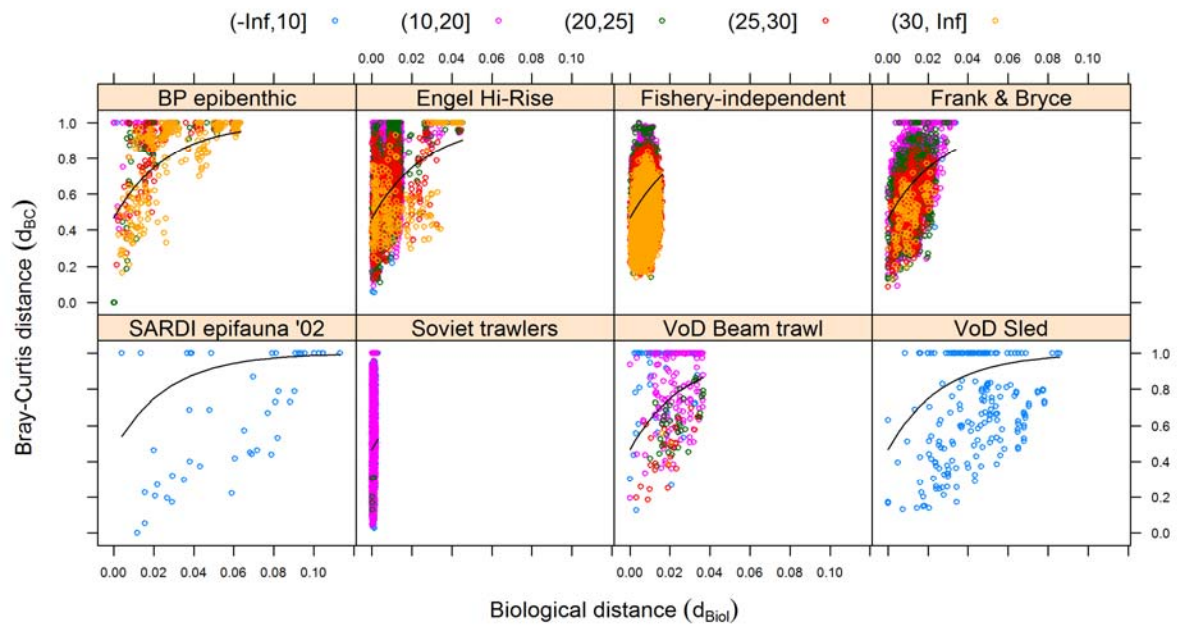
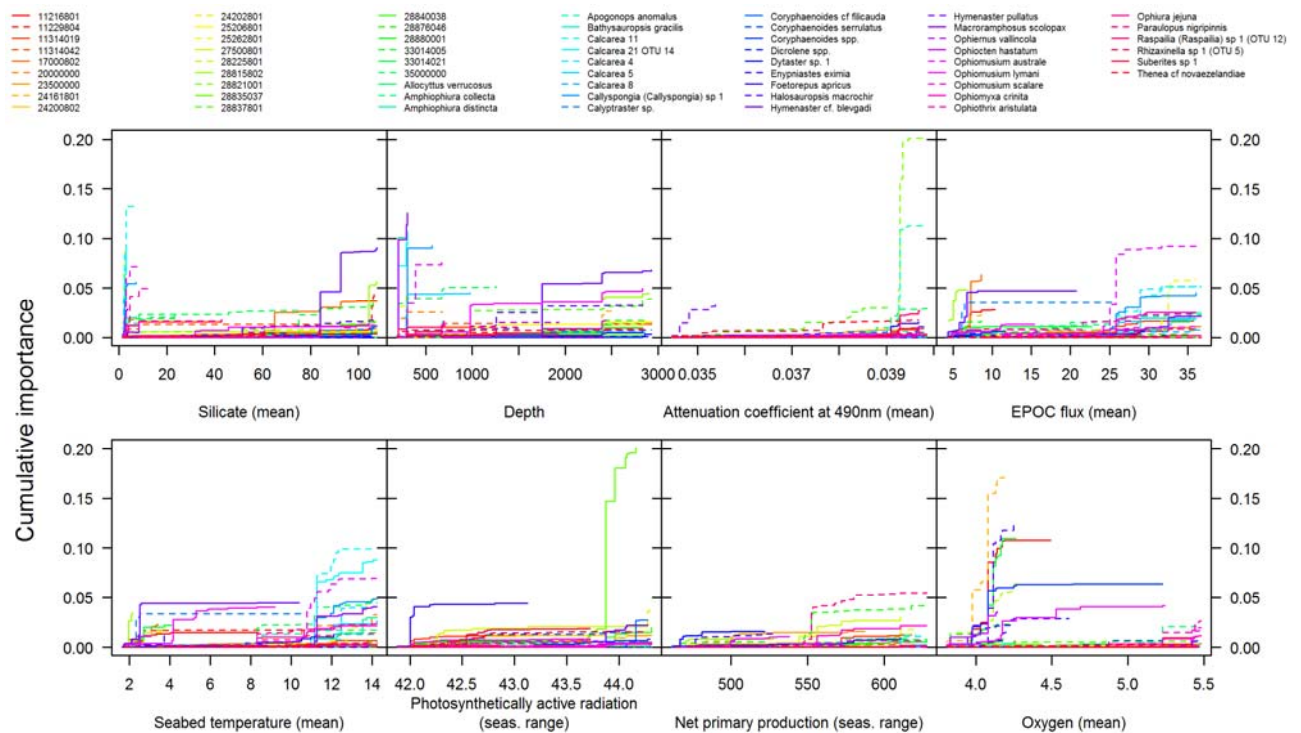


Fig G: Weighted regression of Bray-Curtis distance d_{BC} against biological distance d_{Biol} . Pairs of sites with more species present are given higher weight, and further weighting is applied so that the effective number of observations per survey is proportional to the number of sites in the survey. Points are coloured according to the number of species present.

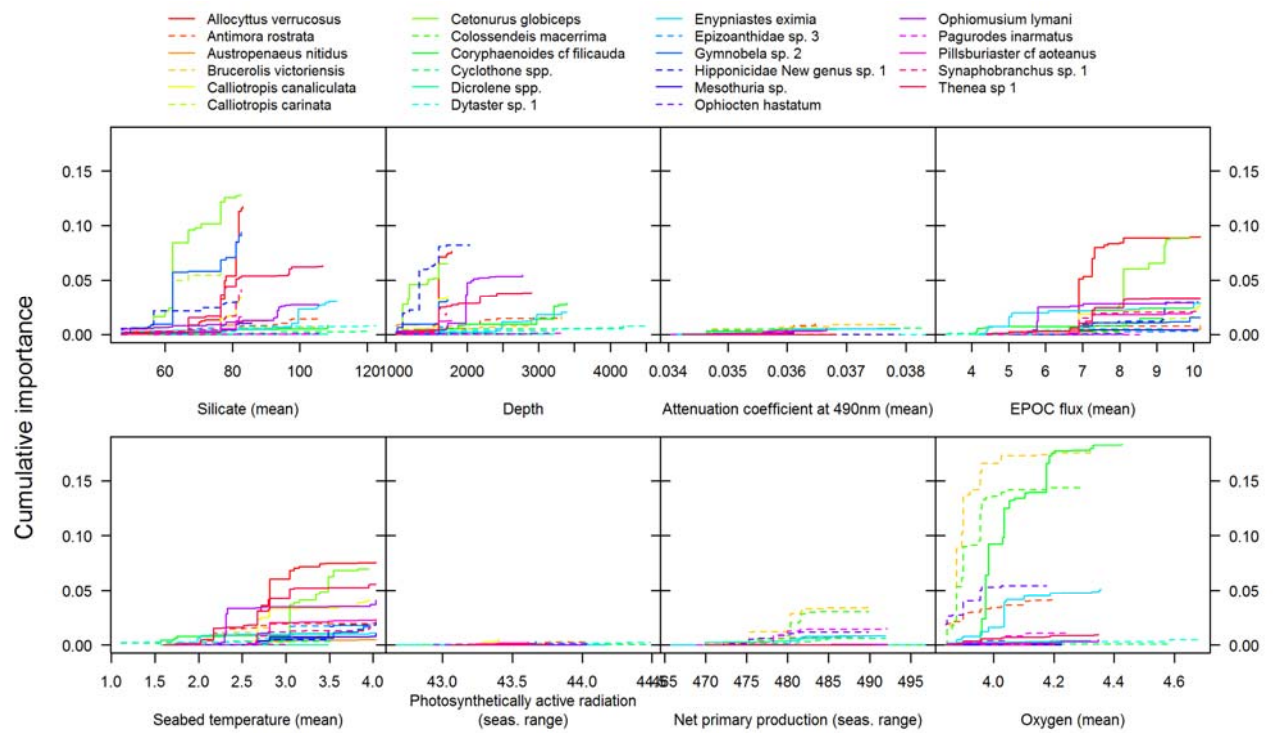
20.3.3 Turnover curves per species

The following diagrams show the individual turnover curves within survey for each taxon for the most influential predictors. These curves are combined to produce the turnover curve for the survey as a whole, as shown in Figure 11.1. Species are identified by their CAAB (Rees et al., 2017), except for the BP epibenthic survey where not all taxa had been assigned to a CAAB at the time of analysis, and SARDI epifauna survey where project internal OTUs were used.

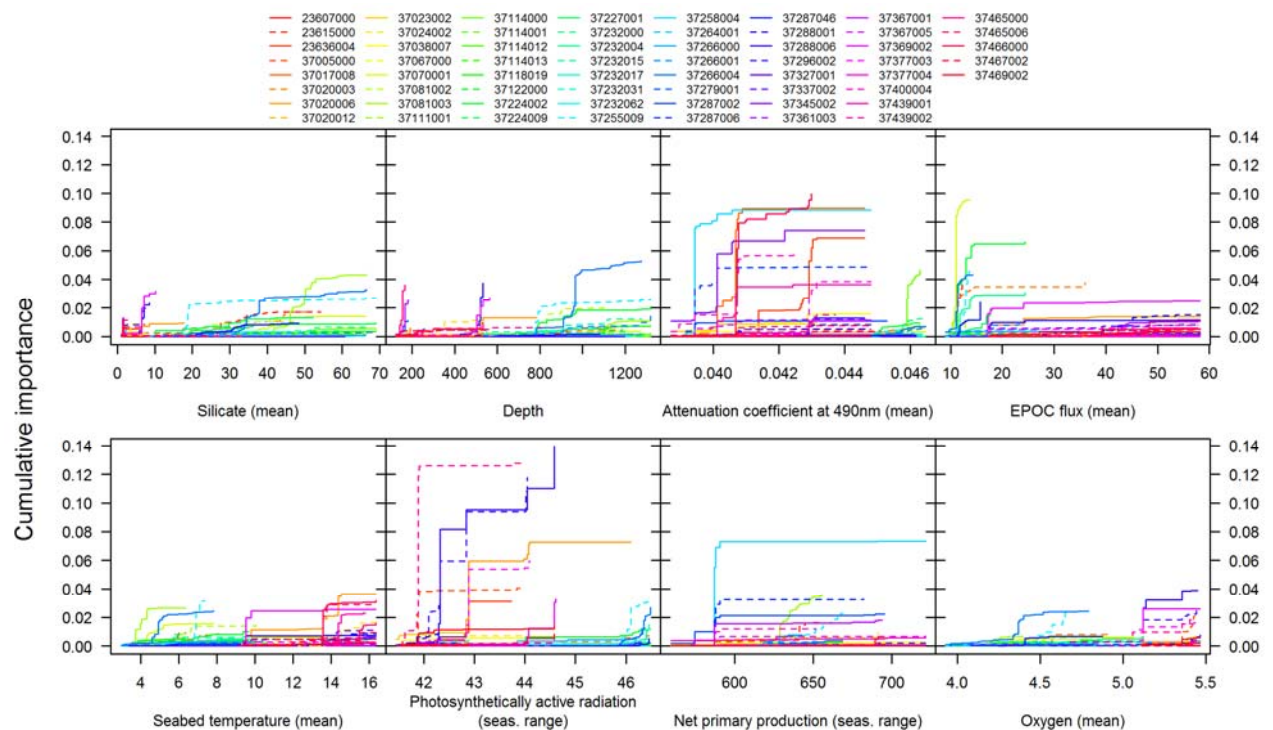
BP epibenthic survey



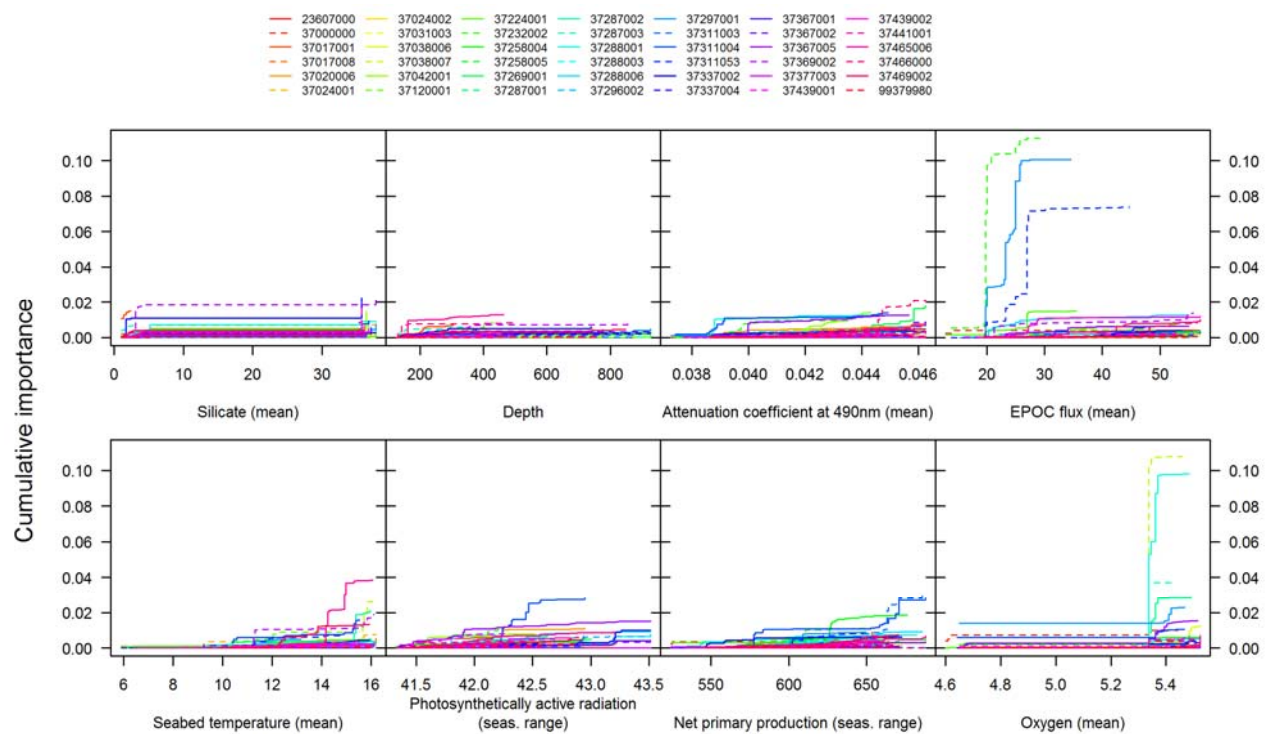
Chevron epibenthic survey



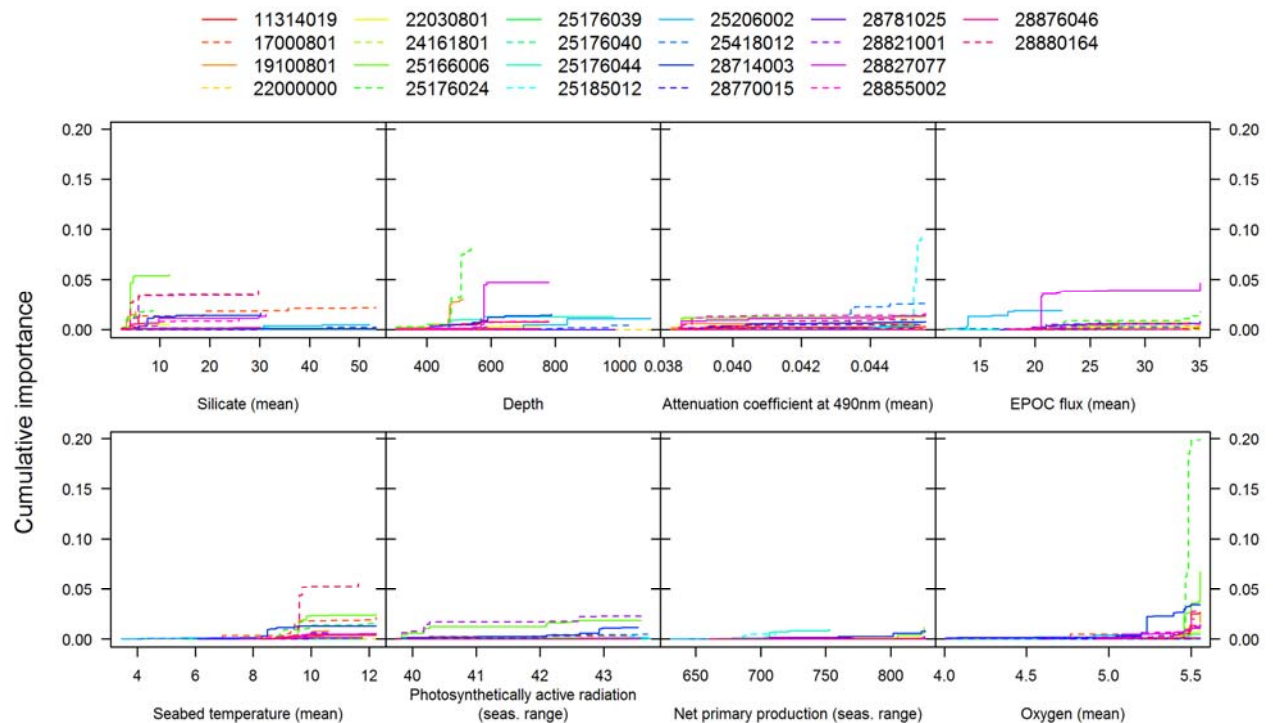
Data-trawler surveys: Engel Hi-rise gear



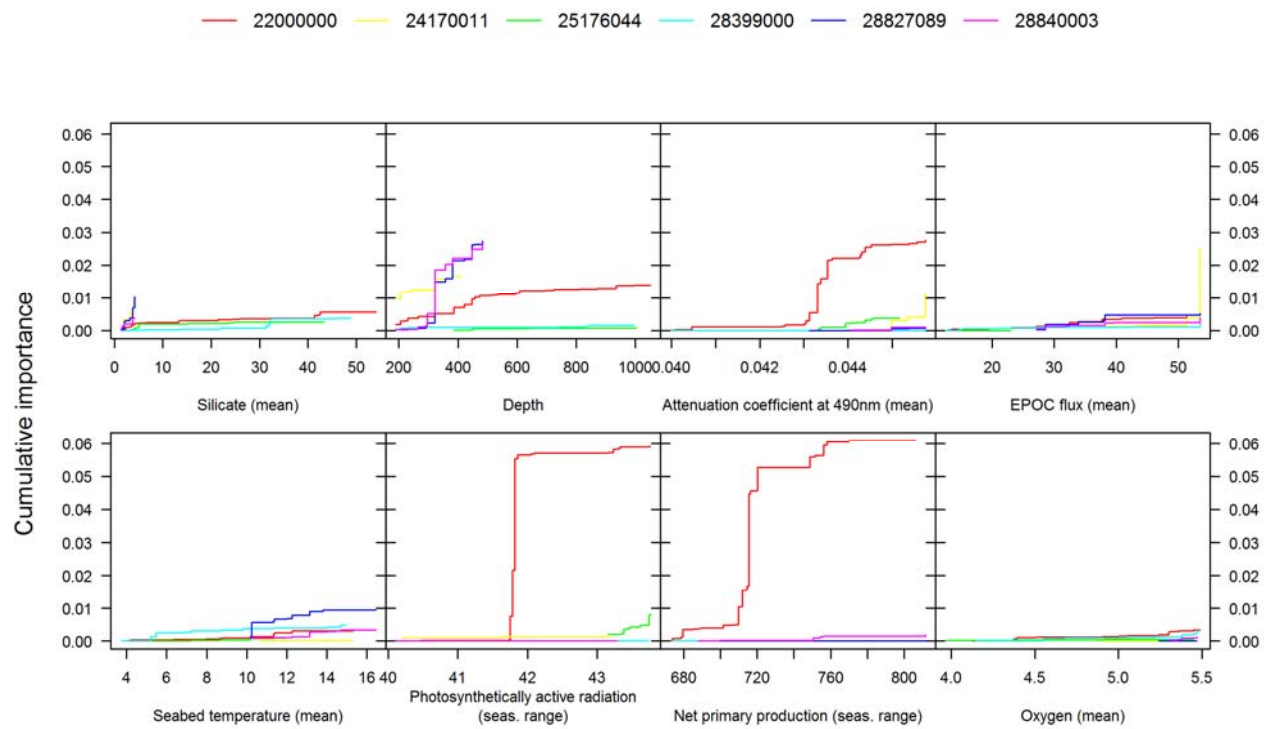
Frank and Bryce gear



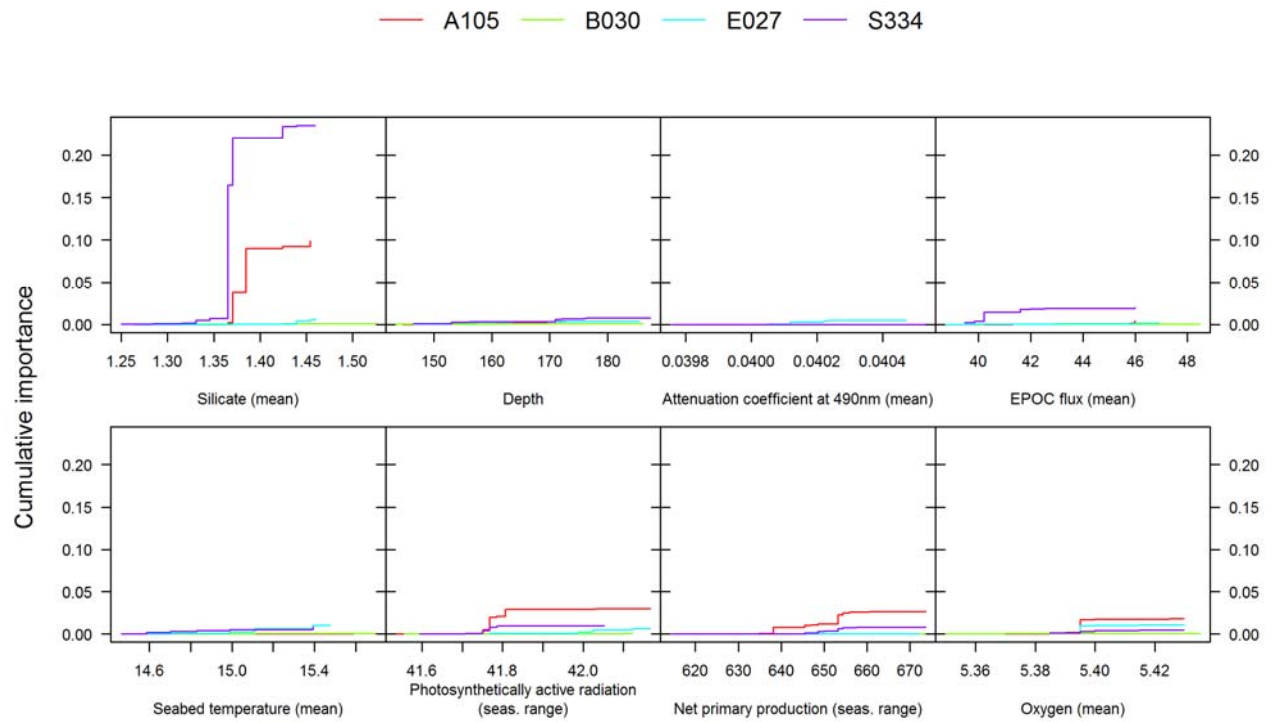
Voyage of Discovery survey: Beam trawl gear



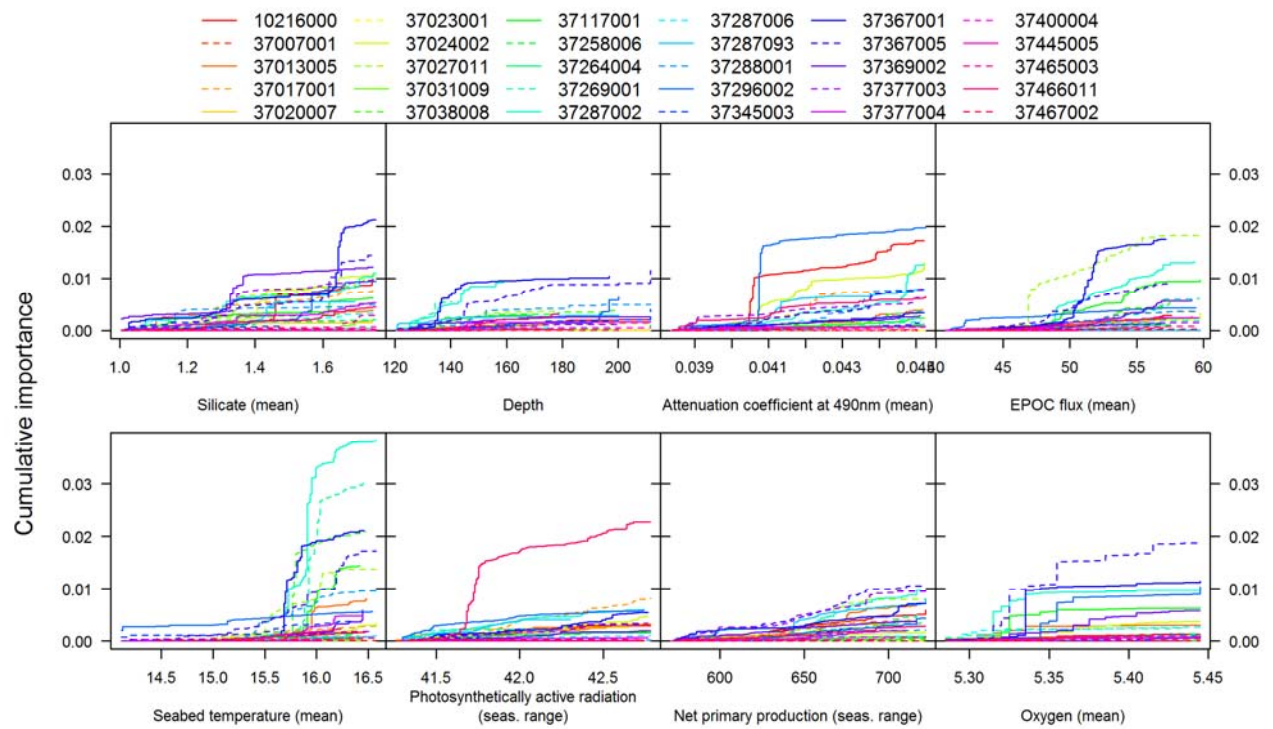
Sled gear



SARDI epifauna survey



Fishery-independent survey



Soviet trawlers

