

Mapping Benthic Habitats for Representation in Marine Protected Areas

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Abstract

Virtually all marine conservation planning and management models in place or proposed have in common the need for improved scientific rigour in identifying and characterising the marine habitats encompassed. An emerging central theme in the last few years has been the concept of representativeness, or representative systems of Marine Protected Areas (MPAs). The habitat classification and mapping needed to incorporate considerations of representativeness into MPA planning must logically be carried out at the same scale at which management occurs. Management of highly protected areas occurs almost exclusively at local scales or finer, independent of the reservation model or philosophy employed.

Moreton Bay, on Australia's east coast, was selected for studies at the local scale to map and classify macrobenthic habitats. In a site scale (1 km) trial for the major habitat classification study, remote underwater videography was used to map and characterise an unusual assemblage of epibenthic invertebrates on soft sediments. The assemblage included congregations of the comatulid crinoid *Zygometra cf. Z. microdiscus* (Bell) at densities up to 0.88 individuals.m⁻², comparable to those found in coral reef habitats. There was no correlation between the distribution of this species and commonly used abiotic surrogates depth (6 – 18 m), sediment composition and residual current. This site scale trial is the first quantitative assessment of crinoid density and distribution in shallow water soft-sediment environments. The high densities found are significant in terms of the generally accepted picture of shallow-water crinoids as essentially reefal fauna. The findings highlight the conservation benefits of an inclusive approach to marine habitat survey and mapping. Assemblages such as the one described, although they may be of scientific and ecological significance, would have been overlooked by common approaches to marine conservation planning which emphasise highly productive or aesthetically appealing habitats.

Most habitat mapping studies rely solely or in part on abiotic surrogates for patterns of biodiversity. The utility of abiotic variables in predicting biological distributions at the local scale (10 km) was tested. Habitat classifications of the same set of 41 sites based on 6 abiotic variables and abundances of 89 taxa and bioturbation indicators were compared using correlation, regression and ordination analyses. The concepts of false homogeneity and false heterogeneity were defined to describe types of errors associated with using abiotic surrogates to construct habitat maps. The best prediction by abiotic surrogates explained less than 30% of the pattern of biological similarity. Errors of false homogeneity were between 20 and 62%, depending on the methods of estimation. Predictive capability of abiotic surrogates at the taxon level was poor, with only 6% of taxon / surrogate correlations significant. These results have implications for the widespread use of abiotic surrogates in marine habitat mapping to plan for, or assess, representation in Marine Protected Areas. Abiotic factors did not discriminate sufficiently between different soft bottom communities to be a reliable basis for mapping.

Habitat mapping for the design of Marine Protected Areas is critically affected by the scale of the source information. The relationship between biological similarity of macrobenthos and the distance between sites was investigated at both site and local scales, and for separate biotic groups. There was a significant negative correlation between similarity and distance, in that sites further apart were less similar than sites close together. The relationship, although significant, was quite weak at the site scale.

Rank correlograms showed that similarity was high at scales of 10 km or less, and declined markedly with increasing distance. There was evidence of patchiness in the distributions of some biotic groups, especially seagrass and anthozoans, at scales less than 16 km. In other biotic groups there was an essentially monotonic decline in similarity with distance. The spatial agglomeration approach to habitat mapping was valid in the study area. Site spacing of less than 10 km was necessary to capture important components of biological similarity. Site spacing of less than 2.5 km did not appear to be warranted.

Macrobenthic habitat types were classified and mapped at 78 sites spaced 5 km apart. The area mapped was about 2,400 km² and extended from estuarine shallow subtidal waters to offshore areas to the 50 m isobath. Nine habitat types were recognised, with only one on hard substrate. The habitat mapping characterised several habitat types not previously described in the area and located deepwater algal and soft coral reefs not previously reported. Seagrass beds were encountered in several locations where their occurrence was either unknown or had not previously been quantified. The representation of the derived habitat types within an existing marine protected area was assessed. Only two habitat types were represented in highly protected zones, with less than 3% of each included. The study represents the most spatially comprehensive survey of epibenthos undertaken in Moreton Bay, with over 40,000 m² surveyed. Derived habitat maps provide a robust basis for inclusion of representative examples of all habitat types in marine protected area planning in and adjacent to Moreton Bay. The utility of video data to conduct a low-cost habitat survey over a comparatively large area was also demonstrated. The method used has potentially wide application for the survey and design of marine protected areas.

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Dedication

For Pixie, Nik, Jen and Mr Ben, without whom nothing else matters.

Declaration

This work has not previously been submitted for a degree or diploma in any university. To the best of my knowledge and belief, the thesis contains no material previously published or written by another person except where due reference is made in the thesis itself.

Tim Stevens

Chapter 1 Introduction

1.1 Introduction

Over the past 15 to 20 years, a great deal of attention has been given to the needs for conservation of marine ecosystems, through management of human use. There has been a marked evolution of approaches to management, from single species or issue-based approaches, e.g. fisheries stock management or whale conservation, to more holistic ecosystem wide approaches to habitat management, e.g. the biosphere concept (Batisse 1990). Marine protected areas (MPAs) in their various forms have become central tools for marine conservation (Kelleher and Kenchington 1991, Jones 1994).

Current marine conservation planning and management approaches, including large-scale zoned MPAs (Kelleher and Kenchington 1991), the biosphere concept (Batisse 1990, Kenchington and Agardy 1990) and coordinated networks of highly protected MPAs, whether or not within a zoned framework (Attwood *et al.* 1997), underline the role for science in quantifying patterns of marine biodiversity and ecosystem function. Such quantitative information is vital to improving the capacity of resource managers to conserve marine environments.

Whilst there is no single agreed approach to marine conservation, virtually all the models in place or proposed have in common the need for improved scientific rigour in identifying and characterising the marine habitats and processes encompassed, to support the decision-making processes involved in MPA design (see Ray and McCormick-Ray 1992, Connor *et al.* 1995, Agardy 1995, Zacharias and Howes 1998). Such rigour is important for both efficiency of reserve selection, and transparency (and hence better understanding and compliance) of the MPA planning process.

Agardy (1995) lists four general areas in which science should be used in solving problems related to marine conservation. The first and probably most important of these is the definition of true ecological boundaries of natural systems. Similarly, Zacharias and Roff (2000) discuss the need to maximise the ecological integrity of MPAs by establishing ecologically defensible boundaries.

A characteristic of most MPAs is a multiplicity of objectives (Jones 1994). However, an emerging central theme in the last few years has been the concept of representativeness, or representative systems of MPAs (and similar terms, e.g. representation, representivity - Parks Canada 1993, Kelleher *et al.* 1995, Boersma and Parrish 1999, Zacharias and Roff *in press*), although precisely what is meant by the term has not always been clearly defined. International Union for Conservation of Nature and Natural Resources (IUCN) guidelines for highly protected areas (categories Ia, II and III), including marine areas, now include representativeness as a major criterion (IUCN 1994). Representativeness and similar terms are used in a variety of different senses in the current literature (sometimes in the same document) and their utility in describing a concept is in danger of being compromised. There is a need to define the terms as they are currently used, as a means to minimising confusion in the concepts they represent.

The current call for representativeness as a major criterion for MPA design has as a prerequisite mapping of true ecological boundaries, as discussed earlier. In order for representativeness to be incorporated into MPA planning with a sound scientific basis, the habitat classification and mapping on which it is based should be at the scale at which management occurs. It is therefore necessary to assess the scale at which most MPA management is carried out. Specifically, if the drawing of a boundary (and then

excluding or regulating use within such an area) is the primary management measure, at what scales are such boundaries drawn?

Representativeness is clearly not the only criterion on which planning decisions should, or can, be made. There are many other layers that are integrated into the decision making process, both scientific (e.g. critical habitats for endangered species, nursery areas for commercially important species) and socio-political (e.g. existing uses and rights, indigenous uses, fisheries economics). It is also clear that in recent years, selecting and designing candidate MPAs to encompass a range of habitat types not sufficiently (or at all) represented in reserve systems has become important (e.g. Zacharias and Roff 2000). This follows similar trends in terrestrial reserve planning (Nicholls and Margules 1993).

This chapter has three main objectives: a) to resolve confusion in conflicting meanings of the terms such as representation, representative, representativeness and representivity as they are currently used; b) to quantify the scales at which area-based management generally occurs; and c) to provide recommendations for incorporating greater rigour into habitat classification and mapping at those scales, so that representation can be quantified and incorporated into MPA planning.

1.2 What is meant by representativeness?

The term “representativeness” (or “representativity”, “representation”, “representative”) is applied in the recent literature in two distinct senses. It is applied to describe some concept of a type of **system** of MPAs (e.g. Kelleher *et al.* 1995), and as a specific **criterion**, amongst a range of others, for the selection of core protected areas (Thackway 1996). It can be a source of considerable confusion, especially when used in

both senses in the same document without definition (e.g. Environment Australia 1998). It also has overlaps with other commonly used terms, such as “distinctiveness” (Zacharias and Roff in press, and see section 1.2.3 below). Like some other common terms (e.g. “biodiversity” - Angel 1991), its utility in describing a concept is compromised by the different subtleties of meaning it carries to each user, unless the term has been defined for that particular use. Therefore, an initial attempt is made here to describe the two uses of the term as they appear in current literature.

1.2.1 *Sensu lato*

In its broader sense, “representative” is applied to mean that MPAs within a system so described should contain core areas that meet at least one (preferably more) of the following criteria: high biodiversity, uniqueness, critical habitat for ecosystem function or for a species of particular interest, high productivity, "representativeness" *sensu stricto* (section 1.2.2 below), and so on. A far longer list of criteria can be derived, depending on the objectives of the individual MPA (Jones 1994, see also the reviews by Attwood *et al.* 1997 and McNeill 1994), but the use of “representative” as an adjective to describe a system of MPAs carries the implication that the component MPAs will collectively encompass this range of criteria, including "representativeness" *sensu stricto*. This use seems to derive from the intention that such a system will “represent” all these types of important habitat characteristics. However, in this context it is self-referential, and potentially misleading, especially in the case where representativeness *sensu stricto* is not clearly identified as the primary criterion. Its use in this broad sense without a clarifying definition should be discouraged.

1.2.2 *Sensu stricto*

“Representativeness” in its narrow sense is used as a noun to describe the concept that a sample of every type of habitat occurring in the area under consideration should be included in an MPA. Habitat here means an area of relatively higher homogeneity derived at a certain nominal scale. The candidate areas selected from each habitat are typical of that habitat, rather than exceptional in any way. Representativeness *sensu stricto* includes the implication, often not stated, that each habitat type has an intrinsic functional position in marine ecosystems, and thus an inherent conservation value, irrespective of its characteristics such as diversity, uniqueness and endangered species habitat. For representativeness to be useful in providing the required rigour in MPA design, it must be at the scale at which area based management occurs, as discussed in section 1.3. Representativeness *sensu stricto* is often used at broad (regional) scales to define relatively homogenous areas, within which other criteria are used to select candidate MPAs at finer scales (Zacharias and Roff in press). A MPA system derived in this way cannot accurately be described as a representative system, since MPAs are still being selected on the basis of exceptional (distinctive, see below) values rather than typical characteristics.

1.2.3 *Related terms*

The term “distinctive” (or “distinctiveness”) is sometimes used to describe reserves established to encapsulate particular values. In this sense it means exceptional in the context of surrounding areas, rather than similar or typical (representative). Distinctive in this use is therefore close in meaning to representative *sensu lato*, and is often used in that way.

1.3 Scale of management

Any process for determining boundaries, or at least gradients (ecotones) between areas of relative homogeneity, rests on the critical question of scale. As Ray and McCormick-Ray (1995, p. 26) point out, “one must view ecosystems as nested within varying time and space scales”.

A formalised series of spatial scales can be used (IMCRA Technical Group 1998), based on a Log_{10} hierarchy (Table 1.1). Ideally, identification and mapping of marine environments would occur within this hierarchy of scales, allowing a structured (nested) analysis of representation at each scale. Indeed, in the terrestrial context this is more or less the case. There is a substantial body of literature on the processes and practise of locating and designing terrestrial parks to meet a range of objectives. These virtually all have as a common first step the definition of biogeographic areas (e.g. Purdie 1987), and then the development of fine scale mapping before the application of sophisticated reserve selection and design optimisation algorithms (Nicholls and Margules 1993, Csuti *et al.* 1997, Possingham *et al.* 2000).

In the marine situation, whilst the need for such a structured and systematic approach has been recognised for some time (Ray 1975, Hayden *et al.* 1984), progress in applying such an approach to reserve selection and design lags far behind terrestrial reserve planning. At the broadest level in the above hierarchy, Kelleher *et al.* (1995) have recently produced a continental scale summary and classification for the global marine environment. At the next scale in the hierarchy, progress internationally has been somewhat sporadic, and based on a range of approaches (Connor *et al.* 1995, Dethier 1992, Harper *et al.* 1993). In general, classification approaches at the regional scale or finer are hampered by a lack of good comparative biological data, and tend to rely on

abiotic surrogates (e.g. Roff and Taylor 2000) and so-called “delphic” datasets (derived from expert opinion rather than quantitative data) (e.g. Hockey and Branch 1997, Chevis 1995).

Table 1.1: Log₁₀ hierarchy of spatial scales
(after Ortiz and Burchmore 1992 and IMCRA Technical Group 1998)

Scale Reference	Linear Extent	Scale Term	Name(s) of Derived Units	Typical Components
Macro-scale	1000s of km	Continental	Provinces	Geopolitical boundaries, oceanic basins, climatic zones.
Meso-scale	100s of km	Regional	Regions, Bioregions, Biophysical Regions	Major discontinuities in physical, oceanographic and biological distributions.
Micro-scale	10s of km	Local	Local Units, Biounits	Functional structural units with recognisable natural boundaries and internal homogeneity.
Pica-scale	<10 km	Site	Sites	Individual physical and biological habitats (e.g. reefs, algal beds).

Recently, a group of studies has produced a regional scale classification of Australian marine and coastal environments, as presented by the Interim Marine and Coastal Regionalisation of Australia (IMCRA) Technical Group (1998). Although the component studies (principally Chevis 1995, Edgar *et al.* 1995, Edyvane and Baker 1995, Ferns and Billyard 1995, Ortiz and Pollard 1995, Stevens 1995, VIMS *et al.* 1994 – for a complete bibliography see IMCRA Technical Group 1998) used a wide range of disparate techniques in deriving their classifications, the basis for objective methods in defining areas of relative homogeneity at the regional scale was demonstrated. Similarly, regional scale classifications for the purpose of defining marine conservation

and management priorities have been constructed in Canada (Parks Canada 1993, Zacharias and Howes 1998).

To determine the scales at which MPAs are managed, the dataset provided in Kelleher *et al.* (1995) was examined (Figure 1.1 and Table 1.2). It is clear that management of MPAs worldwide in general occurs at scales finer than the regional scale. Therefore, if MPAs are intended to have a major goal of representativeness (IUCN 1994), however that may be defined (see section 1.2), then further classification to finer scales is required.

In numerical terms, more than 90% of the world's MPAs are drawn at the local or site scales (Kelleher *et al.* 1995). In areal terms, the picture is skewed by the large size of a few multiple-use MPAs, most notably the Great Barrier Reef Marine Park. However, analysis of the size of highly protected polygons within this MPA gives an interesting result.

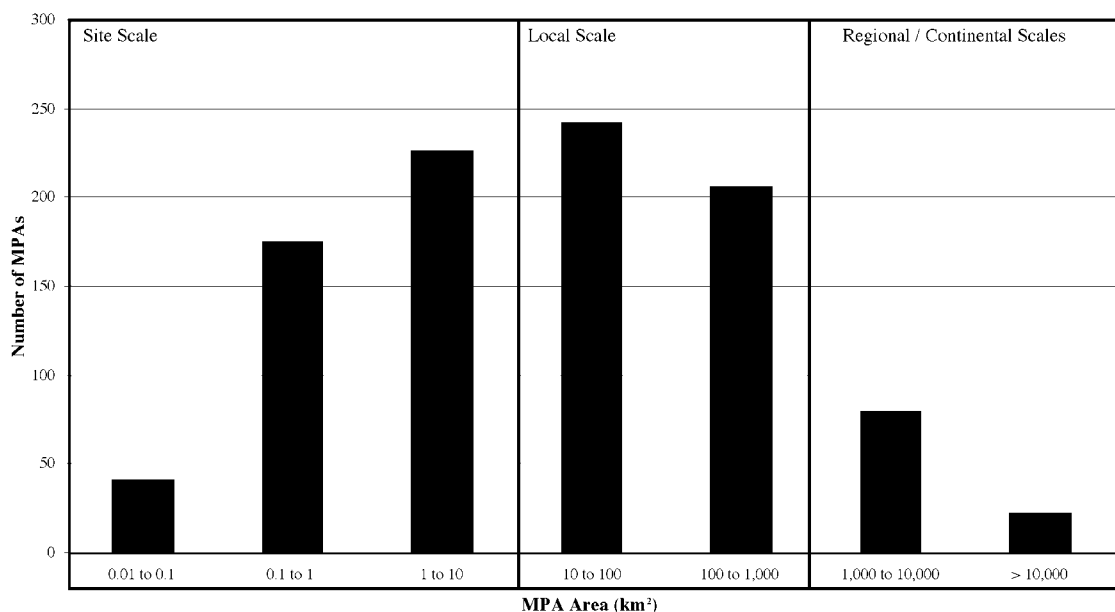


Figure 1.1: MPA size class distribution worldwide (Data from Kelleher *et al.* 1995)

Table 1.2 presents an analysis of polygon sizes in two contrasting types of MPA systems. One is the well-known Great Barrier Reef Marine Park (GBRMP) and the other is from the North West Atlantic region of the review by Kelleher *et al.* (1995), a discontinuous association of reserves enacted under various pieces of legislation and for various purposes.

Table 1.2: Comparison of polygon sizes in contrasting MPA models
(Data from GBRMPA digital zoning plan and Kelleher *et al.* 1995)

IUCN Category	Great Barrier Reef Marine Park			North West Atlantic MPAs		
	Total Area (km ²)	Mean Polygon Area (km ²)	Derived Scale	Total Area (km ²)	Mean Polygon Area (km ²)	Derived Scale
VI	231,376	28,921	Regional			
V				4,671	389	Local
IV	45,621	210	Local	13,825	265	Local
III	1,305	16	Site			
II	12,986	122	Local	5,046	210	Local
I	453	15	Site			
Total	291,740			23,542		

It can be seen that despite the differences in establishment history and MPA philosophy, in highly protected (IUCN Cat I and II) areas, polygons are all drawn at local or site scales. In other words, where the drawing of a boundary constitutes the main management measure (e.g. by excluding access to or take within the area), then this almost invariably occurs at local or site scales. The scale at which highly protected polygons are drawn appears to be independent of the MPA model employed, at least in the two examples examined. This reinforces Kenchington's (1990, p. 34) "15 kilometre approximate limit of applicability of protected area status as a management measure", conceptually derived from considerations of scale in the life cycles of marine biota

relevant to marine area management. This derived 15 kilometre limit is clearly local scale. Indeed, Table 1.2 shows that in all but the lowest levels of protection (IUCN Cat VI), MPA polygons in these two examples are all drawn at local or site scales.

Murdoch and Aronson (1999) provide an example of a field-based assessment of the effects of scale in reserve design. They examined the relationship between scale and the degree of spatial variability in coral assemblages in Florida, and found the highest variability to be among reefs, at the 10 – 20 km scale. This equates to local scale using the definitions in Table 1.1. The authors found that estimates from an individual reef did not adequately characterise variability of nearby reefs, or of entire sectors. Therefore representation derived from larger scale classifications would entirely miss the between-reef variability found, and yet management measures, as illustrated above, are usually at reef-by-reef scales.

Some current initiatives (Environment Australia 1998) seek to derive a representative system of MPAs from an existing regional scale classification (IMCRA 1998), without carrying out the crucial intervening step of deriving local scale marine environment classifications. This approach is at odds with the expressed need for improved rigour, since it is neither logically possible nor scientifically valid to draw management boundaries aimed at representation on the local scale from maps of relative homogeneity of marine environments at the regional scale.

1.4 Methods for local scale mapping and classification

The major obstacles to providing detailed data to decision-makers, in both terrestrial and marine contexts, are the constraints imposed by budgets and time on data collection and analysis. Field surveys, by their nature, are labour intensive and expensive,

especially in marine environments. In the terrestrial field, the advent of high-resolution satellite imagery and aerial photography, sophisticated processing and analysis tools, and the relative accessibility of sites for ground-truthing has meant that a large proportion of the costs of field survey have been offset, although at an inevitable sacrifice of information content (Verbyla 1995).

In the marine context, such optical remote sensing has proved to be of value in some settings. The primary applications were initially oceanographic, such as monitoring fronts, water circulation and near-surface chlorophyll concentrations (Yoder and Carcia-Moliner 1995). In relatively shallow water, optical remote sensing has been used for cartographic and bathymetric mapping (Jupp 1989, Pasqualini *et al.* 1997). The application of optical remote sensing to mapping marine biological distributions has been successful in some tropical coastal marine areas (Chauvaud *et al.* 1998) but is limited to areas of shallow (generally < 15m) and consistently clear water (Pasqualini *et al.* 1998).

As pointed out in the review by Green *et al.* (1996), remote sensing in the marine environment has great application in littoral, shallow and clear waters, as well as sea surface applications. However, in deeper or more turbid waters it is not especially useful for mapping marine biological distributions, leaving the vast majority of continental shelf waters beyond the reach of this technology.

Consequently, in the absence of biological data of the requisite scope and quality, recent attempts at habitat classification at both regional and local scales have tended to rely on more easily available physical and / or oceanographic data as surrogates for biological distributions (Zacharias and Howes 1998, Roff and Taylor 2000) or reverted to delphic

methods of classification (Hockey and Branch 1997, Chevis 1995). Non-biological information clearly is relevant, and in some instances can predict biological distributions quite accurately (Long *et al.* 1997). However, there are disadvantages in basing habitat classification solely or primarily on physical surrogates (Edgar *et al.* 1997). Given that the objective is to represent patterns of biodiversity, in order to provide the requisite rigour the predictions of biological distributions from physical data would involve extensive ground-truthing. Whilst in shallow or intertidal areas this can both be effective and efficient (Zacharias *et al.* 1999), in areas deeper than about 12 metres, the difficulties of major underwater (SCUBA-based) ground-truthing surveys quickly erode the cost and logistical savings of using surrogate datasets.

However, methodologies have recently been developed combining relatively low-cost sonar and visual sampling techniques that highlight the potential application of new technologies to marine environment mapping. The capacity for visual sampling using underwater video techniques to enable more extensive sampling than that provided by either SCUBA surveys or grab sampling techniques is now well established. Significant studies have been carried out using both hand-held (Sweatman 1997) and sled or remotely operated vehicle-mounted (Engel and Kvitek 1998) video units, and operational and analytical procedures developed to ensure quantativity. Sampling design, data collection methods and statistical treatments to provide acceptable rigour in these techniques are quite mature (Christie *et al.* 1996, Ward *et al.* 1998). Development of the technology is continuing, for example Davies *et al.* (1997) report on the integration of acoustic ground discrimination systems with biological information to produce biological resource maps (see also Sotheran *et al.* 1997). Low-cost underwater video technology has in recent years been applied to a wide range of uses from simple observations (Villanueva *et al.* 1997) to highly quantitative measurements (Gledhill *et*

al. 1996, Parry *et al.* 2003). A growing body of work is concerned with quantitative habitat characterisation, especially in areas beyond the capabilities of both SCUBA and optical remote sensing (Engel and Kvitek 1998, Cailliet *et al.* 1999).

Once survey data has been compiled, multivariate techniques are usually used to search for patterns of relative homogeneity within the area studied. Typically, concurrence of more than one method of classification is used to ensure rigour of the derived patterns, for instance agreement between groups of sites derived by both cluster analysis and MDS derived ordination (Clark and Warwick 1994).

1.5 From maps to management

A map of marine habitats at the local scale is, more precisely, a model of patterns of relative homogeneity constrained by the spatial limits of management (ie. local scale). Polygons are defined on the basis of the small subset of biodiversity which is relatively observable and quantifiable.

A question of special importance for the present discussion is how representation is derived from such a map. If some reserve system already exists, assessment of the amount of representation is straightforward. It could be simply expressed in terms of an areal extent, or as a proportion of each derived unit contained in the current system. However, determining how much **should** be contained within a reserve system is more complex.

It is important to emphasise here that representation of patterns of biodiversity is not the same as **maximising** the representation of biodiversity in a MPA system, as is frequently cited as a conservation goal (e.g. Margules *et al.* 1988). The difference is not

just semantic. Agardy (1995 p. 4) criticises the preoccupation of reserve planners and conservationists with so-called “hot-spots” of high biodiversity as misplaced effort, not necessarily linked to areas of most ecological importance, or under the greatest threat: “...high diversity areas may not necessarily be priority areas for protection from an ecological point of view. This is particularly true in marine systems, where pockets of endemism are rare and habitats are functionally linked over wide distances ... and physical spaces that act as critical areas, if only seasonally, may fall off the tail end of diversity indices altogether.” Similarly, as Agardy (1995) points out, while planners have concentrated on the inclusion of high-profile ecological elements (e.g. seagrasses, mangroves, coral reefs) within reserve systems, other equally crucial elements (especially unvegetated soft substrate areas) are generally not considered in allocating priorities for research, survey and inclusion in the planning process. The concept of representation *sensu stricto* includes the idea that each habitat type has an intrinsic functional position in marine ecosystems, and thus an inherent conservation value, which is not based on being the biggest, richest or rarest **anything**.

At its simplest, then, representation *sensu stricto* of all habitat types is achieved when at least one spatial unit of each defined habitat type, at the minimum of the scale mapped (so at the local scale, a linear dimension of 10km) is included in the MPA system. Algorithms are available (e.g. Nicholls and Margules 1993) for optimising reserve selection so that efficiency in meeting multiple objectives (e.g. critical habitat as well as representation) is maximised. These are based on terrestrial systems and will need to be adapted to marine applications to take account especially of the greater degree of interchange between habitats. Vanderklift *et al.* (1998) and Ward *et al.* (1999), amongst others, have recently developed and evaluated the use of numerical methods for

selection of representative areas for a marine reserve network, using the comprehensive dataset derived from exhaustive surveys of Jervis Bay on Australia's southeast coast. Inevitably, it is not this simple. Representativeness *sensu lato* includes notions of adequacy, redundancy and maintenance of ecosystem function, all interlinked concepts whose central aim is to ensure that the processes driving the collection of habitats, the ecosystem, are able to continue. Without additional information on ecological processes within and between the habitat types derived, these questions are difficult to answer. However, local scale habitat classifications and mapping provide a framework for the understanding of ecological processes, by identifying the functional units with greater precision than is currently available. It would be possible, for instance, to determine for any given habitat type, what area is required to encompass (say) 95% of the observed diversity of macrobenthos, physical substrate types, and water chemistry regimes using optimisation algorithms.

1.6 Conclusions

While significant progress has been made in advancing the conceptual and information base for marine conservation over the last several years, much work remains to be done. The concept of representativeness in MPA planning, while valuable, is at risk of being undermined due to its now widespread use in two quite distinct senses, often without definition.

If representative MPAs are to be implemented, there is no escaping the need to carry out habitat classification analyses at the scale at which management occurs; it is simply not valid to expect that representation at the regional scale will have any measurable benefits for marine conservation, whilst (local scale) management decisions are made without information at the appropriate scale and without the context of adjacent

functional units. Affordable technology and methods are available, and being progressively refined, to allow local scale analyses to be carried out over the next several years, in identified high priority regions, providing the required level of detail for MPA planning efforts. It should not be inferred, however, that the difficulties and challenges inherent in designing MPAs to provide for representativeness with an acceptable degree of scientific rigour have all been solved. There remain considerable technical and conceptual challenges, for instance in the concepts of adequacy and the provision of ecological process information.

All such habitat classifications are necessarily subsets, both in spatial scale and complexity, of the real world. Even observed and measured biological distributions are themselves surrogates for biodiversity at scales from genes to ecosystems (Ward *et al.* 1998). Which (biological) surrogates are chosen, and how they are analysed, will determine the final form of any habitat mapping exercise (Ward *et al.* 1999). There is no definitive set of surrogates and analyses; however there are more (or less) rigorous and relevant methods to move toward representative MPAs.

The aims of this thesis were therefore to:

- Develop and test video survey methods using off the shelf technology to permit cost-effective and quantitative surveys of macrobenthos over a relatively large area.
- Determine the ability of abiotic surrogates to predict patterns of biological distributions in macrobenthos at the local scale.
- Survey macrobenthos in Moreton Bay and adjacent offshore waters and derive habitat types by numerical classification.
- Determine the extent to which the habitat types are represented in the existing marine protected area, Moreton Bay Marine Park.

1.7 Arrangement of this thesis

The Introduction (this chapter) was written and published during the course of the studies for this degree as:

Stevens, T.F. 2002 Rigour and representation in marine protected area design. *Coastal Management* 30: 237 – 248.

It is presented here with only minor stylistic alterations and the addition of this section.

Chapter 2 deals with a site scale (Table 1.1) pilot study conducted to test and refine the video survey, data extraction and analytical methods for the full (local scale) study (Chapters 3 – 6). During the course of the trials an unusual benthic assemblage was encountered, providing an ideal focus for the pilot study. Chapter 2 was therefore written and accepted for publication during the course of the studies for this degree as:

Stevens T.F. and Connolly R.M. (in press) Shallow water crinoids are on soft sediments too: evidence from a video survey of a subtropical estuary. *Bulletin of Marine Science*.

It is presented here with minor stylistic alterations and additions to aid the logical flow of the thesis. The contribution of the second author (the candidate's supervisor) to the chapter content was minor.

Chapter 3 details the equipment, field methods, data extraction methods and survey design considerations developed for the major study. It has not been submitted for publication separately.

Chapter 4 examines the relationship between abiotic surrogates and biological distributions in Moreton Bay. It was written during the course of the studies for this degree as a stand alone paper and has been submitted for publication as:

Stevens T.F. and Connolly R.M. (in review) Testing the utility of abiotic surrogates for marine habitat mapping at scales relevant to management. Submitted to *Biological Conservation*.

It is presented here with minor alterations to aid the cohesiveness of the thesis. The contribution of the second author (the candidate's supervisor) to the chapter content was minor.

Chapter 5 is concerned with the relationship between similarity and between-site distance as a prerequisite to mapping habitats by spatial agglomeration. It was written during the course of the studies for this degree as a stand alone paper and has been submitted for publication as:

Stevens T.F. (in review) Scales of similarity in soft sediment macrobenthic assemblages: implications for marine protected area design. Submitted to *Marine Biology*.

It is presented here with minor alterations to aid the cohesiveness of the thesis.

Chapter 6 presents the macrobenthic habitat classification of Moreton Bay and adjacent offshore waters and the analysis of representation within the existing MPA. It was written during the course of the studies for this degree as a stand alone paper and has been submitted for publication as:

Stevens T.F. and Connolly R.M. (in review) Assessing representation in a marine protected area using an inclusive benthic habitat classification. Submitted to *Marine and Freshwater Research*.

It is presented here with some alterations to aid the cohesiveness of the thesis, specifically by removing some parts of the discussion to avoid repetition, and some additional material. The contribution of the second author (the candidate's supervisor) to the chapter content was minor.

Chapter 7 briefly summarises the outcomes of the component studies that constitute the studies for this degree, and places them in a broader comparative framework. The implications of their findings, in terms of both rapid marine benthic surveys and marine protected area design, are discussed in the context of current practices in Australia and around the world.

Chapter 2 Site-Scale Pilot Study

2.1 Introduction

The developing field of remote underwater videography is allowing exploration of areas and community types not previously given priority. Remote videography allows cost-effective visual surveys without many of the logistical limitations of SCUBA or crewed submersibles (Holme 1985, CSIRO 1994). The recent emphasis on representativeness in marine conservation planning and management has given impetus to quantitative surveys of areas not previously regarded as having high conservation or productivity values (Agardy 1995).

This chapter stems from site scale field trials for the more broad ranging study (Chapters 3 – 6) to characterise and map marine benthic habitats at scales useful to managers. During the initial stages of that study, an unusual benthic assemblage from a subtropical estuary was noted. A surprisingly high density of comatulid (unstaked) crinoids occurred amongst an otherwise quite depauperate macrobenthic community. Continental shelf crinoid species (Phylum Echinodermata; Class Crinoidea) are not a noted component of soft substrate macrobenthos. They are obligate suspension feeders, long assumed to have a low tolerance to turbidity (Hyman 1955). Moreover, since all extant shallow water species are unstaked (Order Comatulida) as adults, they must use their cirri, or in some cases adhesive pinnules, to attach themselves to a perch on the substrate and elevate their arms in one of several types of filtration fan array (Macurda and Meyer 1983). For these reasons, shallow water crinoids are assumed to be characteristic of hard substrate, usually reefal environments (e.g. Fabricius 1994).

The crinoid faunas of tropical and subtropical regions, where they have been described, are characterised by high species richness but generally low abundance (Rutman and Fishelson 1969, Macurda 1973, Meyer 1973, Zmarzly 1984, Bradbury *et al.* 1987, Stevens 1989, Fabricius 1994). Assemblages with high density and low species richness have been described from polar and cool temperate waters (Marr 1963, Könnecker and Keegan 1973).

This chapter presents descriptions and mapping of the benthic assemblage in the trial study area derived from the low-cost remote videography techniques developed for the wider study. The significance of this assemblage is discussed in ecological and marine conservation contexts.

Specifically, the field trial had two aims: to characterise and map benthic assemblages at the site scale in the trial study area, and to find and map the extent of a local soft-substrate crinoid population.

2.2 Methods

2.2.1 Study area

The soft-sediment biota was surveyed within a 2.5 x 3 km area in Moreton Bay (153° 15' E; 27° 20' S), Queensland, Australia (Figure 2.1). Moreton Bay is a large (c.1500 km²) roughly triangular embayment opening to the Coral Sea towards the north. It is mostly shallow (< 20 m), although there are deep (40 m) channels in the north. It is protected on the eastern side by large sand islands. The bay receives significant freshwater and sediment inputs from the Brisbane River and several streams entering on its western shores year round, but especially during summer. Consequently there is a strong gradient in mud and silt fraction in sediments from west to east (Lang *et al.*

1998) and a corresponding gradient in turbidity for much of the year (Dennison and Abal 1999). The area sampled may, after heavy and sustained rainfall (principally in summer), experience lowered salinity (Dennison and Abal 1999), however significant rainfall did not occur during or in the two weeks prior to sampling (February 2001).

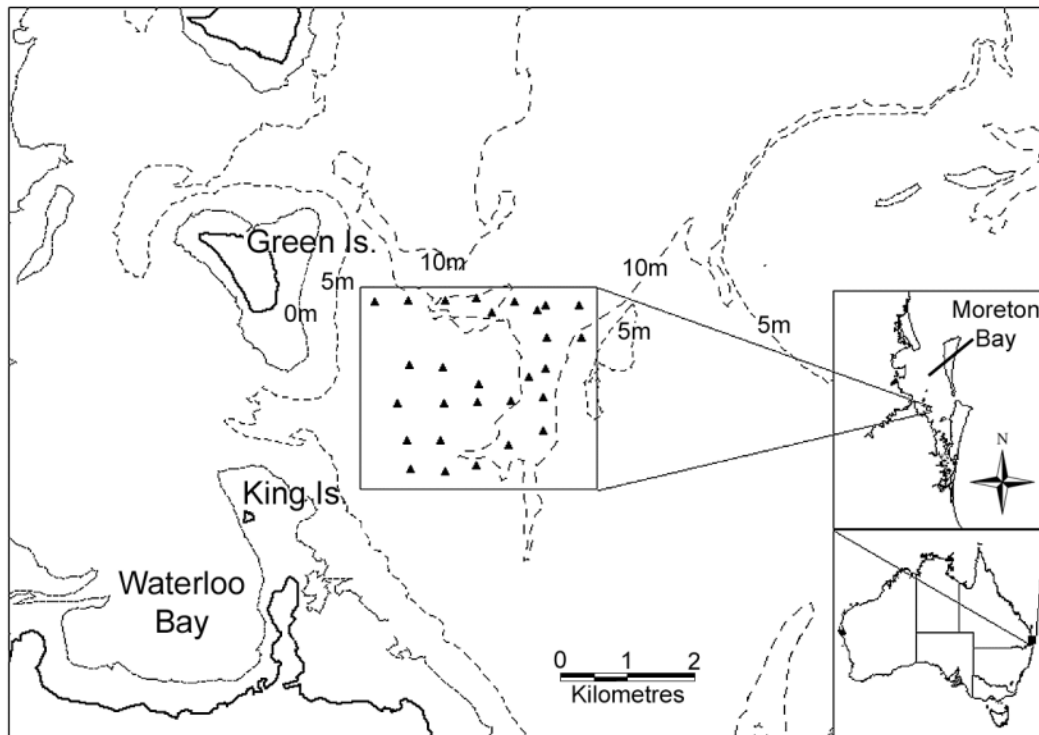


Figure 2.1: Map of the site scale study area showing location of sampling sites. Depth contours are at 5 m intervals. (Redrawn from Moreton Bay Series Chart MB8, Queensland Department of Transport, 2000)

2.2.2 Field sampling

A digital video camera was used to obtain visual samples of macrobenthos in soft-sediment habitats in the study area. The SONY Digital-8 format camera was deployed in an IKELITE underwater housing. The camera was deployed attached to a frame with the camera mounted at a fixed angle (45° down). The camera array was positively buoyant, and was kept at a fixed distance above the bottom by a short length of chain attached to the frame, in a simplified version of the arrangement described in detail by Barker *et al.* (1999). The field of view of the camera is known (± 3 cm) and calibrated for several standard distances above the bottom. The video imagery analysed for this paper was all taken with the camera lens suspended 30 cm from the substrate

because visibility at this inshore site was rather low (surface Secchi depth < 3 m, visibility often < 1.5 m at the bottom). At this height, the field of view of the substrate was slightly over 50 cm wide at the nearest visible point to the camera, allowing a 0.25 m² frame to be superimposed on the video images to quantify the density of benthic organisms.

The camera frame was attached by a 5 m tether to a 20 kg drop weight, which was suspended about 2 m above the substrate beneath the survey vessel. This arrangement minimises the positional uncertainty that would occur with a conventional long (unweighted) towline. In keeping with the low-cost aims of the overall project, the video array was small, lightweight and able to be easily deployed from a small craft.

In this pilot study, 28 sites were sampled within a 3 x 2.5 km block, at a nominal spacing of 500 m (Figure 2.1). Each site is represented by a single video transect of nominally 50 m. Due to the time taken in deploying and recovering the unit, 100 m was allowed from deployment to recovery at the vessel, to ensure that at least 50 m was sampled on the bottom. With the camera at only 30 cm from the substrate, towing the unit even with the engine at idle resulted in blurred images, so a transect was effected by allowing the vessel to drift with wind and tide. Selection of sample sites was “blind” in that the substrate was not visible from the surface, and there was no video feed to the surface to influence selection of images. Sampling was conducted on 4 days between 14 February and 1 March 2001.

A Global Positioning System (GPS) receiver was used to determine the position of the deploying vessel. Since the camera array was on a 5 m tether from a weighted drop line which remains relatively vertical at all times, it was assumed to be within 10 m

horizontally of the vessel at all times, giving sufficient positional resolution for the scale at which mapping of marine habitats for conservation purposes is required (Stevens 2002). Depth (+ / - 0.5 m) was recorded at the beginning of each run and corrected for the state of the tide.

The video images were supplemented by two dives to collect reference specimens for identification. Identifications were verified with the Queensland Museum, and reference specimens deposited there (Voucher reference: QM G218354).

2.2.3 Image processing and data extraction

Video tapes were first viewed on a large colour monitor to identify organisms to the highest taxonomic resolution possible. Quantitative analysis was performed with digital images on computer. The digital signal stream was captured at a nominal rate of 1 frame per second and saved as a digital movie file. The movie file was post-processed using digital filters to enhance image clarity and contrast, which greatly aids recognition of benthic organisms. Further processing was undertaken to add timecode and frame number data. A mask was overlaid to delineate a known sample area of 0.25 m².

Data extraction was carried out by viewing each movie frame by frame. Counts of solitary and discrete colonial organisms (ascidians and sea whips) were scored by recording the number within the mask overlaid on each frame. These were then summed for the entire run, and converted to densities for analysis. Formal decision rules were used to determine the usefulness of each frame. Frames were discarded if the image was blurred, partially or completely obscured, out of correct orientation (camera tilted or at the incorrect distance from the bottom), a partial or complete overlap of a preceding

image, insufficiently lit or overexposed. The number of frames per run varied from 64 to 246 with a mean of 114.

For the purpose of these analyses, a whole transect (rather than individual frames) was considered a single sample. Other work (Stevens unpubl. data) has shown that one run is sufficient to characterise a 50 m swath, provided that the frame spacing is optimised to maximise coverage without overlap.

2.2.4 Analysis

Density values were plotted on spatial co-ordinates, representing the mid-point of each transect, to produce raw distribution plots of crinoids and other taxa. The distribution of crinoids was examined for possible relationships with abiotic parameters depth, mud and sand fraction in sediments, and residual current velocities (background water movement after removal of tidal effects – derived from summing tidal velocity vectors over the entire cycle) obtained from Dennison and Abal (1999). Relationships were tested using regression analysis for depth and by visual comparison of maps for the other parameters since numeric data at the scale of this study was not available.

Densities of crinoids and other taxa were compared using correlation analyses to test for relationships of co-occurrence or spatial separation. Non-parametric (Spearman's Rank) analysis was necessary because preliminary testing showed that data distributions for all taxa were non-normal.

Multivariate techniques were used to look for patterns of relative homogeneity in community structure within the study site. The sites by taxa matrix was $\log(x+1)$ transformed to limit the influence of the few very high density sites / species. A

combination of K-means divisive clustering and more conventional agglomerative clustering (unweighted pair group method with arithmetic means) was used and the results compared to ordinations derived from multi-dimensional scaling. The Bray-Curtis similarity measure was used because it ignores conjoint absences, particularly important in this depauperate dataset (Clarke and Warwick 1994).

Memberships of groups derived from multivariate analyses were plotted on real spatial co-ordinates of sampling sites, and notional community boundaries derived from a smoothed 250 m buffer around sampling points.

2.3 Results

2.3.1 General characteristics of the study area

Depth in the sampled area varied from 6 to 18 m (Figure 2.1), in a general gradient from west to east. Sediments were assessed visually as ranging from mud and shell grit in the northwest to sandy mud with less shell grit in the southwest, with an increasing proportion of sand, and loss of shell grit, toward the eastern side of the sampled area. This agrees in broad terms with the mapping from Dennison and Abal (1999), although their map is interpolated from relatively widely spaced data points.

In terms of the sedimentary environments of Moreton Bay, the study area lies within a zone of minimal deposition, but clearly represents a gradient of influences from an inshore prodelta mud and silt depositional zone to the west (Waterloo Bay), and the marine tidal delta sand zone to the east (Amity Banks) (Lang *et al.* 1998).

2.3.2 Species Distributions

The survey revealed a depauperate epibenthic community. Densities of only eight macrobenthic taxa were quantified from the video data (Table 2.1). Of these, two occurred as single individuals in only a few sites. Of the 168 cells in the remaining 6 taxa by 28 sites matrix, 66 (39%) were zero values. Seagrass and macroalgal cover was not quantified, because it almost never occurred, although evidence of rhizome mats was visible in sites in the southwest corner of the study area. Occasional patches of sparse seagrass *Halophila ovalis* were noted in several of the deeper sites, but did not appear within the sampling mask.

Table 2.1: Abundance of benthic macrofauna over 28 sites within the study area
Mean density over all sites, maximum site density, and frequency of occurrence as a percentage of all sites. Density units are individuals m⁻²

Taxon	Common Name	Mean Density	Maximum Density	% Frequency
<i>Polycarpa papillata</i>	Solitary ascidian	0.366	1.143	100
<i>Eudistoma elongatum</i>	Colonial ascidian	0.174	1.116	79
<i>Zygometa cf. Z. microdiscus</i>	Crinoid	0.114	0.883	64
<i>Guaiaigorgia sp.</i>	Seawhip	0.096	0.696	64
<i>Sphenopus marsupialis</i>	Zooanthid	0.074	0.329	64
<i>Virgularia gustaviana</i>	Short Quill Sea Pen	0.033	0.235	29
<i>Holothuria sp.</i>	Holothurian	0.008	0.071	14
<i>Cerianthus sp.</i>	Anemone	0.003	0.076	7

The most unusual feature of the dataset was the presence at relatively high densities of a single species of the comatulid crinoid genus *Zygometa*. This species was identified from the keys in Clark and Rowe (1971), the most recent treatment of this family. However, the taxonomy of the Zygometridae is unclear, with Clark and Rowe (1971) noting that some of the species of *Zygometa* in the Indo-West Pacific are probably

untenable (p. 17). Specimens from the study site were compared to those of the genus *Zygometra* held by the Queensland Museum. Whilst there is a lot of variability within the specimens held in the Museum, those from this study are more like *Z. cf. microdiscus* than any other species in the genus. The Queensland Museum (Davie *et al.* 1998) lists the form occurring on local reefs as *Zygometra sp.* and states that it may be a new species (p. 221). Given this uncertainty, for the purposes of this paper the species is referred to as *Zygometra cf. Z. microdiscus* (abbreviated as *Z. cf. microdiscus*), while acknowledging that the taxonomy of the genus *Zygometra* is in need of review.

Crinoids occurred over most of the study area (Figure 2.2). Higher densities were found on the central western side of the study area. The highest density of crinoids occurred in site 5, where there were 0.88 individuals.m⁻². Mean crinoid density over all 28 sites was 0.11 individuals.m⁻² (SD = 0.18 individuals.m⁻²). *Z. cf. microdiscus* occurred in 64% (18 of 28) of sites. The maximum density recorded in any single frame was 20 individuals.m⁻² (the highest for any taxon). All individuals were within the range of approximately 150 – 200 mm across and were therefore considered adults (Davie *et al.* 1998). No juvenile specimens were observed.

The most abundant species over the study area was the solitary ascidian *Polycarpa papillata* (Table 2.1). Mean density was 0.37 individuals.m⁻² (SD = 0.29 ind.m⁻²), with a maximum of 0.92 individuals.m⁻² in site 5. This species was also the most widespread, occurring in all sites.

Other taxa that occurred regularly (in more than half of the sites) were the colonial ascidian *Eudistoma elongatum*, a seawhip of the family Gorgonidae, probably *Guaiaogorgia sp.*, and the zooanthid *Sphenopus marsupialis*.

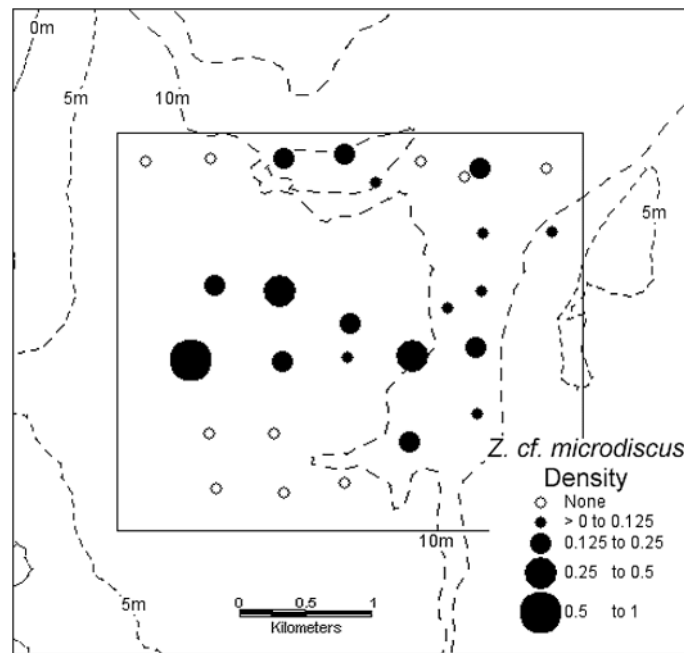


Figure 2.2: *Zygometra cf. Z. microdiscus* densities at the 28 sampling sites
Units are individuals.m⁻²

2.3.3 Assemblages

The two clustering methods gave identical results at the four group solution and agreed well with the relationships apparent in the MDS ordination plot (Figure 2.3). Stress level in the MDS (0.18) was acceptably low for two dimensions, given the agreement with the clustering results (Clarke and Warwick 1994). The derived group membership when plotted onto the real spatial co-ordinates of the sites gives the community map shown at figure 2.4. Comparing the groups with the original data matrix showed that group 1 consisted of a single site containing very high densities of both crinoids and solitary ascidians. Group 2 contained 4 sites in the southwest corner of the study area characterised by moderate to high densities of solitary ascidians and colonial ascidians, with no crinoids present. Group 3 was a large group of undifferentiated sites occupying the bulk of the study area, characterised by a mix of most taxa. Group 4 also contained a single site, which was characterised by a very high density of seawhips. It is evident from comparison of figures 2.2 and 2.4 that the community composition derived from

the multivariate analyses was not driven strongly by crinoid density, except in the case of the very high density of crinoids at the site which formed group 1.

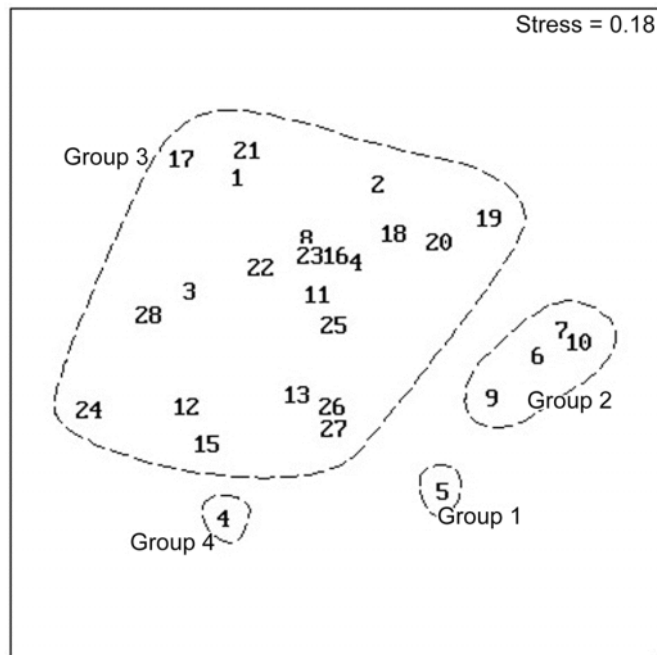


Figure 2.3: MDS ordination plot of taxon density data showing four groups derived from multivariate analysis

Correlation analyses showed no significant relationships between distributions of crinoids and any other taxon, either positively (co-occurrence) or negatively (spatial separation). The only exception to this was a significant negative relationship between crinoid and sea pen (*Virgularia gustaviana*) densities ($r = -0.33, p = 0.042$), indicating that these two taxa are spatially separated. Examination of the data matrix showed that while *Z. cf. microdiscus* occurs in 18 of the 28 sites, and *V. gustaviana* in 8, the two taxa co-occur in only three sites.

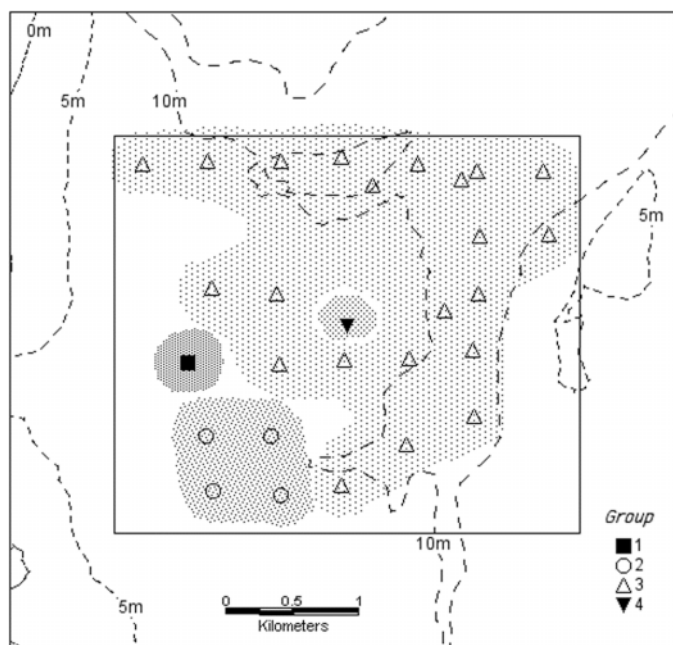


Figure 2.4: Community map derived from groups selected using multivariate analysis
 Notional group boundaries are based on a 250m buffer around sampling points, since nominal site spacing was 500m

2.3.4 Relationships with abiotic surrogates

The relationship between depth and crinoid density was not significant ($p = 0.15$) and the R^2 value was very low (0.08) indicating that depth was not an important determinant of crinoid distribution. This finding is not surprising, as the depth range of 6 – 18m is unlikely to be limiting for crinoids (Stevens 1989). The maps of mud and sand fraction in sediments, and residual current velocities in Dennison and Abal (1999) were derived from interpolation between relatively (compared to the distance between the sites in this study) widely spaced data points, hence no numerical analysis was attempted. From visual examination, there appeared to be no relationship between the distribution of these abiotic factors and crinoid distribution.

2.4 Discussion

2.4.1 *Crinoid densities worldwide*

There have been few quantitative surveys of shallow-water crinoid abundance and species richness worldwide (Table 2.2), and all have been undertaken on tropical or subtropical coral reefs in Jamaica (Meyer 1973), Enewetak Atoll (Zmarzly 1984), Davies Reef (Bradbury *et al.* 1987), other reefs of the central Great Barrier Reef (Fabricius 1994) and Heron Island and Wistari Reefs (Stevens 1989). The only record of comatulid (unstaked) crinoid density estimates on soft-sediment substrates is from dredged and trawled samples from deep to abyssal (75 – 4862m) waters on the Antarctic Shelf (Marr 1963).

The most extensive quantitative survey of crinoid abundance and species richness was undertaken by Stevens (1989), who surveyed almost 10,000 m² in transects on Heron Island and Wistari Reefs at the southern end of the Great Barrier Reef. The current study surveyed about 750m², and while not at the same scale, found maximal and mean densities of a single species at the same order of magnitude as the combined mean or single-transect maximum of all 36 species in Stevens' (1989) study. Densities at similar orders of magnitude are reported in other studies of shallow water crinoids (Table 2.2). It should be noted that the other studies were carried out in areas found by preliminary surveys to be those with high crinoid densities (Zmarzly 1984, Meyer 1973) or with the deliberate intention of characterising reef zones on the basis of crinoid fauna (Bradbury *et al.* 1987, Fabricius 1994). The very high densities found in the study by Fabricius (1994) were partly as a result of the deliberate placement of 1 m² quadrats to sample crinoids, and because the coral substrate beneath quadrats was excavated to extract cryptic species.

Table 2.2: Comparison of quantitative studies on shallow water crinoid species richness and density worldwide

Density units are individuals.m⁻²

- 1 – This study was based on 1 m² transects placed to characterise reef zones on the basis of crinoid fauna, and involved excavation of the substrate to a depth of 70cm to extract cryptic species
- 2 – Overall density value given in Zmarzly (1984) is “within a zone of peak abundance approximately two times the overall densities.” (p. 112), so it is treated here as the maximum, with mean density calculated as half that value
- 3 – Maximum values not given but “The population censused probably represents the maximum size for crinoid populations in this vicinity” (Meyer 1973 pages 244-245) so mean and maximum values are the same

Location	Species Richness	Mean Density	Maximum Density	Source
Moreton Bay, Australia	1	0.110	0.88	Present Study
Central Great Barrier Reef, Australia	43	7.1	70.0	Fabricius 1994 ¹
Heron Island and Wistari Reefs (southern Great Barrier Reef), Australia	36	0.108	1.81	Stevens 1989
Davies Reef (central Great Barrier Reef), Australia	27	0.470	1.02	Bradbury <i>et al.</i> 1987
Enewetak Atoll, Marshall Islands	6	0.071	0.142	Zmarzly 1984 ²
Discovery Bay, Jamaica	4	0.220	0.220	Meyer 1973 ³

Harrison *et al.* (1998) recorded densities of reef benthos at two sites close to the study area: Myora Reef within Moreton Bay (about 13 km from the study area), and Flinders Reef in the open sea north east of Moreton Bay (about 52 km from the study area). The data presented included total numbers of crinoids, although the number and identity of species was not given. No crinoids were recorded from Myora Reef, and densities at Flinders Reef varied from 0.1 to 1.0 individuals m⁻², similar to those found in this study.

In terms of single species densities, *Z. cf. microdiscus* in this study occurred at higher densities than the bulk of species in previous reef-based surveys. For example, only 9 of the 43 species recorded by Fabricius (1994) at central Great Barrier Reef sites occurred

at higher mean densities, even given the bias towards high densities in that study. No single species in Stevens' (1989) study occurred at higher mean densities.

The occurrence of *Z. cf. microdiscus* in the turbid, soft sediment location of the present study at comparably high densities to species, or total crinoid densities, found in coral reef surveys was significant in terms of the generally accepted picture of crinoid ecology. Congregations of comatulid crinoids in soft-sediment, relatively turbid, environments have not been previously described in subtropical and / or estuarine waters, although they occur sparsely in inter-reefal regions of the Great Barrier Reef (Birtles and Arnold 1989). An exception to this is an anecdotal account of an assemblage of the same species (*Z. cf. microdiscus*) on soft substrate in Bowling Green Bay, a marine embayment near Townsville, Australia (D.L. Meyer, pers. comm.). That account supports the contention of this paper that crinoids can no longer be regarded as essentially reefal fauna.

2.4.2 Influences on crinoid distribution

Comatulid crinoids as adults lack the stalk and holdfast retained by their deep-water relatives, and require a perch to which they cling using their cirri or in some species (Family Comasteridae) adhesive pinnules (Macurda and Meyer 1983). They are relatively unselective (although some specialist species have clear perch preferences) and are frequently epizoic (Stevens 1989).

In a soft substrate environment, a firm perch is still required, and might be expected to be a limiting factor. In this study, *Z. cf. microdiscus* was found clinging to a variety of perches including shells (living, whole dead or larger fragments), isolated dead coral clumps, solitary ascidians, zooanthids and artificial objects (bottles and cans). However,

there is no evidence that perch availability was a limiting factor in the distribution of *Z. cf. microdiscus*, since in the majority of sites there were many more available perches (both biotic and abiotic) than crinoids. No correlation was observed between the density of solitary ascidians or zooanthids and that of *Z. cf. microdiscus*. Interestingly, seawhips were never observed to be used as perches, whereas in reefal environments they are commonly used, albeit by a group of specialist crinoid species not occurring here (Stevens 1989).

Crinoids are described as moderately to strongly rheophilic (Meyer 1982), since they are passive filter feeders. Reversing tidal velocities (as distinct from residual current velocities) were noted to be highest in the central western sites, closest to the channel between King and Green Islands, where the water mass must pass through a relatively constricted opening to enter and leave Waterloo Bay. This corresponds in broad terms with the sites of highest crinoid density and may explain the preference of *Z. cf. microdiscus* for these sites. However, it does not explain how crinoids are able to occur in such an environment at all.

A partial explanation for the occurrence of *Z. cf. microdiscus* in the study area may be the ability of this crinoid species, in common with many in this and other non-comasterid families, to swim by undulating alternate arms, and indeed it was observed doing so. The swimming is not powerful, but enables the animal to elevate itself above the substrate, facilitating transport by currents as described by Shaw and Fontaine (1990). Other (non-swimming) crinoids must search for appropriate perches by crawling over the substrate, which may be problematic in a soft-sediment environment. While not tested in this study, it is postulated that swimming activity may also enhance survival on

soft substrates by removing sediment buildup from the filtering pinnules and ambulacral groove.

There are five species of crinoid commonly occurring on local reefs including *Zygometra sp.* (Davie *et al.* 1998), although up to 13 species have been recorded (Stevens unpubl. data). Of these common species, only *Zygometra sp.* is capable of swimming. Given the uncertainty of the taxonomy of the Zygometridae, it is not clear whether this is the same species as *Z. cf. microdiscus*. Until the taxonomy is resolved, it is not possible to say whether *Z. cf. microdiscus* occurs on soft substrates in Moreton Bay because it is the only one of the locally available pool of crinoid species which is able to survive in these conditions, or because it is a soft substrate specialist.

2.4.3 *Significance of the assemblage*

It is not possible to say whether this crinoid population is widespread within the Moreton Bay region, or whether this type of soft sediment assemblage is found in other subtropical estuaries, although the account of Meyer (pers. comm.) suggests it may be. Therefore it is difficult to assign a conservation or representational significance to it. To do so would also require some assessment of threat, and the temporal persistence of the assemblage. However, Moreton Bay is the site of the major port of Brisbane, and several marine research stations. The bay has been quite extensively studied from the perspective of fisheries productivity and benthic ecology (see summaries in Tibbetts *et al.* 1998, Crimp 1992). It is therefore surprising that this crinoid population has not been previously described. Crinoids do not appear in species lists from the extensive benthic sampling carried out in Moreton Bay during the 1970s and 80s (Stephenson *et al.* 1970, Poiner 1977, Stephenson and Cook 1977, Stephenson *et al.* 1978, Young and Wadley 1979, Stephenson 1980, Poiner and Kennedy 1984). Therefore it may be that the

densities described in this report are a localised or recent phenomenon, or that more conventional survey methods (dredge, grab, trawl) under-represent crinoid populations.

The unusual assemblage described in this study also highlights the conservation benefits of a more inclusive approach to marine habitat survey and mapping. An inclusive approach here means one which surveys, and aims to represent, all available habitat types at scales relevant to managers (Stevens 2002.). Common approaches to marine reserve planning rely heavily on the use of abiotic surrogates or obvious structural components in delineating areas as high priority for protection. Historically, this has meant a strong bias towards highly productive or aesthetically appealing (mangroves, seagrass beds, coral reefs) habitats as candidates for protection (Agardy 1995). By this approach, assemblages such as the one described in this study are entirely overlooked although they may be of scientific and ecological significance.

In summary, this study challenges the widely held view of crinoids as essentially reefal fauna. The lack of any strong correlation between the distribution of this unusual assemblage with crude, but commonly used, abiotic surrogates gives added weight to the use of approaches to marine conservation based on biological distributions at relevant scales.

Chapter 3 General Methodology

3.1 Introduction

In order to include representative samples of all habitats in protected areas, it is obviously necessary to know what habitat types are present, and their extent in space. The need for this crucial step of habitat mapping is well accepted and forms the basis of most published methods for terrestrial reserve selection (e.g. Purdie 1987, Margules 1988). In the marine context, the need for quantitative habitat mapping at the scale at which reserves are drawn is recognised, but has not been widely done. This is, at least in part, due to the actual or perceived expense associated with extensive underwater survey. Most marine protected areas are drawn at the local (10 km) scale or finer (Chapter 1) but mapping at this scale has typically relied on abiotic surrogates for biological diversity (e.g. Parks Canada 1993), or has focussed on high-profile habitat types (coral reefs, seagrass beds, mangrove and saltmarsh) rather than being all-inclusive. There is a clear need for methods to survey and classify all the habitats within a given area, at a scale relevant to managers, and in a cost-effective manner.

The rapid development of affordable video technology over the last decade has led to its adoption as a sampling tool. Techniques for the quantitative use of video for sampling marine benthos are mature and well documented (e.g. Christie *et al.* 1996). The expense associated with video sampling is principally in putting the camera where it needs to be. Diver operations for video sampling are logistically complex, depth limited and cover a relatively small area per unit time. Remote deployment requires complex, bulky and expensive equipment and substantial support vessels. This is discussed more fully in section 3.22.

To use video imagery in a quantitative way, several attributes are needed (Holme 1985, CSIRO 1994). The field of view of the camera must be accurately calibrated. The total area or distance of each transect must be accurately known. The locations sampled must be accurately known, relative to the scale of the survey, to allow spatial analysis. Data should be extracted in a numerical form to allow quantitative statistical analysis.

In designing a video survey, several assumptions are made which require evaluation before proceeding to the full survey. It is assumed that the video survey method can quantitatively distinguish between sites that are clearly qualitatively different. The inverse of this is also assumed, that is, that the video method will find replicate surveys at the same site to be the same. A video survey to classify habitats should also be designed to sample a relatively large fraction of the inter-site distance so that extrapolation is valid. There are operational reasons for minimising the number of replicates at each site. The objective of the survey is to quantify between-site similarity at the target scale of mapping, in this case 5 - 10 km. Variability at the next scale down (500 m – 1 km) is treated as patchiness; surveys are designed to characterise at this scale, not to separate elements within it. It is implicit that with a 5 km grid spacing, habitat elements less than 5 km in extent may not be captured.

Data can be extracted from video in several ways, and at differing intensities. The method(s) and intensity of data extraction for greatest discriminatory power need to be determined. The same analyses can determine the most efficient extraction methods, that is, those that can minimise the effort (principally time) required in extracting numerical data from video without significant loss of discriminatory power.

The aims of this chapter were to:

- Describe the local scale study area.
- Describe the development, attributes and use of the video array.
- Test the sampling and analytical methods for surveys at a 5 km grid spacing to determine:
 - How best to combine cover and density data into a single analysis.
 - The ability of the video method to distinguish qualitatively different sites.
 - Whether a single long transect per site is equivalent in terms of between-site relationships to several shorter transects.
 - The intensity at which data can be extracted from video without significant loss of accuracy.

3.2 Methods

3.2.1 Study Area

Moreton Bay (27°15'S, 153°15'E), on the east coast of Australia, is a shallow coastal embayment covering approximately 1,500 km² (Figure 3.1). The bay is roughly triangular in shape, about 35 km wide in the north and narrowing in the south into a maze of mangrove-lined waterways. It is protected in the east by large sand islands with its main ocean entrance in the north east and a smaller entrance in the east. Most of the bay is less than 15 m deep, but reaches depths greater than 25 m in the north-eastern part, adjacent to the main ocean entrance. The western parts of the Bay are heavily influenced by terrestrial inputs year round, but especially during summer (Costanzo *et al.* 2001). Inputs are principally from the Brisbane River (Eyre *et al.* 1998) and smaller river systems entering on the western shore. Consequently there is a strong gradient in mud and silt fraction in sediments from west to east (Lang *et al.* 1998) and a corresponding strong gradient in turbidity for much of the year (Dennison and Abal, 1999). The eastern part of the bay is essentially under oceanic influence (Udy and Dennison 1997).

The offshore portion of the study area extends seaward from the two large sand islands to the 50 m isobath. In general the bottom is of soft substrate and slopes quite evenly away from the ocean beaches. The north-eastern extremity of each island is formed by a rocky headland with associated offshore outcrops. In the north-east part of the study area a sandstone platform provides a substrate for Flinders Reef, a coral reef community of surprisingly high diversity given its latitude (Davie *et al.* 1998, Harrison *et al.* 1998).

The bay and adjacent offshore waters are included within Moreton Bay Marine Park (Figure 3.1), a zoned multiple-use MPA declared in 1993 and managed to “provide for

the ecologically sustainable use of Moreton Bay Marine Park and to protect its natural, recreational, cultural heritage and amenity values.” (Anon 1997, page 9). The park covers about 3,800 km² and extends from highest astronomical tide to between 3 and 20 km offshore to a maximum depth of about 150 m.

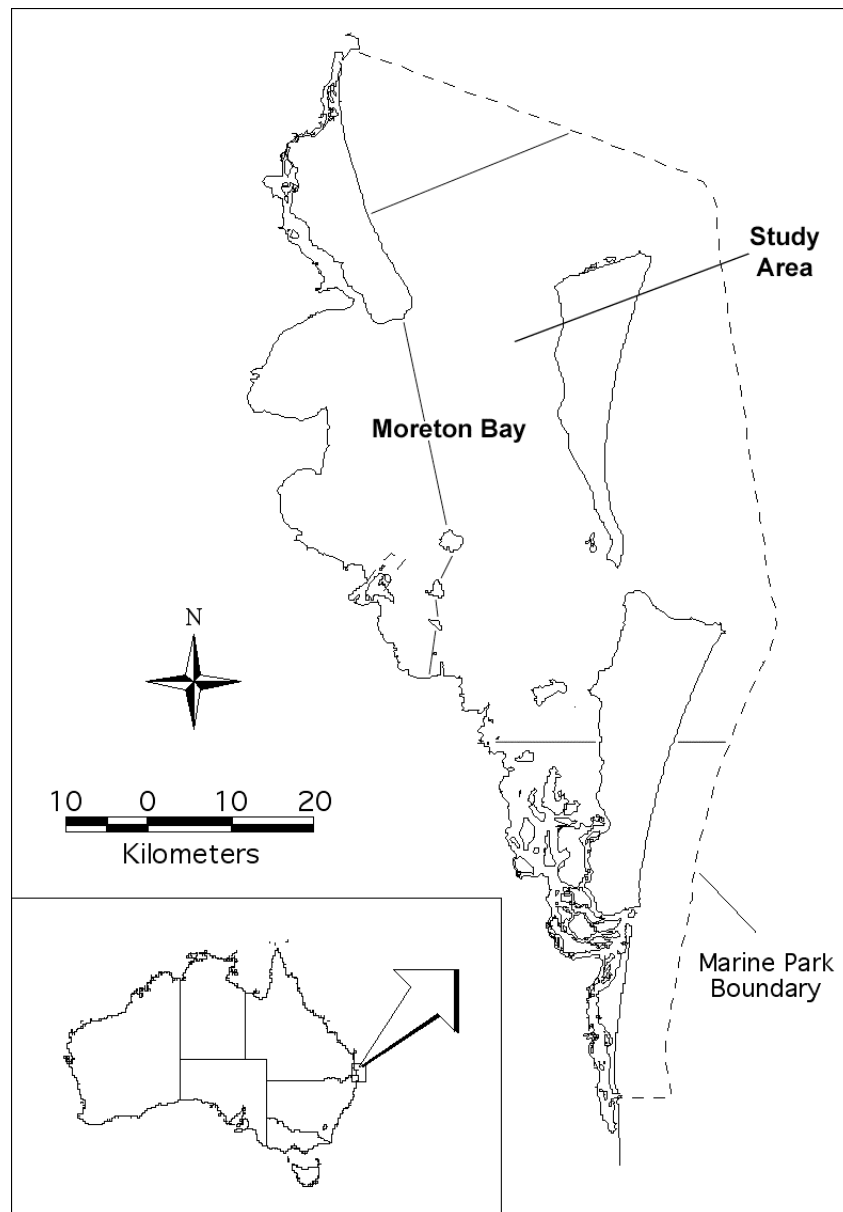


Figure 3.1: Local scale study area showing the Marine Park boundary

3.2.2 Video array

Previous quantitative video surveys have used a variety of methods to deploy the video sensor. These can be grouped into diver operated (e.g. Christie *et al.* 1996), sled-

mounted (e.g. CSIRO 1994), buoyant array (e.g. Bax and Williams 2001), or self propelled ROV (e.g. Parry *et al.* 2003). Each of these methods has its logistical limitations. Diver operated surveys are effective over small areas, but limited in terms of depth and scope by diver endurance. Diving operations are complex, entail a degree of risk especially in extended operations, and require significant top-side support. Sleds, buoyant arrays (e.g. figure 3.2) and ROVs are generally bulky, complex and expensive pieces of equipment. They require substantial support vessels equipped with winches and cranes to deploy the gear and generators to power it. Because of the expense associated with operating large vessels and / or teams of divers, video sampling, in spite of its advantages, has been viewed as expensive.

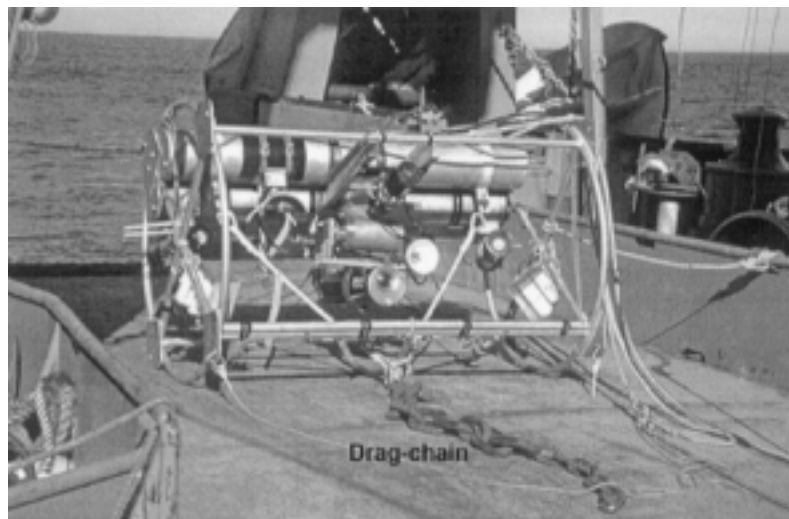


Figure 3.2: Example of buoyant video array on RV Southern Surveyor
Source: Barker *et al.* 2001. The array weighs approximately 170 kg

It was therefore an operational aim of this study to develop an inexpensive method for video survey. This involved two main strategies – keep it small, and keep it simple. In practise this meant adapting readily available off-the-shelf technology to the task, rather than custom built oceanographic hardware.

The array (Figure 3.3) supported a small, high quality, video sensor. These have recently become widely and inexpensively available with the growth in home security systems. The unit used was a 12v “lipstick cam” delivering high resolution (480 lines) colour images in PAL format from a sensor only 7 cm long and 2 cm in diameter (Figure 3.4a). An underwater housing for the camera was fabricated using high-pressure 4 cm diameter PVC pipe and plumbing fittings, available from hardware outlets. The camera was mounted on a lightweight riveted aluminium frame. The unit was powered, and the video signal returned to the surface, via a 3-core cable. Power source was a 12v car battery, and the video signal was recorded on a SONY Digital-8 ‘handycam’, which doubled as a video monitor with its 6 cm LCD screen (Figure 3.4b). Two laser diodes mounted parallel to each other projected dots onto the bottom a constant 0.5 m apart, allowing calibration of the video images and checking for correct orientation and elevation of the array.

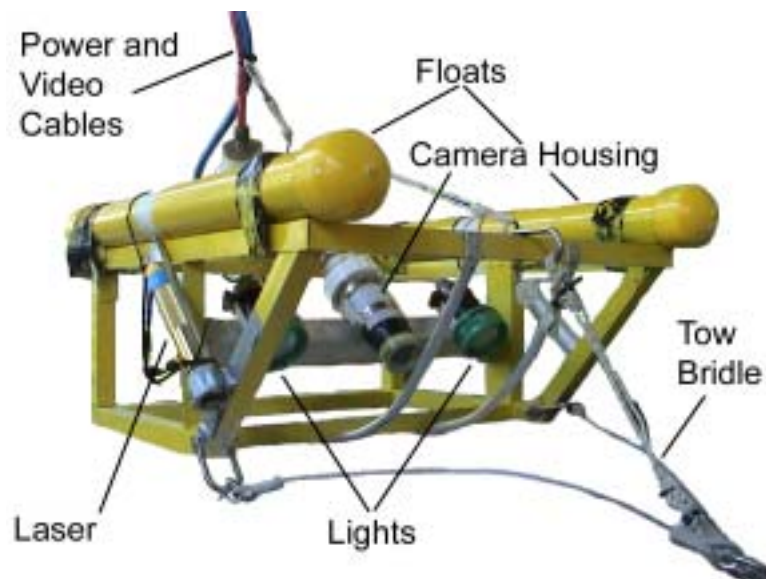


Figure 3.3: Compact video array developed for this study
Weight excluding the dropweight is less than 10 kg

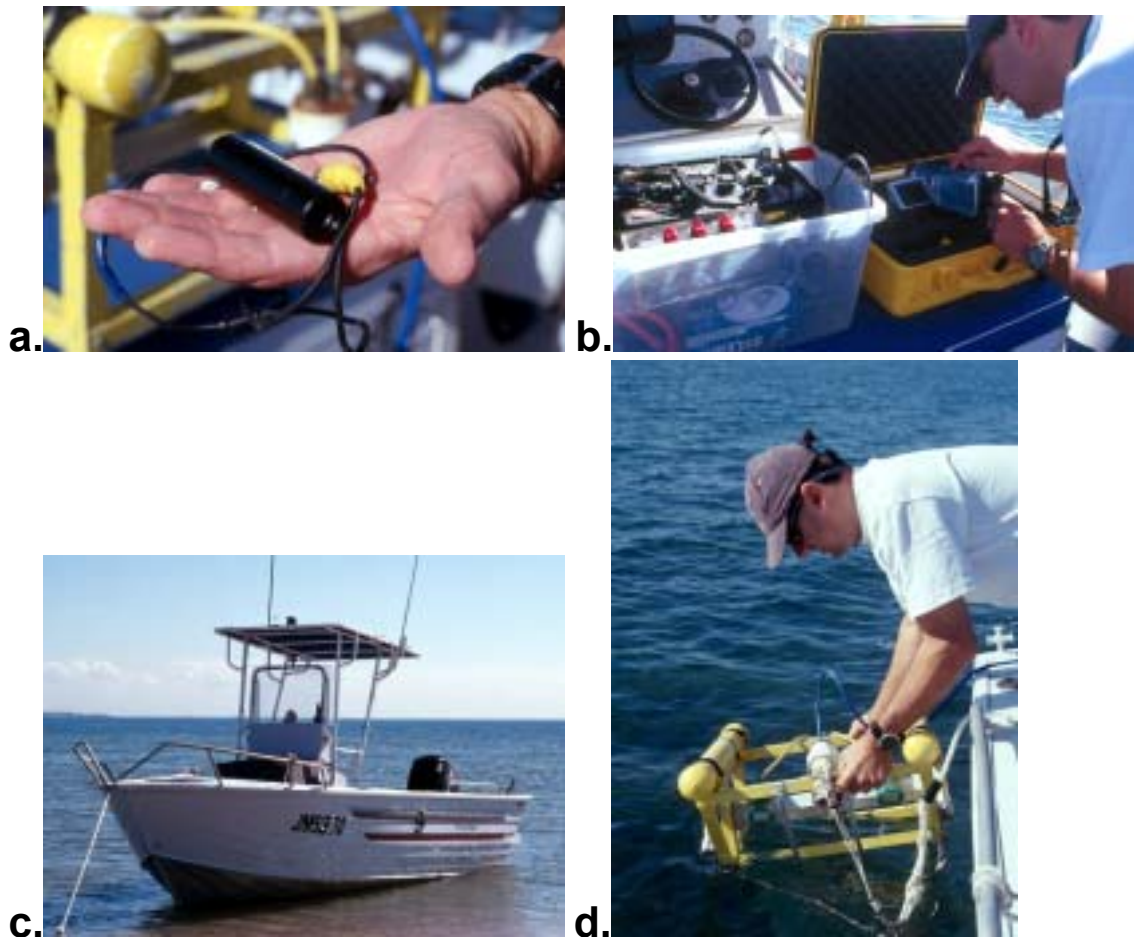


Figure 3.4: Using the video array

- a. High-resolution 480-line PAL “lipstick-cam” video sensor
- b. Power source and video recording on SONY digital-8 handycam
- c. Survey vessel
- d. Lightweight video array allowed easy deployment and recovery

The general arrangement follows the design principles of Barker *et al.* (1999), but much reduced in size and complexity. The overall size of the array was 0.5 m x 0.5 m x 0.3 m and it weighed less than 10 kg, making it easy to deploy and retrieve from a small vessel (Figure 3.4d), in this case a 5.75 m open boat powered by a 90 hp outboard (Figure 3.4c). The array was towed on a 10 m tether behind a 20 kg drop weight suspended beneath the survey vessel approximately 2 m above the substrate (Figure 3.5). The array was slightly positively buoyant and “flew” a constant and adjustable distance above the substrate by trailing a length of light chain, which allowed the array to self adjust to irregularities on the bottom. This arrangement can be used on rough substrates where comparable sled-based equipment is at risk of damage or

entanglement. The array was successfully deployed to a maximum depth of 52 m.

Although 12 volt halogen lights were mounted on the array, in practise they were not used since the video sensor provided excellent resolution even in the low light at 50 m.

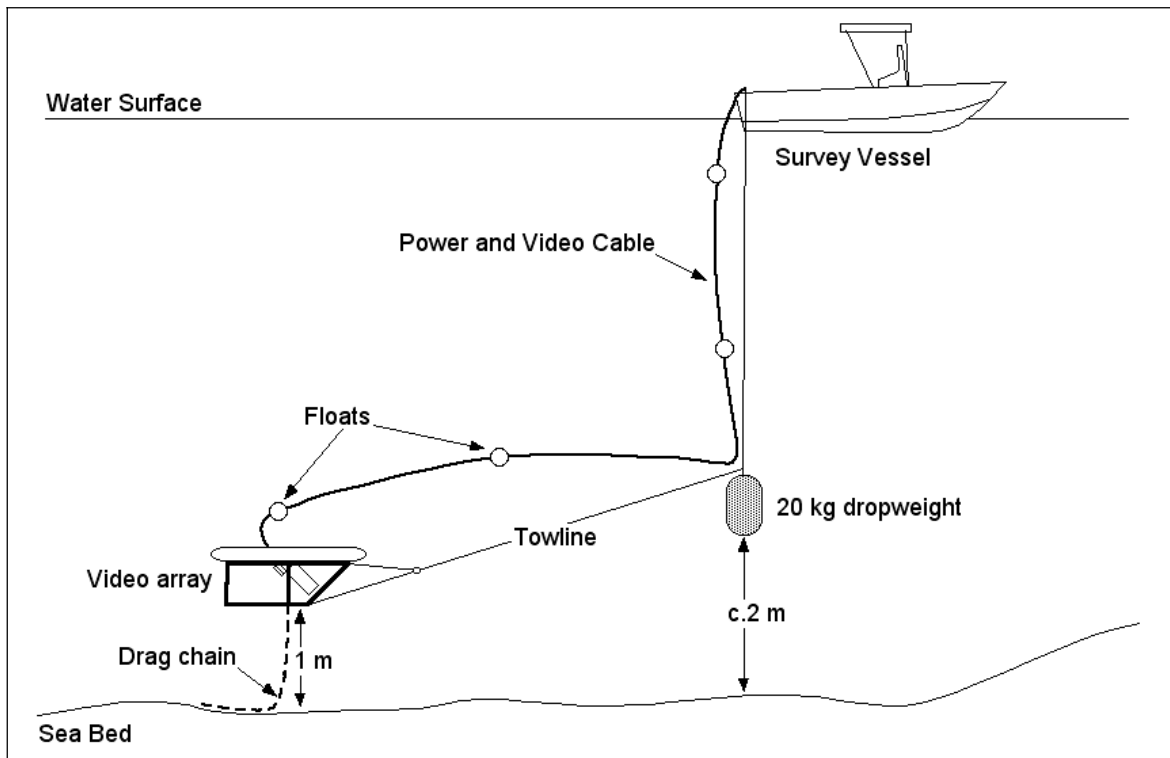


Figure 3.5: Arrangement for deployment of the video array (not to scale)

The field of view of the video camera was calibrated by towing it over a grid marked in 10 cm intervals placed on the bottom. Still images were extracted and used to construct a trapezoidal frame which accurately represented 1 m² frame on the substrate. The sides of the trapezoid are slightly curved as a result of spherical distortion in the source image.

Transects were located using GPS, which gave sufficient positional accuracy (about 15 m) compared to the target mapping scale (10 km). Start position was noted and the transect commenced. Transects were normally effected by allowing the survey vessel to drift with wind and tide until the required distance had been covered, or by towing at very low speed ($< 0.5 \text{ m}\cdot\text{sec}^{-1}$) using a small auxiliary engine. Finish position was then noted, the video recorder turned off, and the video array recovered.

3.2.3 *Image processing and data extraction*

After sampling, video images were captured on a Macintosh G3 laptop computer via IEEE 1349 digital interface to preserve image quality. Images were captured at the highest possible frame rate to avoid overlap whilst maximising coverage of the transect. In practise this was a rate of a frame every 2 to 5 seconds, depending on the speed of the camera over the ground. Each frame series was saved as a Quicktime movie file, and post-processed using digital filters to correct colour balance and improve contrast where necessary.



Figure 3.6: Sample video image showing 1 m² counting frame and 9 point array

Numerical data were extracted from the Quicktime movies by adding counting masks as overlay layers. The 1 m² frame was overlaid, within which all solitary or discrete colonial organisms were counted, as well as arrangements of points for calculating % cover (Figure 3.6). For each frame, the taxa present at each of the points were recorded, and cover calculated by dividing by the total number of points. Arrangements of 25, 16, 9, 4 and 1 points were trialed. Presence and abundance of bioturbating organisms was

quantified by scoring variables for occurrence of biogenically worked sediment surfaces, and counts of burrows or holes in 3 size classes.

3.2.4 *Analyses*

For each transect the biological data took the form of two arrays, each arranged as species (columns) by frames (rows), one row per frame. The first was derived from point data and expressed in the form of the number of points lying on top of each taxon. The second was derived from count data and expressed in the form of the number of individuals or discrete colonies within the 1m² box.

For comparing transects each array was summarised into species (columns) by transects (rows), one row per transect. The first (point data) was expressed as % cover of each taxon for the entire transect, and the second (count data) as density (individuals.m⁻²) for the entire transect.

A range of analyses were carried out on data from an initial set of 10 transects to determine the form of the final sampling, data extraction and analytical design. All the datasets in these initial analyses were not transformed.

3.2.4.1 Combining % cover and density data

The two data types, % cover of benthic plants or colonial organisms, and density of solitary or discrete colonial organisms, generally sample different subsets of the macrobenthos, although there is some overlap. Analyses were carried out to determine the relative discriminatory ability of each data type. Matrices of Bray Curtis similarity between the 10 sites were constructed for % cover, density and both data types

combined. The combined dataset was derived by separately standardising each data type into the range 0 – 1 and amalgamating them. Non-metric multidimensional scaling (MDS) was used to visually compare between-site relationships derived from the three datasets. The similarity matrices underlying the MDSs were compared using the RELATE routine in the Primer analytical package, a type of Mantel's test correlating corresponding cells in pairs of similarity matrices (Manly 1996). RELATE generates a Spearman's rank correlation statistic ρ ranging from 0 (no correlation of ranks) to 1 (perfect correlation of ranks). Because the cells within a similarity matrix are not independent, significance cannot be determined from standard statistical tables, but is estimated using Monte Carlo randomisation.

Analyses could be run on cover and density data in parallel, but for the sake of clarity and simplicity it is far preferable to include both the datasets in a single analysis that draws on the discriminatory power of both, rather than to have two parallel and potentially confusing classifications. However, some method of standardisation is required, since the two datasets have different units (% and ind.m⁻²) with different sensitivities (cover data is relatively independent of the field of view, whereas accurate calibration is crucial to density data). Analyses compared between-site relationships derived from several methods of standardising the datasets to allow them to be combined. Methods compared were: datasets simply combined with no standardisation (none), datasets combined and then uniformly standardised to the range 0-1 (uniform), datasets separately standardised to the range 0-1 and then combined (separate), and datasets standardised using an indexed scaling (indexed). In this last method taxa common to both data types are required. Colonial species where all or most of the colony could be seen in the frame were counted as well as truly solitary or discrete species, although this imposes an additional overhead when extracting numerical data

from the video images. The relative values of the most abundant taxon common to both datasets are then used to standardise the datasets to a common scale. The overlapping taxa are then removed, and the combined dataset uniformly standardised. The effects of the four methods on between-site relationships were visualised using MDS ordinations, and correlation analyses (RELATE) were used to compare the underlying Bray Curtis similarity matrices.

Further analyses investigated the sensitivity of similarity matrices to scaling between cover and density data. Two extreme case datasets were derived from the separately standardised combined dataset, using weightings for cover vs density data of 1:100 and 100:1. A scale difference of up to 10,000 times therefore exists between these extreme case datasets. Correlation analyses (RELATE) were used to compare the two weighted combined datasets with the unweighted, separately standardised, combined dataset.

3.2.4.2 Replication

One assumption of a 5 km spaced grid array is that each point sampled reflects the species and abundance within a reasonably large area (500 m radius) compared to the distance between sample points (5 km, so a 10:1 between:within ratio). A conventional sampling regime would characterise each site by using replicate transects randomly placed within 500 m of the target site. However, given that within-site variability was not of interest for the purposes of the overall habitat classification, and that there are clear advantages in minimising the number of times deep water gear has to be deployed and recovered (in terms of time, effort and risk of gear damage), analyses were conducted to determine if a single 500 m transect would be sufficient as a sampling unit. Five 100 m transects were randomly placed within 500 m of the centroid of a

single 500m transect. Data from the short transects were pooled and compared to those from the single long transect.

A conventional multivariate ANOVA approach was not valid because the data violated assumptions of normality. Therefore a one-way Analysis of Similarity (ANOSIM) from the Primer analytical package was used to determine whether there was significant difference between the 5 replicate short transects and the single long transect. For the purposes of the ANOSIM analysis, the long transect was considered to comprise 5 sequential 100 m transects, since values from a single transect allow no estimate of variance. Thus a 2 sites x 5 replicates design was employed. The analysis was also performed using the values of the first 50 frames of each of the short transects with the first 250 frames of the long transect to eliminate any bias associated with different numbers of frames per transect. ANOSIM generates a test statistic R which ranges from -1 to +1. Values close to 0 indicate that the null hypothesis of no difference between sites is accepted. Large positive values indicate a difference between sites, and large negative values indicate higher similarity across sites than within sites (Clark and Warwick 1994). Significance is estimated by Monte Carlo randomisation since the test is based on a similarity matrix whose cells cannot be considered independent.

As a further check, paired Pearson's product moment correlation analyses were used to examine the similarity between the single long transect and pooled short transects across the taxon list. Three sets of analyses were conducted. All frames from the short transects were pooled (n = 585) and compared to all frames from the long transect (n = 262). Since the short transects had unequal numbers of frames (range 82 - 157, mean = 117), there is potential for bias. Therefore a second analysis pooled the mean values from each of the short transects and compared these to the long transect. A third

analysis compared the pooled values of the first 50 frames of each of the short transects with the first 250 frames of the long transect.

Since the total number for frames from the long transect (262) was less than half that of the pooled short transects (585), the impact of this lower sampling effort on species richness was assessed. For rare or sparsely distributed species, differences in the area sampled can have a major influence on relative abundance. Therefore, species richness from the single long transect was compared to that from pooled short transects.

The basic analytical method of the video sampling program is to compare the relationships between sites by placing them relative to each other in multidimensional (multi-taxon) space to determine relationships of similarity. Therefore, an analysis was carried out to determine whether points representing the various estimators of the test site (pooled short transects and long transects) were co-incident, or nearly so, relative to an array of other points in multi-dimension space. An MDS ordination plot was constructed based on Bray-Curtis similarity, which plotted all estimators of the test site relative to 6 other sites.

3.2.4.3 Extraction Intensity (% cover data only)

Effect of reducing number of points

In deriving % cover from video, the number of points that have to be counted in each frame is a major determinant in the time taken to analyse the video images. Analyses were therefore carried out to determine the minimum number of points per frame required to give the same between-transect relationships as the maximum number sampled. Symmetrical arrays (to give even cover over the 1 m² frame) of 25, 16, 9, 4

and 1 point per frame were used. Extraction at 25 points per frame was soon abandoned as unwieldy, with so many points in the frame that recognition of taxa was impaired. Point data were therefore extracted at 16, 9, 4 and 1 points per frame. Derived % cover for each site was compared using correlation analysis. Pearson product-moment correlation was used because it is a more stringent test than other correlation measures, in that high correlation demands the compared curves be close to parallel (Zar 1999).

Relative effect of reducing number of frames

In a single 500 m transect, over 250 non-overlapping frames may be extracted from the raw video. The number of frames analysed is clearly another determinant in the time taken to extract data from the video images. Analyses were used to determine the minimum number of frames within each transect to give the same between-transect relationships as the maximum number sampled. The total set of frames was compared with progressively halved datasets comprising every 2nd, 4th and 8th frame. These were also compared to progressively halved datasets comprising 16 (all) points per frame, 8, 4, 2 and 1 point per frame. Both methods of data reduction involve progressive loss of the same proportions of the dataset. Matrices of Bray Curtis similarity (based on % cover only) were constructed for each combination of data reduction, and compared to the entire dataset using correlation analysis (RELATE). The correlation values gave a relative measure of the loss of accuracy associated with each method in losing the same proportion of the dataset.

3.2.4.4 Discriminatory ability

Runs from qualitatively different habitats were compared to verify that the video method was able to effectively discriminate between them. In the same analysis,

repeated runs at the same site were compared to verify that the video method found them to be identical. Table 3.1 represents the set of sites selected to test the discriminatory ability of the video method.

Table 3.1: Transects selected for discriminatory ability analysis

Transect	Qualitative description
A	<i>H.spinulosa</i> / sponge bed (replicate)
B	<i>H.spinulosa</i> / sponge bed (replicate)
C	<i>H.spinulosa</i> / sponge bed (replicate)
D	Soft coral bed
E	Soft coral bed
F	Bioturbated community, no cover
G	No cover, sparse mobile fauna
H	Sparse cover, sparse mobile fauna

For the video method to be considered a useful tool, numerical analysis would group the the replicate transects of the same habitat types together, whilst clearly separating those of different habitat types. Sites A, B and C were replicate parallel transects with start points less than 50 m apart. Sites D and E were in qualitatively similar areas, but separated by 500 m. Sites F, G and H were similar only in that they were quite depauperate, with little cover and only a few mobile taxa in low numbers. Between-site relationships were visualised using cluster analysis (group average sorting) and MDS ordination based on Bray Curtis similarity.

3.3 Results

3.3.1 Data combination

3.3.1.1 Relative importance of data types

Correlation analyses showed that while there were similarities, the correspondence between similarity matrices derived from % cover and density was not good, highlighting the fact that cover and density data have different and incomplete discriminatory properties (Table 3.2). Cover data failed to discriminate between sites characterised by different mobile or bioturbating fauna, whilst density data didn't discriminate well between partly or mostly covered sites. Density data also correlated far better with the combined dataset than did % cover data, indicating that it is more important in discriminating between sites than is % cover, at least in the test datasets. The combined dataset showed the improved discriminatory ability of density data when added to cover data.

Table 3.2: Correlation between data types

Spearman's rank correlation (ρ) between similarity matrices derived from cover, density and combined datasets. Significance values derived from Monte Carlo randomisation are given in parentheses

	% Cover	Density
Density	0.35 (0.03)	-
Combined	0.19 (0.15)	0.86 (0.00)

It can be seen that the addition of density data improves discriminatory capability by separating sites F and G (Figure 3.7), unvegetated sites but with very different degrees of bioturbation (density data includes burrow counts in three size classes). The addition of density data also tightens the HIJ group, which consists of three replicate sites (Figure 3.7). It seems therefore clear that both types of data are required to give the most complete picture of patterns in the distribution of macrobenthos.



Figure 3.7: Comparative MDSs for % cover only, density only, and combined datasets. Note that in the density plot, site I is co-incident with site H.

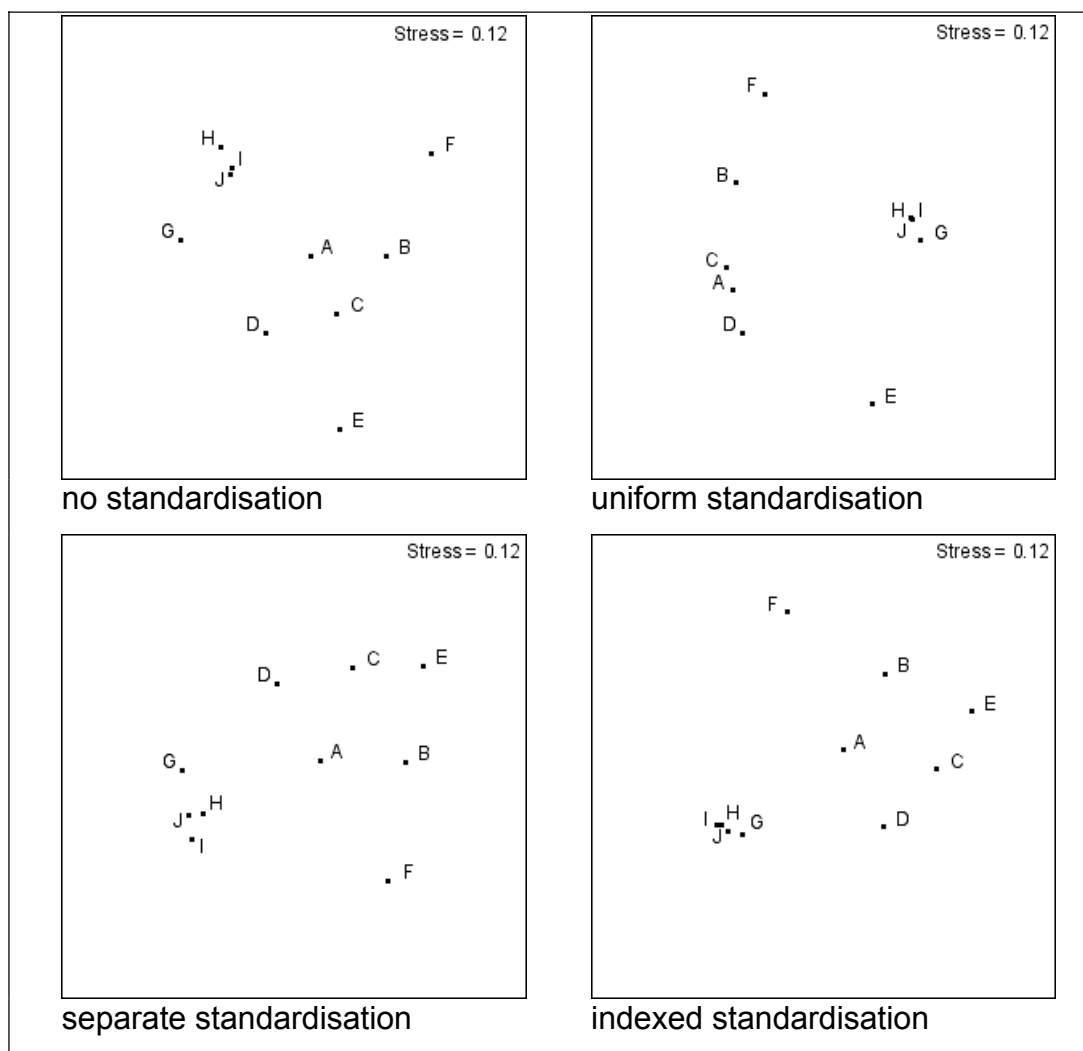
3.3.1.2 Methods of standardisation

Perhaps surprisingly, there is little difference between the methods of standardisation to combine the datasets. Correlation values for comparisons between similarity matrices derived from each type of standardised dataset are all > 0.90 (Table 3.3) and highly significant. Visually, the MDSs are very similar, the main difference being in how tightly the HIJ group (3 replicates) is clustered, and the separation of G (a qualitatively very different site) from it (Figure 3.8).

Table 3.3: Correlation between methods of standardisation

Spearman's rank correlation (ρ) between Bray-Curtis similarity matrices derived from combined datasets using none, uniform, separate and indexed standardisation. All correlations were highly significant ($p < 0.001$, derived from Monte Carlo randomisation)

	None	Uniform	Separate
Uniform	0.99	-	
Separate	0.93	0.93	-
Indexed	0.94	0.94	0.97

**Figure 3.8:** Comparative MDSs of none, uniform, separate and indexed standardisation

This result indicates that between-site relationships were relatively insensitive to differences in scaling between data types, and that therefore relationships were driven more by the taxa present than by relative abundance, even though these data were not transformed.

3.3.1.3 Sensitivity to scaling between data types

The correlation values (Table 3.4) show that the similarity matrix derived from the unweighted combined dataset is virtually identical to that derived from the 1:100 weighted dataset (that is, where standardised density was multiplied by 100). This is consistent with the previous analysis in indicating that the patterns of similarity are driven more by density than by % cover data. However, correlation between the similarity matrix derived from the unweighted (1:1) combined dataset and that derived from the 100:1 weighted dataset, although lower than the 1:1 vs 1:100 correlation, is also good, and highly significant. Moreover, the correlation between the two extreme case datasets is also quite good, and highly significant.

Table 3.4: Correlation between weighted datatypes

Spearman's rank correlation (ρ) between similarity matrices derived from 1:1 (cover:density), 1:100 and 100:1 standardised combined datasets. All correlations were highly significant ($p < 0.001$, derived from Monte Carlo randomisation)

	1:1	1:100
1:100	0.99	-
100:1	0.76	0.72

It is therefore clear that between-site relationships for these sites are relatively insensitive to issues of scale between % cover and density data. It can be concluded that there is no particular advantage in an indexed form of data standardisation, and there is no need to collect overlapping data from the video footage. It is logical, and seems prudent, to place equal weight on each dataset by using the separate (1:1) standardisation of % cover and density data, but the results of this section indicate it is not critical to the analysis.

3.3.2 Replication

The ANOSIM analysis tests the hypothesis that variation between sites is significant. A non-significant value of R, close to 0, indicates that sites are not different. For both the all-frames and the 250 frames analyses, the ANOSIM results were clearly non-significant ($p > 0.05$, Table 3.5) and values of R very close to 0, indicating that the single 500 m transect was not significantly different to 5 randomly placed 100 m transects.

Table 3.5: Analysis of Similarities (ANOSIM) between single long and pooled short transects

Analysis	R	<i>p</i>
All frames	-0.01	0.486
first 50	-0.01	0.516

Pearson's product moment correlation values (Table 3.6) for all three analyses were high, 0.85 or above, and highly significant ($p < 0.001$). Therefore the patterns of relative abundance of taxa between the long transect and the pooled short transects were very similar. There appears to be no appreciable effect for using a single long transect rather than multiple replicates.

Table 3.6: Correlation between long transect and pooled short transects for relative abundance of taxa. Pearson's product moment correlation

Analysis	r	<i>p</i>
All pooled frames	0.86	<0.001
Pooled mean Frames	0.87	<0.001
250 pooled frames	0.85	<0.001

An analysis was conducted to determine whether there was any appreciable difference between species richness from the single long transect compared to pooled data from

the five 100 m transects. Species richness was equal or higher in the single long transect compared to the pooled short transects (Table 3.7).

Table 3.7: Comparison of species richness from the single 500m transect and five 100m transects

Transect	No. spp.
Long, All frames	20
Long, 1 st 250 frames	18
Short, Pooled all frames	18
Short, Pooled 1 st 50 frames	11

The MDS plot (Figure 3.9) shows that the 5 estimators of the test site (all frames from the long transect, first 250 frames from the long transect, all frames from the pooled short transects, pooled means of short transects, pooled first 50 frames from each short transect) were virtually co-incident in multidimensional space, relative to the other sites plotted. Stress value in the MDS was acceptably low (0.10). Clearly there is no effect on between-site relationships of using the single long transect compared to multiple short transects.

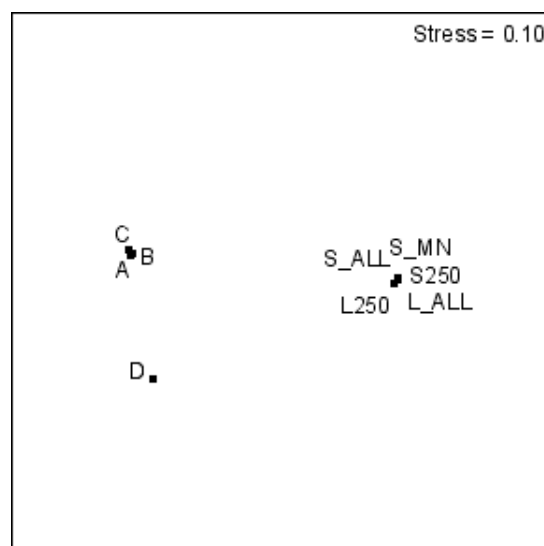


Figure 3.9: MDS plots of successive estimators of test site, relative to 4 other sites. Test site estimators designated L_ALL (long transect, all frames), L250 (long transect, first 250 frames), S_ALL (pooled short transects, all frames), S_MN (pooled means of short transects, all frames), S250 (pooled short transects, 50 frames each). Comparative sites designated A,B,C (replicates) are from seagrass and sponge dominated location >5km distant from test site; D is from bioturbated site >5km distant from test site. Labels have been separated for clarity

3.3.3 *Extraction intensity*

3.3.3.1 Effect of decreasing points per frame

Correlation values for this analysis were uniformly high and highly significant, with every value > 0.90 ($p < 0.001$) (Table 3.8). All correlation values for 4 points per frame or greater are > 0.99 . The between-site relationships based on estimates of % cover derived from reduced numbers of points per frame are clearly very consistent even when only 1 point is used, and at 4 points or 9 points they are virtually identical. Clearly, in this analysis there is very little loss of accuracy associated with extracting point data at 9, 4 or even 1 points per frame compared with 16.

Table 3.8: Effect of decreasing points per frame

Pearson's product moment correlation for 16, 9, 4, and 1 points / frame. All correlations are highly significant ($p < 0.001$)

	16	9	4
9	0.99	-	
4	0.99	1.00	-
1	0.94	0.93	0.94

3.3.3.2 Relative effect of decreasing number of frames or points per frame

The dataset was clearly more robust when halved by dropping points per frame than when dropping frames (Table 3.9). However, it could sustain being halved by either method without significant difference from the entire dataset. Reduction could not be sustained beyond one half when dropping frames, or beyond one quarter when dropping both points and frames (Figure 3.10).

Table 3.9: Relative effect of methods of data reduction

Spearman's rank correlation (ρ) between similarity matrices derived from progressive halving of the datasets with the complete dataset. Progressive halving was either by reducing number of points per frames, or by reducing the number of frames. Significance values estimated by Monte Carlo randomisation are in parentheses. *nt = Not tested, since higher value was non-significant
 Shaded cells indicate non-significant results or correlations not tested

Points per Frame	All Frames	Every 2 nd Frame	Every 4 th Frame
16	(test sample)	0.90 (0.016)	0.333 (0.117)
8	0.98 (0.007)	0.88 (0.025)	0.624 (0.098)
4	0.84 (0.010)	0.66 (0.089)	nt
2	0.77 (0.033)	nt	nt
1	0.65 (0.090)	nt	nt

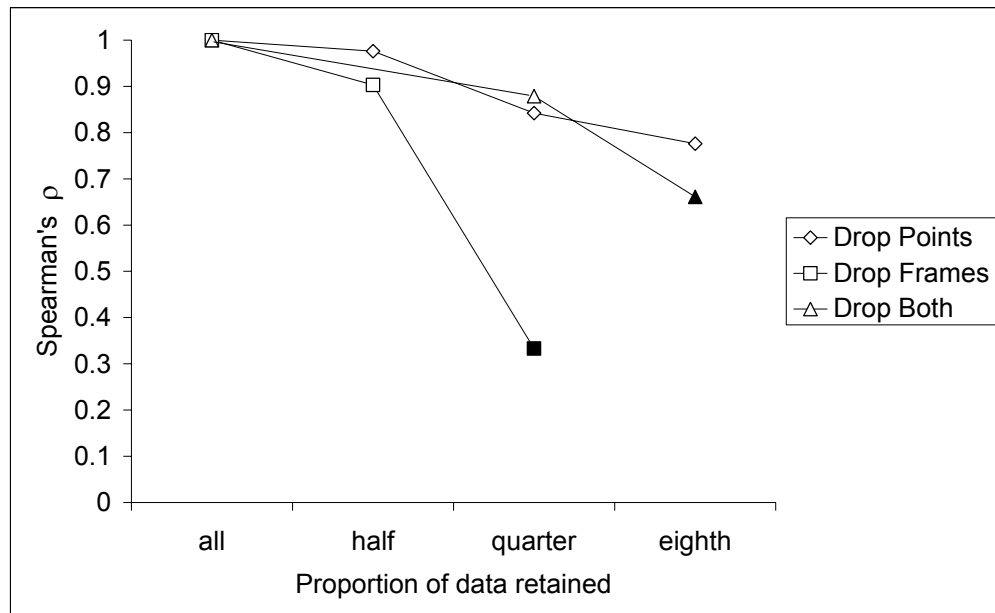


Figure 3.10: Comparison of dataset reduction methods
 Filled symbols denote non-significant correlations

This analysis has examined the impact of data reduction on point data extracted to estimate % cover. Clearly, reducing the dataset by dropping frames would have the additional effect of removing the density data for each frame removed. This has not been assessed in this analysis, it can be assumed that the effect on accuracy (in terms of the correlation with the complete dataset) would be a further significant reduction. Therefore, it appears that reducing effort in extracting data by dropping frames is not an option for the full study.

3.3.4 Discriminatory ability

Cluster analysis (Figure 3.11) showed that the three replicate sites (ABC) were grouped together at high similarity levels. Similarly, sites D and E, which were qualitatively similar but spatially separate, were grouped together at a relatively high similarity level. The MDS ordination (Figure 3.12) is consistent with the cluster analysis.

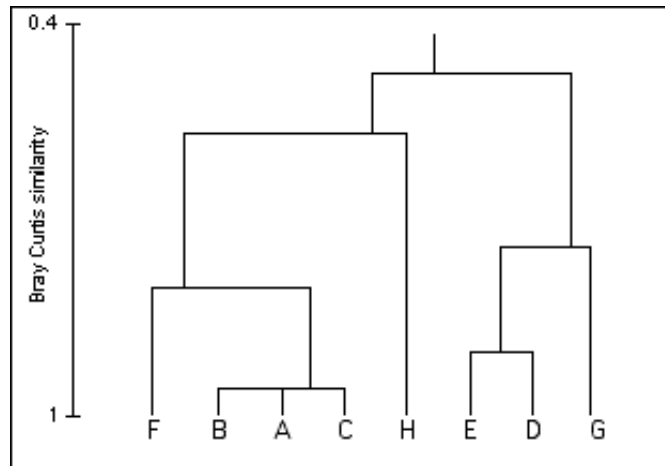


Figure 3.11: Cluster analysis dendrogram of discriminatory ability

Bray Curtis similarity with group average sorting. Site identifiers correspond to the habitats listed in table 3.1

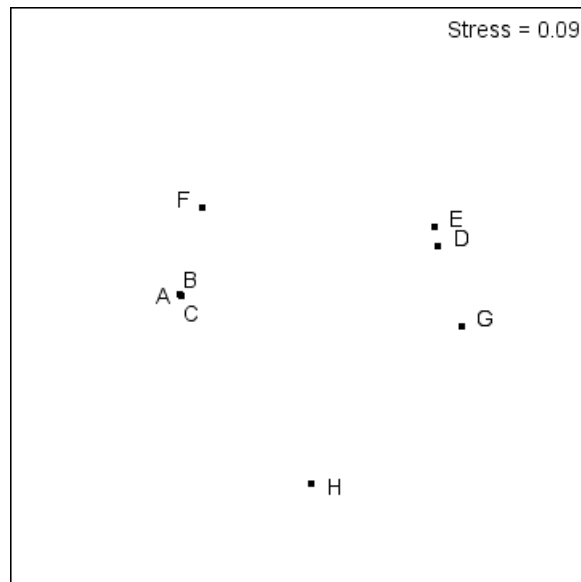


Figure 3.12: MDS plot of discriminatory ability from Bray Curtis similarity matrix

Site identifiers correspond to the habitats listed in table 3.1. Labels for sites A, B and C have been separated for clarity

The three replicate sites (A,B,C) were virtually co-incident on the plot, and clearly separated from the other sites. Sites D and E, as in the cluster analysis, were more

similar to each other than any other sites. Based on this group of test sites, between-site relationships found by numerical analysis of data obtained by the video sampling method closely matches relationships predicted from qualitative observation.

3.4 Conclusions

3.4.1 *Sampling Design*

Between-site relationships based on % cover and density data were clearly different. They sample different components and when combined provide additional discriminatory ability than either data type used alone. Density data appears to have greater influence than cover data in this set of sites. The fact that patterns of similarity based on the separate data types are different shows that for a more complete picture of diversity in macro-benthic habitats for the broader study area, it is desirable to extract both types of data for the full study, and to combine them into a single dataset for analysis.

Comparisons of methods of combining the datasets showed that derived patterns of similarity are quite insensitive to issues of scaling between data types. It is prudent to adopt a separate, but unweighted standardisation technique, but this does not appear to be critical to the analysis.

The approach of replication through length by using a single long transect, with considerable practical benefits, gave equivalent results to the more conventional approach of using multiple randomly placed replicates. All the estimators of the test site, whether from single long transect or multiple short transects, were essentially coincident in multidimensional space, and clearly separate from other sites. This was consistent across several analyses, and indicates that this sampling design is valid for the full study.

There is clearly a greater loss of accuracy in reducing data extraction effort by dropping frames, rather than by dropping points. Additionally, the effect of the loss of density

data by dropping frames was not assessed, but can be assumed to entail an additional loss of accuracy. A conservative approach to data integrity dictates therefore that all frames be analysed for the full study. It is clear that estimating % cover from 4 or 9 points per frame gives virtually identical results to 16 points. The same conservative approach dictates that % cover be estimated from 9 points per frame in the full study.

The correlation and MDS analyses indicated that the survey method using the video array and data extraction techniques tested here was a valid tool for discriminating between different sites while preserving the relationship of similar sites. Replicate sites were found to be co-incident in multidimensional space, and clearly separate from qualitatively different sites.

3.4.2 Benefits of video

The video array designed and tested for this study fulfilled the operational requirements of the study. It used inexpensive, off-the-shelf, consumer-level technology combined with easily available materials. The array was lightweight (< 10 kg) and easy to use from a small vessel, and therefore made the survey program a cost-effective operation.

The relative performance of remote video versus diver census in surveying soft bottom habitats was not investigated in this study, since video was clearly the only method that would permit the study to proceed on the scale desired. Miller and Cheshire (1999) compared the two methods and concluded that, in spite of its poorer taxonomic resolution (see also Berkelmans 1992, Carleton and Done, 1995) the video method matched diver surveys well in detecting patterns at the community level. They also assessed the cost effectiveness of video versus diver sampling and concluded that video represented a 15% saving in cost, with significant logistical advantages as well.

However, their trial was structured so that the video survey design matched a typical diver-based survey design, with multiple short transects (Miller and Cheshire 1999). The current study realised far greater cost-effectiveness, in part because it was structured to take advantage of the strengths of video sampling, viz; essentially unlimited endurance allowing long transects, and depth capability beyond the range of divers.

Typically, four to six 500 m transects, each 1m wide, could be sampled in a single person-day, including towing the sampling vessel to and from the nearest boat ramp, launching and retrieving the vessel, and transit to and from the sampling area. Extracting the data in the laboratory took approximately the same amount of time as sampling. So 2,000 to 3,000 m² was sampled, and data extracted and entered into the database, in 2 person-days. In comparison, a typical SCUBA-based survey to cover the same area (2,000 – 3,000 m²) would take 21 – 30 person-days (conservatively estimating 2 divers, 1 boat person, 3 x 100 m² transects / day) and be effectively limited to half the depth range.

Chapter 4 Accuracy of Abiotic Surrogates for Marine Habitat

Mapping

4.1 Introduction

Planning and design of Marine Protected Areas (MPAs) over the last decade has increasingly adopted the concept of representativeness as a major criterion, including its use in IUCN guidelines for highly protected areas (IUCN 1994). Representativeness in this case means the desire of planners to incorporate samples of each habitat, landscape or community type, depending on the scale of the MPA and the issues being addressed.

Representation can be assessed within a nested series of scales from continental (1000 km) to site (1 km). Kelleher *et al.* (1995) produced a continental scale classification of marine environments. In some parts of the world, including Canada, Australia and South Africa, regional scale (100 km) classifications have been produced as a basis for establishment of MPA systems (e.g. Parks Canada 1993, Hockey and Branch 1997, IMCRA Technical Group 1998, Zacharias and Howes 1998).

For highly protected areas (Category II or above, IUCN 1994), which contain the core values of most MPAs including multiple-use examples, polygons are generally drawn at the local scale (10 km) or smaller (Stevens 2002). Planning for, or assessment of, representation cannot logically be carried out without the crucial step of habitat mapping at the requisite planning scale. Classification and mapping of marine habitats at the local scale has not been widely done, generally due to the (actual or perceived) lack of available information, and the expense associated with subtidal surveys.

Therefore, current classifications done at this scale (e.g. Zacharias *et al.* 1999) rely heavily on abiotic surrogates, rather than directly reflecting biological distributions.

Abiotic data lend themselves well to habitat classification exercises because they often come in mapped form (e.g. from remote sensed imagery), or are already georeferenced (e.g. sediment samples with co-ordinates attached). A recent trend is the use of sophisticated sonar systems to classify the seabed on the basis of physical properties deduced from analysis of the returning acoustic signal (e.g. Davies *et al.* 1997). In basing habitat mapping for the purpose of representation on abiotic surrogates, it is implicitly assumed that the surrogates predict, or at least correlate with, patterns of biological distributions reasonably well. This assumption is not often tested.

In some cases, abiotic factors have proved to be good predictors. Long *et al.* (1997) found that current stress predicted the distribution of epibenthos in Torres Strait (between Australia and New Guinea). Zacharias and Roff (2000) reported that a combination of salinity, temperature and fetch predicted intertidal species richness in British Columbia (on the Canadian west coast). Both of these studies were at the regional (100 km) scale, and are not directly applicable to representation of habitats within MPAs at the local scale.

Recent calls in the literature for improved rigour in MPA design (Agardy 1995, Stevens 2002) demand reasonable confidence in the accuracy of habitat mapping for representation. If abiotic surrogates for patterns of biodiversity are used, two types of errors are possible: *false homogeneity*, where sites with similar or identical abiotic (geophysicochemical) conditions support different biological distributions, or *false heterogeneity*, where sites with different abiotic conditions support very similar

biological distributions. Both types represent an inability of analyses that are based on abiotic conditions to accurately model biological distributions. Habitat mapping (and subsequent management decisions) based on abiotic factors subject to these errors will necessarily be inaccurate and misleading. This may be ameliorated by extensive ground truthing, however in subtidal areas this is expensive and logistically difficult. It could be argued that the additional survey effort required to accurately ground truth the predictive power of abiotic surrogates would be better spent directly surveying the biota, since they are of primary interest in planning for representation in MPA design.

Remote underwater video survey provided an opportunity to compare biological and abiotic data at the scale used by MPA designers and managers. The aims of this chapter were to:

- Determine the predictive ability of abiotic factors for observed patterns in biological distributions.
- Quantify the frequency of errors of false homogeneity and false heterogeneity and thereby;
- Assess the utility of abiotic information in habitat mapping for representation in MPA design at this scale.

4.2 Methods

4.2.1 Study site

Moreton Bay (27°15'S, 153°15'E) on the east coast of Australia, is a shallow coastal embayment, covering approximately 1,500 km² (Figure 4.1). The bay is protected on the eastern side by Moreton and North Stradbroke Islands, with its main ocean entrance in the north east. It is approximately 35 km wide at the widest point, and narrows in the south into a maze of mangrove-fringed waterways. Most of the bay is less than 15 m deep, but reaches depths greater than 25 m in the north eastern part, adjacent to the main ocean entrance. The drainage catchment is substantial (21,000 km²) and contains urban centres with populations totalling about 1.5 million people (Dennison and Abal 1999). The western parts of the Bay are heavily influenced by terrestrial inputs (Costanzo *et al.* 2001) dominated by inputs from the Brisbane River (Eyre *et al.* 1998) plus 3 smaller river systems. The eastern side is essentially under oceanic influence (Udy and Dennison 1997), with ocean entrances in the north and east.

The bay and adjacent offshore waters are included within Moreton Bay Marine Park, a zoned multiple-use MPA declared in 1993 and managed to “provide for the ecologically sustainable use of Moreton Bay Marine Park and to protect its natural, recreational, cultural heritage and amenity values.” (Anon 1997, page 9).

Sample sites for both abiotic and biological data were set out in a staggered 5 km spaced array covering the central, eastern, and southern parts of the bay (Figure 4.1). The 5 km spacing was chosen to facilitate construction of polygons of relative similarity at the local (10 km) scale. The western portions of the bay were not included because they are generally too turbid for video-based survey.

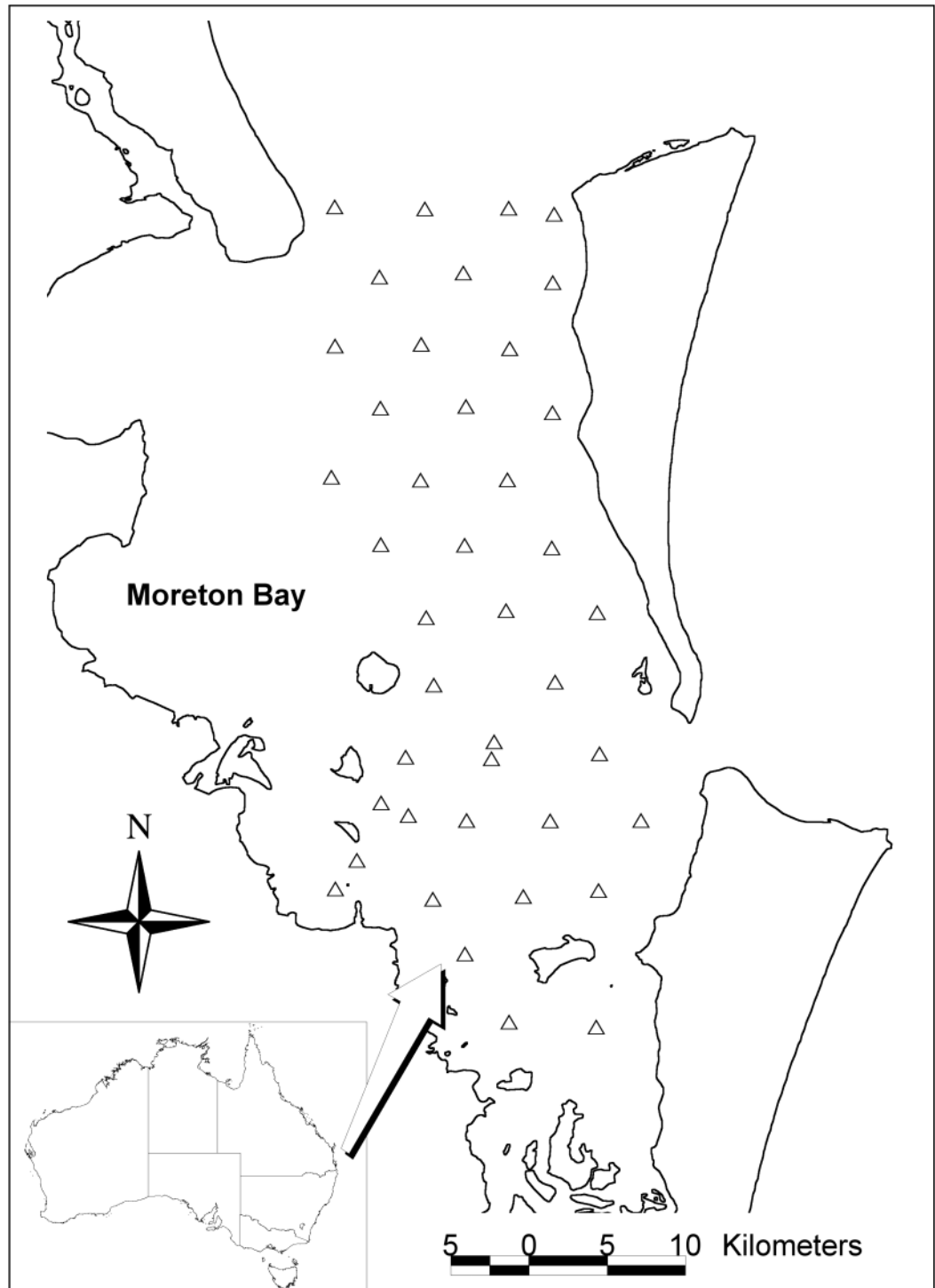


Figure 4.1: Location of study area with sample sites

4.2.2 *Abiotic datasets*

Contemporary studies were examined to determine a typical suite of abiotic factors used to construct habitat classifications (e.g. Zacharias *et al.* 2001, Bax and Williams 2001).

It should be noted that such studies may be carried out by Government agencies or

NGOs, and are often only reported in internal documents or limited circulation reports (e.g. PISCO 2002, Marine Reserves Working Group 2000).

Parameters could be subdivided into three themes; those concerned with the nature of the substrate (depth, sediment type [mud, sand, gravel, rock], sediment constituents [e.g. carbonate fraction]); the nature of the water body overlying the substrate (temperature, pH, salinity, turbidity), and influences on the local environment (exposure, current velocities, proximity to major river entrances, nutrient inputs). These operate at a range of scales and not all were relevant to this study. From examining the suitable information available for Moreton Bay, a suite of parameters was selected as the basis for an abiotic classification of the bay.

The parameters selected were: depth, mud content of sediment, sand content of sediment, reversing tidal current velocity, residual current velocity, distance from Brisbane River mouth, distance from northern oceanic entrance, distance from eastern oceanic entrance (South Passage), fetch from southeast direction, and fetch from northeast direction (major prevailing winds).

The 41 sites used for the biological surveys (locations determined as the mid-point of each transect – see field methods below) were scored for each of the variables. From this initial matrix, variables were combined or eliminated to give approximately even weight to variable types, and avoid redundancy. Correlation analyses were used to highlight areas of potential overlap. Mud and sand content were reduced to a single variable since they are almost exactly the reciprocal of each other, and the second therefore adds no additional information to the analysis. The two current parameters were highly correlated and subsequently reduced to a single variable. The distances to

the two ocean entrances were reduced to a single variable, weighted by the ratio in cross-sectional area between the northern and eastern entrances, to allow for the much greater flow volume through the northern entrance (Dennison and Abal 1999). Fetch variables were combined (root sum of squares) to give an index of exposure. The final abiotic matrix was therefore 41 sites by 6 variables (Table 4.1) all standardised to the range 0 – 1 to give equal weight.

Table 4.1: Variables for abiotic classification

Dn = direct measurement from site to closest point on closing line across northern entrance

Dsp = direct measurement from site to closest point on closing line across south passage

R = ratio of approximate cross-sectional areas (south passage / northern entrance)

Fne = distance to nearest land or drying bank in NE direction

Fse = distance to nearest land or drying bank in SE direction

Variable	Units	Definition	Source
Depth	m	Corrected to low water datum	As measured
Mud fraction	%	Fraction of total sediment, 10 classes, spatial extrapolation (contour plot) from point data.	Dennison and Abal 1999
Current Velocity	m s ⁻¹	Five classes	McAlister and Patterson 1999
Distance to River	km	Direct measurement from site to midchannel point at Brisbane River mouth	AUSLIG 1:250,000 digital mapping
Distance to Ocean	km	Dn + (Dsp*R)	AUSLIG 1:250,000 digital mapping
Fetch	km	$\sqrt{(Fne^2+Fse^2)}$	Queensland Dept of Transport charts

Some parameters that have been used in other studies (e.g. Zacharias *et al.* 2001), such as tidal range, salinity and temperature, were not used because they were considered to be either almost uniform over the whole of the study area, or functions of other variables already included (e.g. Distance to Ocean). Other common variables (slope and form of rocky shores) are applicable to intertidal studies but not to the present, wholly

subtidal, and wholly soft-bottom, investigation. Terrestrial influences such as nutrient loads and pollutant volumes were not included because several studies (Costanzo *et al.* 2001, Gabric *et al.* 1998, Dennison and Abal, 1999) show that these factors rarely penetrate into the eastern side of the bay, the effects remaining concentrated on the western bay.

4.2.3 *Biological datasets*

4.2.3.1 Field methods

Surveys were carried out using a towed self-adjusting array developed especially for the study following the design principles of Barker *et al.* (1999) but much reduced in size and complexity. It had the advantage of being small and lightweight, and therefore easily deployed from a small vessel, in this case a 5.75 m open boat. It was relatively low-cost, using off-the-shelf consumer-level technology, and had virtually no impact on the area surveyed.

The array was towed on a 10 m tether behind a drop-weight suspended beneath the survey vessel. It was slightly positively buoyant but maintained a constant distance of 1m above the bottom by trailing a 2 m length of light chain. This system allowed the array to self adjust to irregularities on the bottom, and coped better with rough terrain than sled-mounted arrays, which are at risk of entanglement and damage. The array was also smaller and lighter than a sled of similar elevation, and more flexible, in that it could be configured to fly at different elevations by changing the weight of the drag chain.

The video sensor was a high resolution (480 lines) colour analogue “lipstick camera” in PAL format. The unit was powered and the video signal returned to the surface via 3-core cable. Video was recorded at the surface on a Sony Digital-8 handycam that doubled as video monitor with its 6.5 cm colour LCD screen. Two laser diodes projected dots onto the bottom a known and constant distance apart to allow calibration of the video images, and check for correct orientation and elevation of the array.

Preliminary studies with this video sampling method showed that a single long transect gave equivalent results in species richness, assemblages and abundance to the more conventional technique of using multiple replicate transects. This “replication through length” approach had substantial practical advantages for boat-based surveys, and allowed a single 500 m transect to be run at each site. Transects were located using GPS, which gave sufficient positional accuracy (about 15 m) compared to the spacing of the sample points.

4.2.3.2 Data extraction

Digital video was captured at 1 frame every 2-5 s, the frame rate giving maximum coverage without frame overlap. The resultant frame series was stored as a Quicktime movie file, and digital image enhancement carried out where necessary to enhance clarity and contrast.

Overlay layers were added to the Quicktime movies to facilitate data extraction. A calibrated 1 m² frame was overlaid, within which all solitary or discrete colonial organisms were counted, as well as a 9 point array for calculating % cover. For each frame, the taxa present at each of the 9 points was recorded, as was the number of individuals of each taxon in the whole frame. Presence and abundance of bioturbating

organisms was quantified by scoring variables for occurrence of biogenically worked sediment surfaces, and counts of burrows or holes in 3 size classes.

Data were pooled for all frames in a transect. Percent cover was calculated from point data, and density calculated from count data and bioturbation indicators. A uniform standardisation technique was used to scale cover, count and bioturbation indicator data into the same range, so that they could be analysed as a single dataset. The resulting data matrix (species by sites) was then analysed using multivariate techniques.

4.2.4 *Analysis*

4.2.4.1 Multivariate classification

Abiotic similarity matrices were derived using the widely-used Normalised Euclidean Distance. Biological similarity matrices were produced for both untransformed and 4th-root ($\sqrt[4]{}$) transformed data (to allow for the influences of both abundant and rarer taxa in the dataset) using Bray-Curtis similarity, widely considered the most appropriate measure for biological information because it ignores conjoint absences (Clarke and Warwick 1994).

4.2.4.2 Whole dataset comparisons

The correlation between abiotic and biological similarity matrices was tested using Spearman's correlation coefficient and Mantel's test. The correlation coefficient values indicate how well abiotic similarity matches observed biological similarity. Mantel's test (Manly 1997) is a similar procedure but uses a more stringent test statistic.

Predictive ability of the abiotic similarity matrices was further tested by regression analysis to give a measure of the amount of the variance explained by the relationship.

For each of these measures (Spearman's correlation, Mantel's test and Regression) the use of standard statistical tables to determine significance is considered invalid because the elements of the similarity matrices cannot be considered independent. Significance was therefore estimated using Monte Carlo randomisation (Clarke and Warwick 1994).

An iterative approach was used whereby similarity matrices from different combinations of the six variables were compared to those from the biological data to find the set of abiotic variables with the best predictive power. Iterations included both continuous data and data aggregated into categories.

4.2.4.3 Extremes of abiotic similarity

The risks of false homogeneity and heterogeneity were determined by examining the 10% most similar and 10% most dissimilar site pairs from abiotic data to see if these were also biologically very similar (or dissimilar). The rationale for this analysis was that whilst it might be expected that there is some error in matching abiotic and biological similarity for site-pairs with intermediate similarity values, at the extremes of the abiotic similarity distribution there should still be reasonable predictive capacity.

The 820 site-pairs in the similarity matrices were ranked on the basis of abiotic similarity and the most abiotically similar 10% selected for further analysis. The biological similarity values for each of these site-pairs were examined to determine the proportion that were biologically similar (see Figure 2 for a diagrammatic explanation of this analysis). Several levels of similarity were used to give a range of measures of error. The frequency of occurrence of site-pairs with Bray-Curtis similarity scores above each of the 90th, 75th, 50th, 25th and 10th percentiles, within the abiotically very similar set of site-pairs, was determined. Similarly, pairs of sites that were the 10%

most different in abiotic terms were examined to determine the proportion of these that were clearly biologically distinct.

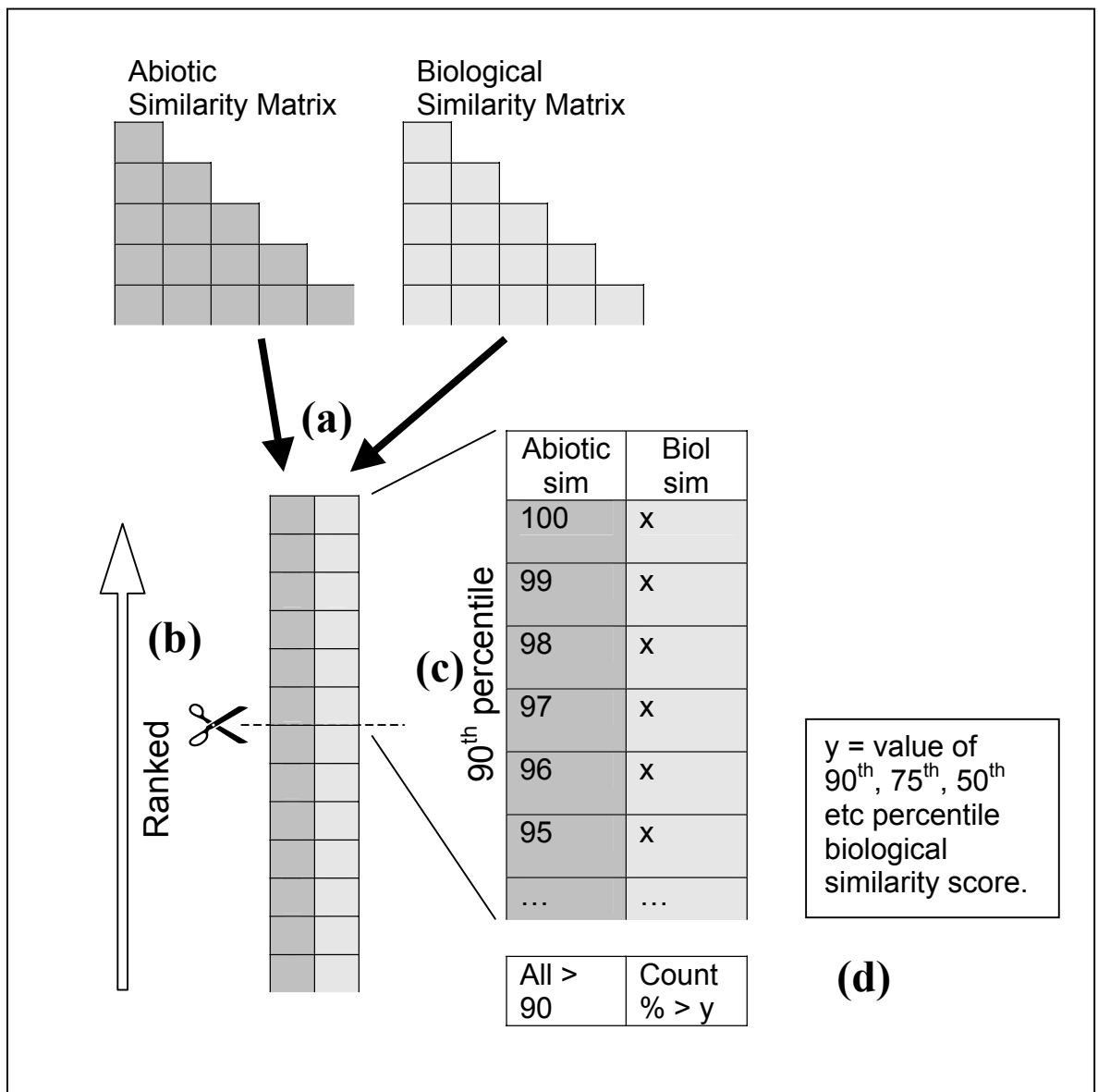


Figure 4.2: Method for extremes of abiotic similarity (Top 10%) analysis

Steps: a) Construct similarity measures by site-pairs matrix; b) rank matrix by abiotic scores; c) select site pairs with abiotic similarity scores above 90th percentile; d) count number of site pairs within the selected set that have biological similarity scores above selected interpretation level (90th, 75th, 50th, 25th, 10th percentiles). Repeat c) and d) with abiotic similarity scores below 10th percentile for bottom 10% analysis

4.2.4.4 Derived group comparisons

The 41 sites were sorted into groups for both abiotic and biological similarity measures on the basis of cluster analysis and MDS ordinations. Several solutions were examined

for each measure, from 2 to 6 groups. The makeup of the groups at each solution was compared and each site scored as to whether it was grouped consistently using abiotic and biological similarity measures. Sites not grouped consistently were considered errors of prediction and assigned to either false homogeneity or false heterogeneity, depending on the nature of the error. The proportion of the 41 sites that constituted each type of error was determined for each solution between 2 and 6 groups.

4.2.4.5 Influence of individual abiotic variables

Correlation and multiple regression analyses were used to determine which, if any, of the abiotic variables could predict the following variables: 1) number of species, 2) the abundance of individual taxa or bioturbation indicators, and 3) abundance of organisms within pooled groups, % cover (estimated from point array), solitary or discrete organisms (density from count per unit area), or bioturbation indicators data (burrow counts in 3 size classes plus occurrence of biogenic working).

4.3 Results

4.3.1 Whole dataset comparisons

Iterative classifications using different combinations of the 6 abiotic variables showed that the best correlation with the biological datasets used continuous data (rather than categorical) from all 6 variables. Spearman's correlation between abiotic and biological similarity from $\sqrt{\sqrt{}}$ transformed data gave $\rho = 0.56$ ($p < 0.001$), slightly better than the correlation with biological similarity from untransformed data ($\rho = 0.51$, $p < 0.001$). Correlation values > 0.5 with high significance suggested that the classification using all six abiotic variables would be a moderately good predictor for biological similarity.

Mantel's test also showed that there was a statistically significant relationship between abiotic and biological similarity from $\sqrt{\sqrt{}}$ transformed data ($r = 0.26$, $p < 0.001$) and between abiotic and biological similarity from untransformed data ($r = 0.18$, $p = 0.030$). The standardised Mantel statistic, r , has a range from 0 (no relationship) to 1 (perfect match), so the values found suggested only a weak relationship.

Although regression analyses showed that there was a positive relationship between abiotic and biotic similarities (in every case $p < 0.01$), R^2 values were low. Abiotic similarity predicted biological similarity from $\sqrt{\sqrt{}}$ transformed data with $R^2 = 0.28$, and the R^2 value was only slightly improved by applying transformations to the y-axis ($R^2 = 0.29$). Predictive ability of abiotic similarity for biological similarity from untransformed data was lower still ($R^2 = 0.13$). At best, therefore, the abiotic variables explain $< 30\%$ of the corresponding biological similarity.

4.3.2 Extremes of abiotic similarity

Only biological similarity from transformed data was used in this and subsequent analyses, since it was better predicted by the abiotic variables than that from untransformed data. Of the 82 most similar site pairs, less than 40% had biological similarity scores above the 90th percentile (Table 4.2). Less than 70% had biological similarity scores above the 75th percentile, and about 90% of these very similar sites had Bray Curtis scores above the median.

Table 4.2: Proportion of biological similarity at extremes of abiotic similarity
Total number of site-pairs was 820, and *n* for each 10% was therefore 82

Abiotic	Biological	Proportion included (%)
Very similar site pairs (top 10 %)	Top 10%	38
	25%	68
	50%	92
	75%	99
	90%	100
Very dissimilar site pairs (bottom 10 %)	Bottom 10%	45
	25%	67
	50%	90
	75%	100
	90%	100

Of the 82 most abiotically dissimilar site pairs, 10% were actually somewhat biologically similar (Bray Curtis scores above the median). Only 45% of these very abiotically dissimilar sites had Bray Curtis scores in the bottom 10%, and less than 70% had Bray-Curtis scores below the 25th percentile (Table 4.2).

Estimates of the risks of false homogeneity and false heterogeneity can be derived from these results, depending on how stringent a test is required (Table 4.3 and Figure 4.3). If a close match is required (10% rule), false homogeneity was predicted by abiotic data in 62% of abiotically very similar site pairs examined. Even at a less stringent

interpretation (25% rule), false homogeneity was predicted in 32% of abiotically very similar site pairs. At the broadest interpretation, false homogeneity is predicted in about 10% of abiotically very similar site pairs. The risk of false heterogeneity was a little lower than that of false homogeneity at the most stringent interpretation (Table 4.3) but was similar at less stringent interpretations.

Table 4.3: Estimates of error (derived from Table 4.2)

Errors represent the proportion of biological similarity not included at extremes of abiotic similarity, and are therefore the inverse of values in Table 2. Errors of false homogeneity are derived from the top 10% abiotic similarity analysis and errors of false heterogeneity are derived from the bottom 10% abiotic similarity analysis

Factor	Error of False Homogeneity (%)	Error of False Heterogeneity (%)
10% rule	62	55
25% rule	32	33
50% rule	8	10

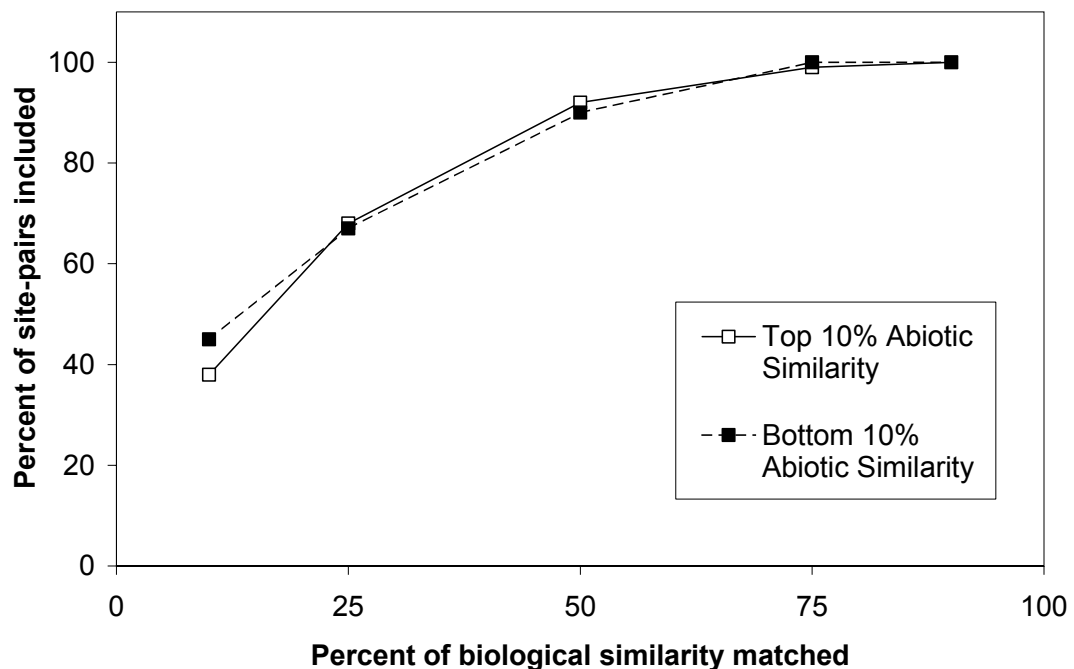


Figure 4.3: Matching abiotic and biological similarity at extremes of abiotic similarity
 Percentage of site pairs within the highest and lowest 10% of abiotic similarity values which have biological similarity values above the ranges shown on the x-axis

4.3.3 Derived group comparisons

An MDS ordination plot coded for both abiotic and biological datasets (Figure 4.4) at a four group solution shows the relatively poor match between the composition of derived groups. When plotted on the site co-ordinates (Figure 4.5) the differences in spatial relationships between abiotic and biological datasets become clear. The number of sites not consistently grouped represents error in the abiotic prediction and can be apportioned as either false heterogeneity or false homogeneity. At the extremes of the available set of group number solutions, 1 and 41 groups, the abiotic and biological group plots will match exactly. At intermediate values the error will vary. At solutions with more than 6 groups, the cluster and ordinations plots began to drop off single sites, rather than discrete sub-groups, and group comparisons therefore became increasingly meaningless. The error in abiotic prediction was at its greatest (50 - 60%) for 4 and 5 group solutions (Table 4.4). The majority of the error was false homogeneity, with false heterogeneity remaining relatively low and quite constant (Table 4.4).

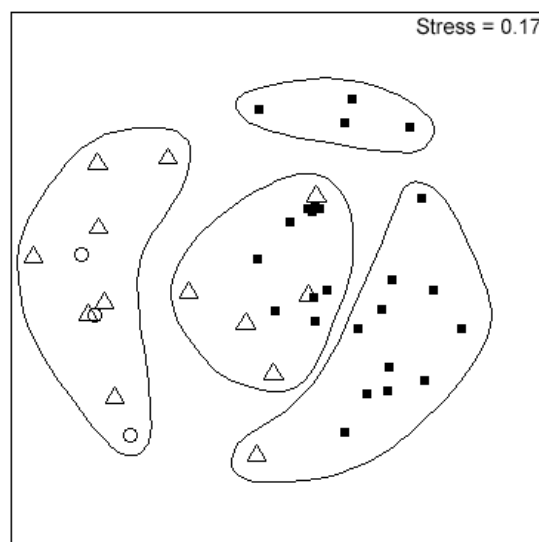


Figure 4.4: Comparison of groups from abiotic and biological classifications at four group solution

MDS ordination plot of biological classification (Bray-Curtis similarity from \sqrt{V} transformed biological data). Biological group membership at 4 group level indicated by polygon boundaries. Abiotic group membership indicated by symbols.

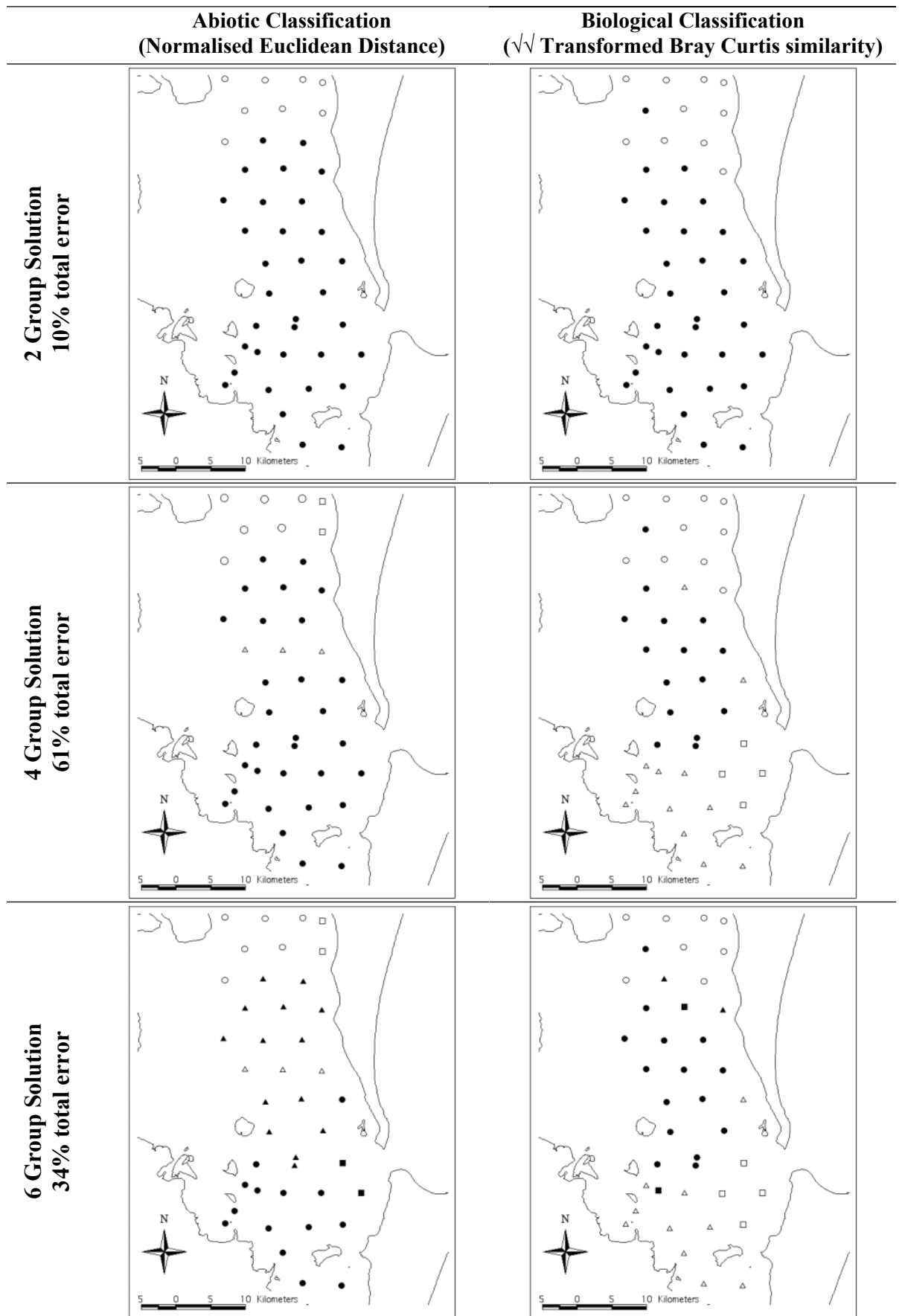


Figure 4.5: Comparative maps of Abiotic and Biological Classifications at 2, 4 and 6 group solutions

Table 4.4: Comparison of group composition from abiotic and biological classifications

Errors are expressed as % of total number of sites (41).

False homogeneity = sites predicted by the abiotic classification to be in the same group, but the biological classification placed them in different ones.

False heterogeneity = sites predicted by the abiotic classification to be in different groups but the biological classification placed them in the same one

Solution No of Grps	No of Sites Consistent	Errors		
		False Homogeneity %	False Heterogeneity %	Total %
2	37	10	0	10
3	31	20	5	25
4	16	49	12	61
5	18	44	12	56
6	27	22	12	34

4.3.4 Influence of individual abiotic variables

Species richness of sites was found to be predicted, but not well, by a combination of Depth, Distance to ocean and Mud fraction (Log-transformed y-axis, $R^2 = 0.34$, $p < 0.001$). Only about 6% of individual taxa or indicators correlated with abiotic factors (Table 4.5). The strongest relationship (highest R^2) was the prediction of frequency of biogenic working of the sediment by a combination of Mud fraction and Distance to ocean ($R^2 = 0.30$, $p < 0.001$). The highest R^2 for a taxon predicted by abiotic factors was density of the heart urchin *Lovenia sp.* by Distance to ocean ($R^2 = 0.28$, $p < 0.001$).

Other results of note were density of an unidentified bivalve by Depth and Distance to river ($R^2 = 0.21$, $p = 0.002$) and density of the spoilt seastar *Astropecten veppa* by Fetch ($R^2 = 0.198$, $p = 0.004$). However, for the overwhelming majority of the 89 taxa observed in the biological data set there was no detectable relationship with any of the abiotic variables (Table 4.5). Even where significant relationships were detected, most of these had little predictive power ($R^2 < 0.2$). Distance to ocean was the factor having most relationships with individual taxa (Table 4.6), with more than twice the number of

correlations of any other factor, yet even for this factor relationships existed with only 18% of the 89 taxa or indicators.

Table 4.5: Number of individual taxa or indicators predicted by abiotic variables
Total number of correlations examined was 534 (89 taxa or indicators by 6 abiotic variables); Regressions with more than one predictor were counted only once

Relationship	No. of correlations	%
Significant correlations ($p < 0.05$)	33	6.2
$R^2 > 0.1$	28	5.2
$R^2 > 0.2$	2	0.4
$R^2 > 0.3$	1	0.2

Table 4.6: Predictive capability of individual abiotic factors
Number of taxa or indicators for which significant relationships were found for each abiotic factor. Total n for each factor was 89 taxa or indicators. Some relationships are attributed to more than one factor

Abiotic Factor	No. of taxa or indicators	%
Dist to Ocean	16	18.0
Dist to River	7	7.9
Depth	7	7.9
Mud fraction	5	5.6
Fetch	2	2.2
Current	0	0.0

Of the three sets of data types, cover organisms, solitary or discrete organisms and bioturbation indicators, only cover organisms were predicted by any abiotic factors.

Total cover was best (but not well) predicted by a combination of Depth and Distance to ocean (Log-transformed y-axis, $R^2 = 0.418$, $p < 0.001$).

4.4 Discussion

While there is clearly a relationship between abiotic factors and biological distributions, the abiotic factors explain only a small proportion of the overall pattern. The whole matrix analysis showed that, at best, abiotic similarity explained < 30% of the pattern of observed biological distributions. It might be expected that at the extremes of the abiotic similarity values there may be reasonable predictive capacity. Yet at the tails of the abiotic similarity distribution (top and bottom 10%), errors of false homogeneity and false heterogeneity were large. A similarly poor match was found in comparing group membership derived independently from abiotic and biological data. At solutions with intermediate numbers of groups (4 - 6), errors of false homogeneity were large although errors of false heterogeneity were lower and more consistent than in the previous analysis.

Abiotic variables were also shown to have poor predictive capacity for individual taxa or indicators. The abiotic factor Distance to ocean had the most value as a predictor, but still showed significant correlations with less than a fifth of taxa or indicators. While this supports the finding of Udy and Dennison (1997) that the eastern side of Moreton Bay is essentially under ocean influence, it is of limited value for habitat mapping.

The generally poor predictive ability of abiotic factors shown in this study contrasts strongly with similar studies, albeit at a different scale. Zacharias *et al.* (1999) and Zacharias and Roff (2001) produced models based substantially and wholly (respectively) on abiotic factors that explained > 70% of the pattern of intertidal diversity at the regional (100 km) scale. In contrast, Schlacher *et al.* (1998) studied benthic community structure in a soft-sediment tropical lagoon at scales similar to the

present study, and also found that sediment characteristics had only weak relationships with the distribution of biota.

The inability of the abiotic classification to accurately predict patterns of biological similarity between sites begs the question: did such patterns exist, or was the abiotic information unable to predict them because they weren't there? The ordination analyses show clearly that patterns do exist, with strong and consistent groupings at solutions from 3 – 6 groups. This chapter does not go into the nature of those groups in detail; that is the subject of chapter 6. The inability of the abiotic data to predict such groups at this scale has implications for reserve planners and managers.

How broadly applicable is this finding? Compared to similar studies at other scales (Zacharias and Roff 2001) the area encompassed by this study is more abiotically homogeneous, although major and obvious differences exist. Of particular note is that all the sampled sites are soft substrate, and all subtidal. Most abiotic habitat classification schemes (e.g. Marine Reserves Working Group 2000) benefit from clear distinctions such as between soft and hard substrates, or coral versus rock versus gravel, and in these conditions abiotic variables can perform well in predicting patterns of biological similarity. At the other extreme, studies in soft sediment environments have found that a single environmental variable, e.g. current stress (Long *et al.* 1997) can predict distribution of epibenthos quite accurately in otherwise homogenous situations.

This study falls between these two extremes but highlights the limitations of using abiotic surrogates for habitat mapping at the local scale. In this study, abiotic variables were not able to predict more subtle and complex patterns of biological distribution in a system that, although exclusively soft substrate, was quite variable in terms of depth,

sediment composition and current velocity. Moreover, the study was conducted to provide mapping at the minimum polygon resolution required by MPA planners (Stevens 2002). The use of abiotic surrogates for habitat mapping in reserve planning is so deeply entrenched that these findings should raise concerns about the validity of that approach.

Could additional abiotic information have improved predictive capacity? Certainly, with more comprehensive datasets, it is possible that an abiotic classification could be constructed that would predict the observed patterns of biological similarity. However, in order to provide abiotic data detailed enough to model patterns of biological similarity, ground truthing would have to be so detailed one might as well survey the biota in the first place. For reserve planning, especially for considerations of representation, it is the biological distributions that are (or should be) the central interest.

What does this mean for MPA planning? At the local scale, it is questionable whether habitat mapping, and resulting analyses of representation for use in MPA design, can be constructed with a reasonable degree of rigour from abiotic surrogates alone. Several authors have constructed classification schemes combining abiotic and biological information, often within nested scales (e.g. Connor *et al.* 1995). The subtext to these schemes seems to be that the abiotic information is necessary to supplement inadequate biological data. When biological data is not available, this is clearly necessary. The danger with this approach is that abiotic or hybrid classifications are then accepted as a basis for representation of patterns of biodiversity, without ever doing robust biological surveys at the appropriate scale. It is questionable, and certainly rarely tested, whether MPAs designed on this basis can have measurable benefits for conservation.

It is acknowledged that the biota captured in this survey does not constitute a comprehensive picture of Moreton Bay benthic biodiversity. It is, of course, a relatively small subset of the total biota, in that it does not sample infauna, nekton or taxa smaller than the optical resolution of the sensor. All surveys capture subsets of the total biota, which are biological surrogates for biodiversity at scales from genes to ecosystems (Vanderclift *et al.* 1998, Ward *et al.* 1999), as are indicator groups proposed as tools for marine reserve selection (Gladstone 2002). Such approaches are logically more robust than the use of abiotic surrogates if representation of patterns of biodiversity is the aim, but all require testing against other components of the total biota.

Chapter 5 Scales of Similarity in Macrobenthic Assemblages

5.1 Introduction

Marine conservation initiatives over the last decade or more have increasingly relied on spatial management measures at a variety of scales, with much emphasis on the establishment of Marine Protected Areas (MPAs) (e.g. Agardy 2000). Increasingly, the concept of representativeness has been adopted as a major criterion in MPA design, including its use in IUCN guidelines for highly protected areas (IUCN 1994).

Representativeness in this case means the desire of planners to incorporate samples of each habitat, landscape or community type, depending on the scale of the MPA and the issues being addressed.

For highly protected areas (Category II or above, IUCN 1994), which contain the core values of most MPAs including multiple-use examples, polygons are generally drawn at the local scale (10 km) or smaller (Stevens 2002) although they may be nested within reserve systems or networks at regional (100 km) or even continental (1000 km) scales (Kelleher *et al.* 1995). Planning for, or assessment of, representation cannot logically be carried out without the crucial step of habitat mapping at the scale at which reserve boundaries are drawn.

A habitat map is a model of relative homogeneity at a nominated spatial scale, such that points within a single polygon are more similar than points in different polygons (Stevens 2002). Typically, such maps are constructed by sampling sites spaced at or below the minimum scale. Sites are numerically classified on the basis of biological attributes and polygons drawn around groups of similar sites. This spatial agglomeration

approach assumes that there is a negative autocorrelative relationship (Koenig 1999) between distance separating sites and their relative similarity. Whilst this seems intuitively true, it is not always the case. Intertidal biota, in particular, have been shown to have very complex spatial patterns. Underwood and Chapman (1996) and others (e.g. Bustamante and Branch 1996, Chapman and Underwood 1998) showed that assemblages separated by metres may be less similar than those separated by 10's of km. Such patchiness is of course a key attribute of benthic biota, at scales from mm to km (Raffaelli *et al.* 2003).

Habitat mapping for MPA design cannot (and indeed should not) attempt to model patterns of similarity across all scales (Levin 1992). The selection of the lower scale limit determines *a priori* (but usually not explicitly) that patches smaller than the practical limits of area-based management are treated as attributes of the habitats defined, not as separate habitat types. However, for spatial agglomeration to be a valid mapping tool, it is necessary to establish that for the range of scales at which MPAs are drawn (from site to local scale, rarely larger - Stevens 2002), there is an autocorrelative relationship between distance and biological similarity. To put it another way, we must have confidence that sites randomly selected within a polygon derived from spatial agglomeration will be more similar than those from different polygons.

If conducted at a range of distances (i.e. across a whole grid of sites) such analyses can provide information about nestedness of patterns of similarity and the scales at which the processes driving such patterns operate.

The developing field of remote videography allows rapid quantitative survey of benthic habitats over quite large areas (Solan *et al.* 2003) and is well suited to documenting

patterns of biological similarity at the scales in question here. Calibrated video imagery was used to quantify the relationship between biological similarity of macrobenthos and distance at site (1 km) and local (10 km) scales in Moreton Bay, Australia. Specifically, the aims of this chapter were to:

- Determine the nature and significance of the relationship between distance and biological similarity at site and local scales.
- Determine the scales of similarity within the bay, within practical limits of habitat mapping.
- Determine if these scales vary between biotic groups to assess whether a common habitat classification can be valid for a range of biotic groups.

5.2 Methods

5.2.1 Study Area

The soft-sediment biota was surveyed in Moreton Bay (153° 15' E; 27° 15' S), Queensland, Australia (Figure 5.1). Moreton Bay is a large (c.1500 km²) roughly triangular embayment opening to the Coral Sea towards the north. It is protected on the eastern side by large sand islands. It is approximately 35 km wide at the widest point, and narrows in the south into a maze of mangrove fringed waterways. Most of the bay is less than 15 m deep, but reaches depths greater than 25 m in the north-eastern part, adjacent to the main ocean entrance. The substrate in the bay is almost all soft sediment, with a decreasing gradient in mud and silt fraction in sediments from west to east as a result of freshwater and sediment inputs from the Brisbane River and several smaller streams (Lang *et al.* 1998). The eastern side is essentially under oceanic influence (Udy and Dennison 1997), with ocean entrances in the north and east. The western portions of the bay were not included in this study because they are generally too turbid for video-based survey, and to avoid the influence of terrestrial inputs.

5.2.2 Survey method

The two components of the study were sampled using remote videography to quantify occurrence and abundance of macrobenthic organisms. Surveys were carried out using a towed self-adjusting array following the design principles of Barker *et al.* (1999) but much reduced in size and complexity. It had the advantage of being small and lightweight, and therefore easily deployed from small vessels. It was relatively low-cost, using off-the-shelf technology, and had virtually no impact on the area surveyed.

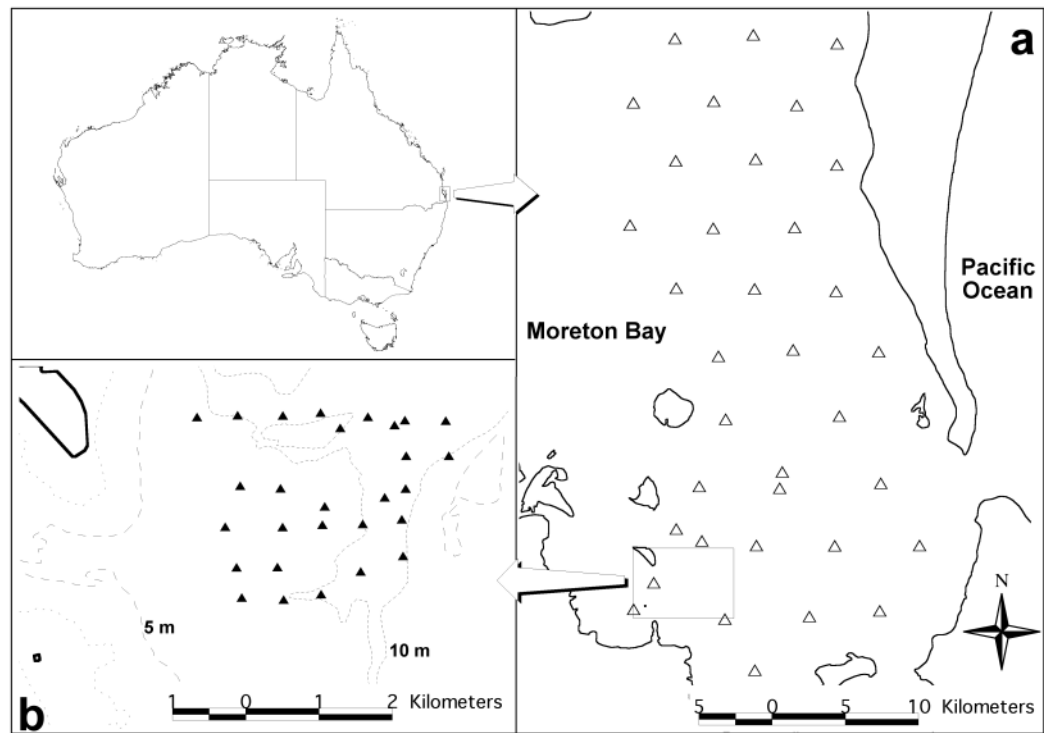


Figure 5.1: Study area showing location of sampling sites
a) Local-scale survey component. b) Site-scale survey component with depth contours

The array was towed on a 10 m tether behind a drop-weight suspended beneath the survey vessel. It was slightly positively buoyant but maintained a constant distance above the bottom by trailing a short length of light chain. This system allowed the array to self adjust to irregularities on the bottom, and coped better with uneven terrain than sled-mounted arrays, which are at risk of entanglement and damage. The video images were recorded with a digital-8 format camera which provides high resolution (480 lines) colour images.

Preliminary studies with this video sampling method showed that a single long transect gave equivalent results in species richness, assemblages and abundance to the more conventional technique of using multiple replicate transects. This “replication through length” approach had substantial practical advantages for boat-based survey, and allowed a single transect to be run at each site. Transects were located using GPS,

which gave sufficient positional accuracy for the scale at which mapping of marine habitats for conservation purposes is required (Stevens 2002).

For the local-scale component of the study, 41 sites within a 54 x 18 km area were sampled at a nominal spacing of 5 km, with a single 500 x 1 m transect at each site (Figure 5.1a). In the site-scale component, 28 sites within a 2.5 x 3 km area were surveyed at a nominal spacing of 0.5 km (Figure 5.1b). Each transect in this component was nominally 50 x 0.5 m.

5.2.3 Data extraction

Digital video was captured at 1 frame every 2 – 5 s, giving maximum coverage without frame overlap. The frame series was stored as a movie file and digital filters applied if necessary to enhance clarity and contrast. Overlay layers were added to the movie files for data extraction. A calibrated grid was overlaid, within which all solitary or discrete colonial organisms were counted, as well as an array of 9 points for calculating % cover.

For each frame, taxa present at each of the 9 points was recorded, as was the number of individuals of each taxon within the grid. Presence and abundance of bioturbating organisms was quantified by scoring variables for occurrence of biogenically worked sediment surfaces, and counts of burrows or holes in 3 size classes.

Data were pooled for all frames in a transect. Percent cover was calculated from point data, and density calculated from count data and bioturbation indicators. A uniform standardisation technique was used to scale point, count and bioturbation indicator data

into the same range, so that they could be analysed as a single dataset. The resulting data matrices (species by sites) was then analysed using multivariate techniques.

5.2.4 *Analyses*

The local-scale dataset consisted of a 41 sites by 89 taxa / indicators matrix, whilst the site-scale dataset was 28 sites by only 8 taxa. Initial analyses were done to determine if there was a direct (autocorrelative) relationship between similarity and distance. Mantel's procedure (Manly 1986), which compares similarity and distance matrices using correlation analysis, was used to quantify the nature and strength of the relationships for each component. Similarity matrices were produced for both untransformed and 4th-root ($\sqrt[4]{}$) transformed data (to allow for the influences of both abundant and rarer taxa in the dataset) using Bray-Curtis similarity, widely considered the most appropriate measure for biological information because it ignores conjoint absences (Clarke and Warwick 1994). For each component, distance matrices were constructed using simple Euclidean distance to give the distance between each site-pair in the matrix in metres. The *Relate* routine in PRIMER numerical analysis package (a type of Mantel's test), was used to calculate correlation (Spearman's ρ) values. The predictive power of distance for similarity was also calculated using regression (R^2) analyses. Significance for both analyses was determined using Monte Carlo randomisation with at least 1000 permutations (Clarke and Warwick 1994), since cells within a similarity or distance matrix cannot be considered independent.

In a regular sampling array, distances between pairs of sites can be considered categorical rather than strictly continuous. The relationship between similarity and distance was therefore also examined by grouping distances into classes defined in multiples of the nominal spacing between sites (plus a small margin to allow for

variation in spacing). Thus distance class boundaries for the site-scale component were 600 m, 1,100 m, 1,600 m, etc., whilst the spacing for the local scale component was 6 km, 11 km, 16 km, etc. Mean similarity was calculated for each distance class, and differences between classes were determined using ANOVA (after checking assumptions) followed by Tukey pairwise comparisons.

Rank correlograms (Somerfield and Gage 2000, Parry *et al.* 2003) were used with the distance classes to estimate maximum patch size and look for evidence of nested patterns of similarity for both components of the study. For each size class, a model distance matrix was constructed in which distance for the site-pairs in that class was set to 1, whilst distance in all other cells was set to 0. Spearman's rank correlation between the similarity matrices and the model matrices was calculated for each distance class, with significance again determined using Monte Carlo randomisation. The results were examined graphically using rank correlograms. The size class at which significant autocorrelation minima occur represents the distance between samples that are least similar, and indicates the maximum radius of a patch of similar biota (Legendre and Fortin 1989). Significant autocorrelation maxima (at distances greater than minima) indicate the distance between successive patches. Multiple minima (separated by significant positive values) indicate a nested patch structure. A spatially homogenous distribution would be represented by a rank correlogram with no correlation values significantly different from zero (Legendre and Fortin 1989).

Mantel's tests and rank correlograms were also used to examine the relationship between similarity and distance for the following discrete biotic groups: annelids, anthozoans, ascidians, bioturbating organisms, echinoderms, macroalgae, seagrasses,

and sponges. This was done only for the local-scale dataset, as too few taxa occurred in the site-scale dataset to make useful analyses.

5.3 Results

5.3.1 Overall distance relationships

In the site-scale component, there was a significant negative relationship with distance (Figure 5.2a, $p \leq 0.001$ for correlations and regressions). Correlation values were, however, low for both untransformed ($\rho = 0.23$) and transformed ($\rho = 0.24$) data, and little of the observed variance could be explained by distance (R^2 approximately 5% for both transformed and untransformed). The regression relationship was close to linear and log-transforming the y-axis term in the regression did not improve the R^2 value.

Mean similarity declined only slowly with increasing distance between points (Figure 5.2b) until the 2.1 – 2.6 km distance class where it tailed off more quickly. Differences in mean similarity occurred (ANOVA: $p < 0.001$ in both cases), and Tukey's pairwise comparisons indicated that only the largest two distance classes were different from the others, whilst the smaller four distance classes were not statistically different.

The rank correlogram showed autocorrelation minima at the 2.1 – 2.6 km distance class, indicating that this was the maximum patch size (Figure 5.2c). There were no subsequent significant autocorrelation maxima, although for the untransformed dataset (emphasizing abundance of common species) the line trends sharply upwards in the largest distance class. The increase in correlation value for the largest distance class also occurred for the transformed data but was less pronounced. The lack of another peak in values at larger distances shows that the distance between patches was greater than the largest between-site distance sampled in this component of the study.

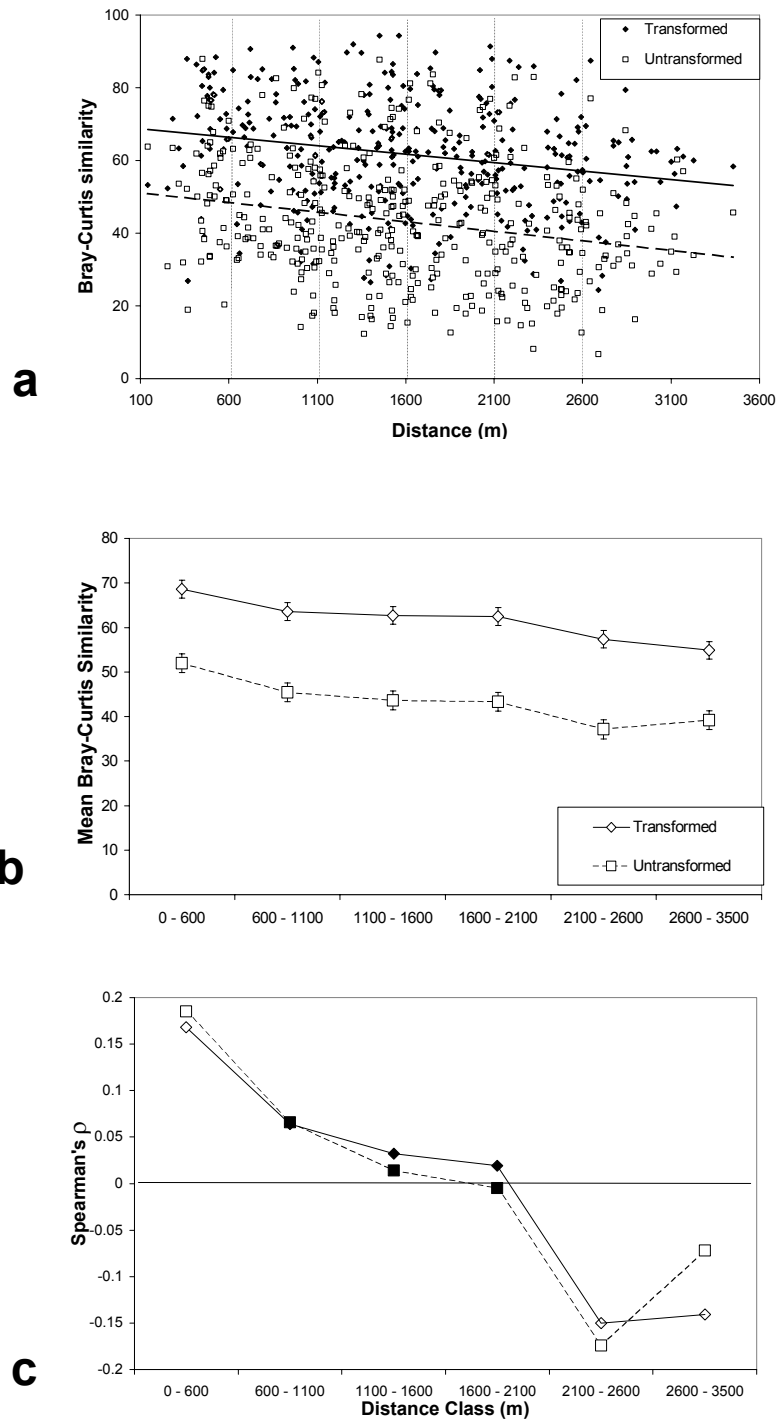


Figure 5.2: Site-scale relationships with distance

- Scatterplot of Bray-Curtis similarity by distance between site-pairs for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data. Vertical lines indicate boundaries of distance-classes used in succeeding analyses. Best-fit regression lines shown.
- Bray-Curtis similarity by distance classes for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data (Mean \pm SE).
- Rank-correlogram of Bray-Curtis similarities for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data. Legend as for 2b. Open symbols indicate significant correlations, filled symbols indicate non-significant correlations, estimated by Monte Carlo randomisation

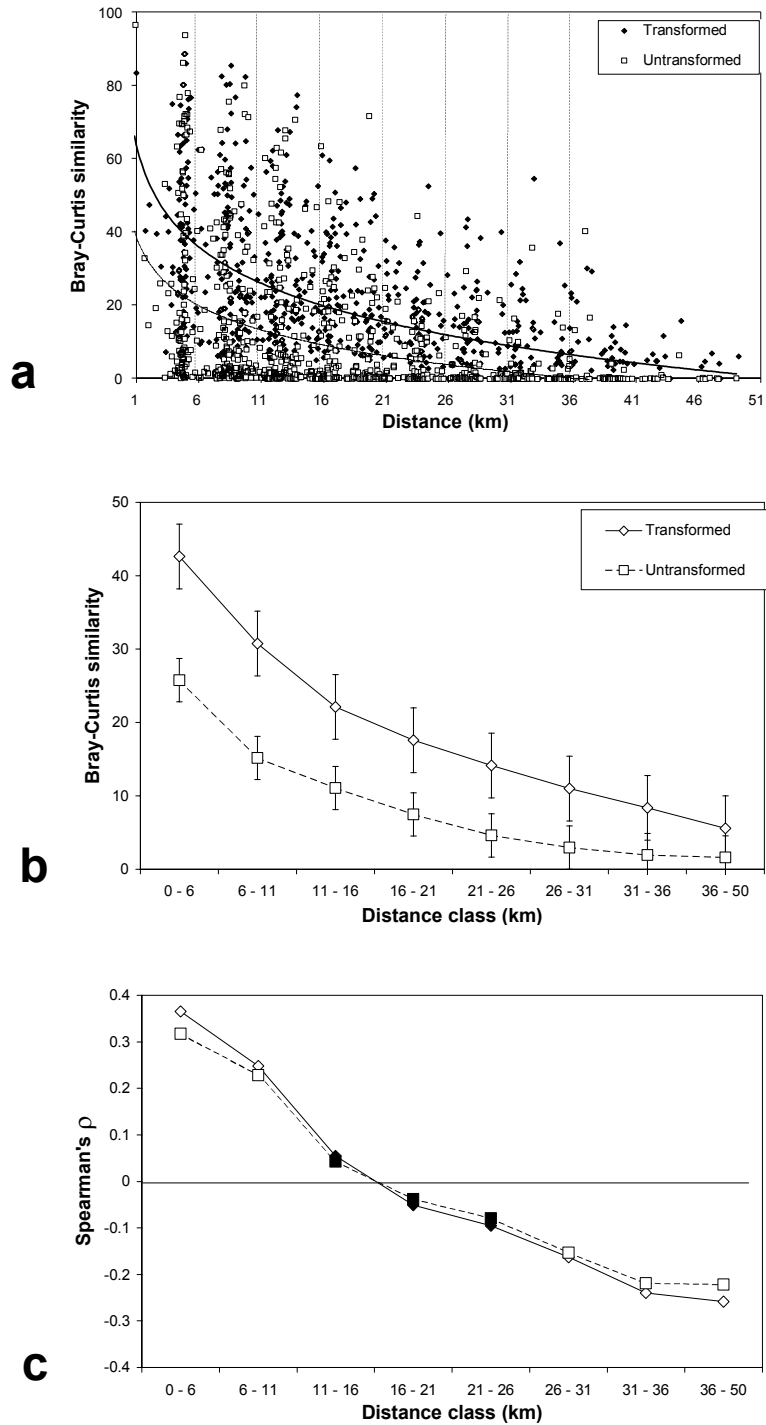


Figure 5.3: Local-scale relationships with distance

- Scatterplot of Bray-Curtis similarity by distance between site-pairs for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data. Vertical lines indicate boundaries of distance-classes used in succeeding analyses. Best-fit regression lines shown.
- Bray-Curtis similarity by distance classes for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data (Mean \pm SE).
- Rank-correlogram of Bray-Curtis similarities for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data. Legend as for 3b. Open symbols indicate significant correlations, filled symbols indicate non-significant correlations, estimated by Monte Carlo randomisation

Within the local-scale component, there was a significant negative relationship with distance (Figure 5.3a, $p \leq 0.001$ for correlations and regressions). Correlation values for both untransformed ($\rho = 0.50$) and transformed ($\rho = 0.56$) data were much higher than in the site-scale component and distance explained far more of the variance ($R^2 = 22\%$ and 28% for untransformed and transformed data respectively). The regression relationship was not linear, best fit being obtained with log transformation of the y-axis term.

Mean similarity of transformed data declined quite quickly with distance but the trend was not linear (Figure 5.3b). Mean similarity fell most quickly between the first three distance classes, then declined almost linearly with increasing distance. The curve for mean similarity from untransformed data was similar, with the largest fall in similarity between the first two distance classes. From the 26 – 31 km distance class to the maximum distance there was virtually no decline. Differences in mean similarity occurred (ANOVA: $p < 0.001$ in both cases), and Tukey's pairwise comparisons indicated that the smallest three distance classes were significantly different from each other and from the largest five distance classes, which were not significantly different.

The rank correlogram (Figure 5.3c) shows no autocorrelation minima below the maximum distance range (36 – 50 km), although the correlation values in the 31 – 36 km range are similarly low. These results indicate that within the scale of this dataset, there are no nested patches, and that at distances greater than 31 km, similarity does not decline markedly. Largest autocorrelation values are in the smallest distance classes, indicating that polygons drawn at the 10 km scale would capture much of the similarity, although at the 5km scale more would be captured.

5.3.2 Biotic Groups

All biotic groups had significant relationships with distance, although correlation values were low for anthozoans and seagrass (Table 5.1). The strongest distance relationships were found in Bioturbators and Macroalgae. Rank correlograms (Figure 5.4) showed that anthozoans, seagrass and echinoderms had correlation minima below the maximum distance class, indicating the presence of patch structures. Both anthozoans and seagrass had multiple minima, indicating possible nested patches, but the minima were not significant, in fact no significant autocorrelation was found for either group other than in the smallest distance class. The only group to show significant autocorrelation minima at less than the maximum distance class were echinoderms at 26 – 31 km (untransformed) and 31 – 36 km (transformed). Ascidiarians were clearly most similar at scales up to 11 km, but the similarity declined markedly at larger distances. This was also evident, but less pronounced, in bioturbators and annelids. Macroalgae appeared to aggregate at scales up to 16 km.

Table 5.1: Mantel’s test for relationships between similarity and distance for Biotic Groups

Spearman’s rank correlation, Bray-Curtis similarity and distance (km). Significance estimated by Monte-Carlo randomisation

Biotic Group	Untransformed		Transformed	
	ρ	p	ρ	p
Annelids	0.30	0.021	0.34	0.003
Anthozoans	0.10	0.001	0.16	0.001
Ascidiarians	0.26	0.001	0.26	0.001
Bioturbators	0.41	0.001	0.41	0.001
Echinoderms	0.34	0.001	0.38	0.001
Macroalgae	0.40	0.001	0.40	0.001
Seagrass	0.13	0.019	0.14	0.014
Sponges	0.26	0.001	0.22	0.002

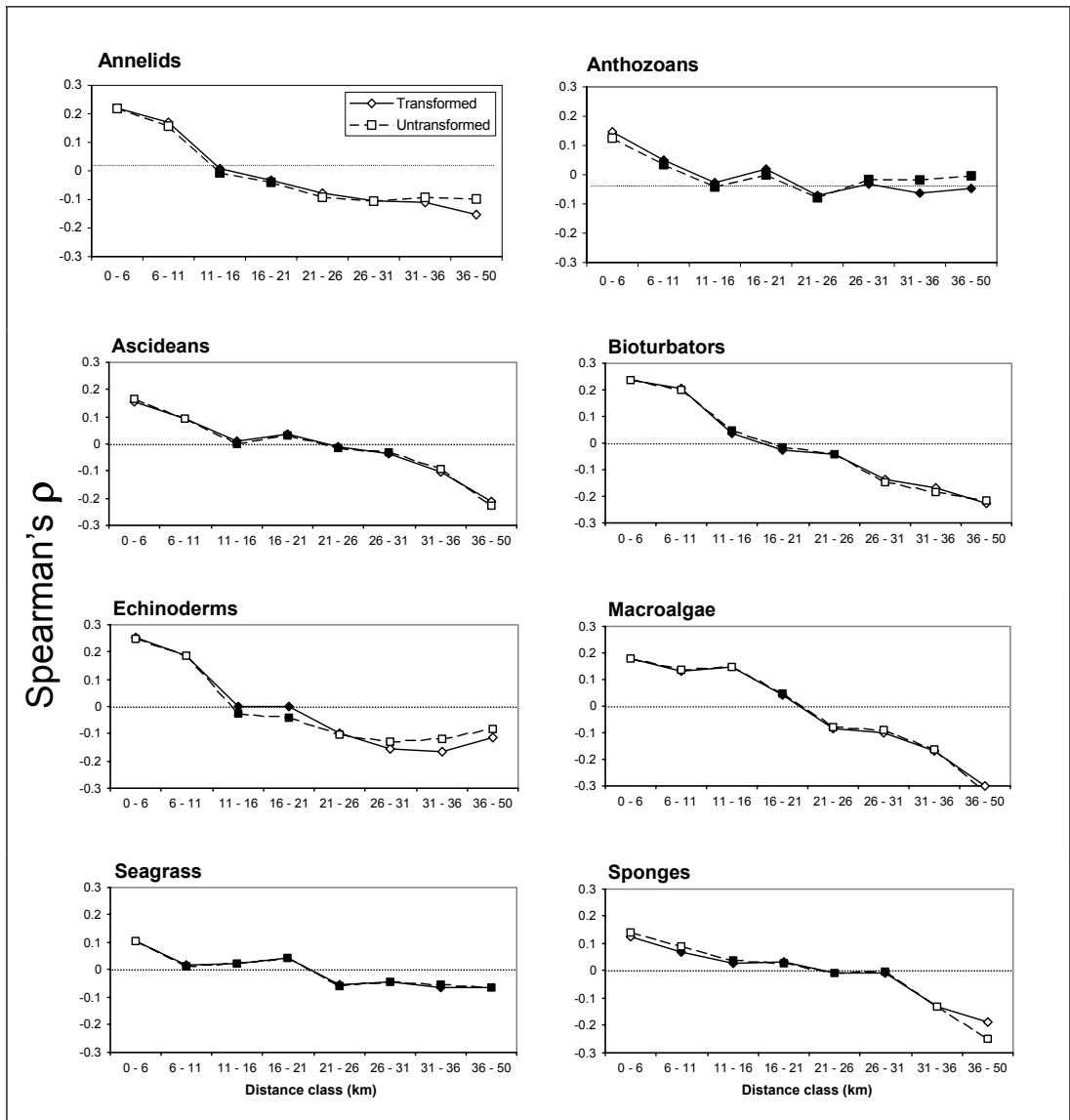


Figure 5.4: Distance relationships of biotic groups
 Rank-correlograms of Bray-Curtis similarities by distance between site-pairs for biotic groups for both untransformed and $\sqrt{\sqrt{}}$ transformed biological data. Open symbols indicate significant correlations, filled symbols indicate non-significant correlations, estimated by Monte Carlo randomisation

5.4 Discussion

There is a significant relationship with distance in all analyses. Locations further apart are less similar than those closer together, so spatial agglomeration of sites into groups is a valid approach to deriving polygons of relative homogeneity. However, the distance relationship within the site-scale component is not strong, with evidence that similarity declines little at patch sizes up to 2.1 – 2.6 km. For the local-scale component there is significant but non-linear relationship with distance, with similarity declining quickly at less than 11 - 16 km, with virtually no change from 21 – 26 km to the largest distance class. Biotic groups in general conformed to this overall pattern, with some departures. Seagrass and anthozoans had clearly aggregated distributions at scales of 11 km or less, indicating quite discrete distributions within the study area. A similar pattern, although less clear, was seen in echinoderms, ascidians, annelids and bioturbators.

When the two components of this study are considered together, a picture emerges of a benthic macrofauna in Moreton Bay that was relatively homogenous at scales up to about 2.5 km, and clearly more similar at 5 and 10 km scales than at larger distances. In this context, the somewhat higher similarity at < 0.6 km (Figure 2c) would be considered as patchiness within biotic distributions.

In the context of habitat mapping for representation in marine protected area planning, the results of the present study show that it is valid to represent patterns of homogeneity at the local-scale. It is clear that a site spacing greater than 10 km (the minimum for a local scale mapping exercise), would under-represent patterns of biodiversity. On the other hand, although positioning of polygon boundaries might be more precise if a site spacing less than 5 km was used, there is evidence that the overall picture of patterns of biodiversity would be changed little by site spacing of 2.5 km or less.

In setting the results of this study in the context of previous work, it is necessary to clarify a point of terminology. Similarity (or biological similarity) has been used in this study to describe how alike sites are in terms of their biological attributes. Many other studies use terms such as variation, variability, and heterogeneity to describe in essence how different samples (sites, transects, locations etc) are from each other. Although not strictly opposites, in comparing the results of prior studies to the present one, similarity is considered the opposite of terms such as variation, variability and heterogeneity, and comparisons drawn accordingly.

A compounding problem with such comparisons is that different studies, apart from having different methods and scales, are expressing variability (or heterogeneity, or dissimilarity) between different components of the biota. A measure of variability relating to species richness cannot be directly compared to that derived from abundance or a mixture of the two (e.g. a diversity index), or to variability in density of a single species. Indeed, Archambault and Bourget (1996), working at nested scales from 10 cm to 100 km, showed that for species richness in intertidal communities, variability was highest at the 1 km scale, whilst for abundance, variability was highest at scales of 20 cm or less. Patterns in the scale of variability will certainly vary between hard and soft substrates, macrobenthos and meiofauna, intertidal organisms and pelagic fishes.

Most previous studies have explored patterns of variability at scales smaller than this study, typically comparing a range of scales all less than 1 km (Smith and Hamilton 1983, Kendall and Widdicombe 1999, Somerfield and Gage 2000, Paiva 2001, Parry *et al.* 2003). Exceptions include studies of meiofauna up to 10 km (Li *et al.* 1997), intertidal communities up to 10 km (Archambault and Bourget 1996), and sperm whale

aggregations 150 – 1200 km (Jaquet and Whitehead 1996). Few studies have explored patterns of variability (or similarity) at the scales at which marine protected areas are drawn (1 km to 10's of km).

A common thread through many, but by no means all, previous studies is that whatever the range of scales studied, similarity is higher at the smaller scales, usually expressed in the inverse, as variability or spatial heterogeneity being higher at larger scales (Li *et al.* 1997, Somerfield and Gage 2000, Paiva 2001, Parry *et al.* 2003,). That this is a common pattern is not surprising, reinforcing the intuitive perception that communities are more different if they are further apart. It is at odds, however, with the evidence presented by Underwood and Chapman (1996) and others showing that for rocky shore communities, variability is as high or higher at very small scales (metres) as it is at large scales (kilometres). James and Fairweather (1996) showed significant variation in intertidal sandy beach fauna at both metre and 100 m scales. The extent to which these findings translate to comparisons between larger scales, or to subtidal soft sediment communities, has not been widely explored.

For mapping of marine habitats for the purpose of MPA design, there are practical constraints on the range of scales that can be considered. Boundaries of highly protected areas are drawn at scales of 1 km to 10's of km, rarely greater (Stevens 2002, Kelleher *et al.* 1995). Patterns of similarity below this range (e.g. the correlation maximum at 0 - 600m in Figure 5.2c) are in practicality considered as patchiness within biotic distributions, and managed by non-area based measures (Schwartz 1999). Within this practical range, this study has demonstrated that for Moreton Bay, sites are most similar in their macrobenthic assemblages at distances of 10 km or less, and that this is generally true for the range of biotic groups analysed. It has also shown that similarity is

consistent at scales up to about 2.5 km. Spacing of survey sites to derive polygons of relative homogeneity should therefore be between 2.5 and 10 km.

Chapter 6 Benthic Habitat Classification and Assessment of Representation

6.1 Introduction

Design of marine protected areas (MPAs) over the last decade has increasingly adopted representation of all habitat types as a major criterion for selection of candidate areas and drawing of management boundaries (e.g. IUCN 1994, Agardy 1995, Great Barrier Reef Marine Park Authority 2003). Representativeness *sensu stricto* (Stevens 2002) logically and practically requires habitat mapping at the scale at which management provisions and protected area boundaries are drawn. Most commonly, this is at the local scale (10 km) or finer (Kelleher *et al.* 1995). Even within the world's largest MPA, the c.350,000 km² Great Barrier Reef Marine Park, boundaries of highly protected areas (IUCN Category I or II) are drawn at this scale (Stevens 2002).

Habitat mapping at the relevant scale allows planners to design MPAs or MPA systems which incorporate samples of every habitat type existing in the candidate area, typically through the use of optimisation techniques (e.g. Possingham *et al.* 2000, Villa *et al.* 2002). In existing reserves, representation can be assessed and habitat types that are not well represented highlighted for inclusion or particular management provisions.

However, design of MPAs to include representative samples of the range of habitats occurring in the area (amongst a range of other criteria, Jones 1994) has been hampered by a lack of mapping at the requisite scale, largely due to the perceived costs of underwater survey. Often, maps have been constructed from abiotic surrogates, but there are clearly inaccuracies resulting from this approach, especially in distinguishing variation in soft bottom communities (Chapter 4).

Underwater videography, either diver operated (Christie *et al.* 1996, Sweatman 1997) or remotely deployed (e.g. Starman *et al.* 1999, Bax and Williams 2001, Parry *et al.* 2003) has emerged as an effective, non-destructive and data-rich method for surveying benthic communities over relatively large areas. The widespread use of this technology has been limited by the logistical constraints of depth and endurance for SCUBA divers, or the size, complexity and therefore expense of remotely deployed equipment and the required support vessels. Recently, Stevens and Connolly (in press) have demonstrated the quantitative use of an inexpensive video array using off the shelf components and compact enough to be deployed from a small (~6 m) vessel.

Moreton Bay Marine Park is a relatively complex example of a meso-scale MPA zoned to reduce conflicts between competing users and to preserve high profile marine habitats and threatened “iconic” species, especially seagrass beds, coral reefs, dugong and marine turtles (Anon 1997). Established in 1993, the planning process for the park predated the emergence of representativeness as a major criterion in MPA design. Park zoning plans are subject to periodic review and alteration where necessary. The Moreton Bay Marine Park zoning plan is due for review shortly (L. Harris, pers. comm.).

The aims of this chapter were to:

- Classify and map all marine habitat types in Moreton Bay and adjacent offshore areas at the local scale, ranging from shallow subtidal estuarine areas to offshore waters to the 50 m isobath.
- Determine the extent to which different taxonomic groups influence the patterns of between-site similarity.

- Assess the extent to which each habitat type is represented within the existing MPA.

6.2 Methods

6.2.1 Study site

Moreton Bay (27°15'S, 153°15'E) on the east coast of Australia, is a shallow coastal embayment, covering approximately 1,500 km² (Figure 3.1). The bay is roughly triangular in shape, about 35 km wide in the north and narrowing in the south into a maze of mangrove-lined waterways. It is protected in the east by large sand islands with its main ocean entrance in the north east and a smaller entrance in the east. Most of the bay is less than 15 m deep, but reaches depths greater than 25 m in the north-eastern part, adjacent to the main ocean entrance. The western parts of the Bay are heavily influenced by terrestrial inputs (Costanzo *et al.* 2001) principally from the Brisbane River (Eyre *et al.* 1998) and smaller river systems. The eastern side is essentially under oceanic influence (Udy and Dennison 1997). The offshore portion of the study area extends seaward from the two large sand islands to the 50 m isobath. In general the bottom is of soft substrate and slopes quite evenly away from the ocean beaches. The north-eastern extremity of each island is formed by a rocky headland with associated offshore outcrops. In the north-east part of the study area a sandstone platform provides a substrate for Flinders Reef, a coral reef community of surprisingly high diversity given its latitude (Davie *et al.* 1998, Harrison *et al.* 1998).

The bay and adjacent offshore waters are included within Moreton Bay Marine Park (Figure 3.1), a zoned multiple-use MPA declared in 1993 and managed to “provide for the ecologically sustainable use of Moreton Bay Marine Park and to protect its natural, recreational, cultural heritage and amenity values.” (Anon 1997, page 9). The park covers about 3,800 km² and extends from highest astronomical tide to between 3 and 20 km offshore to a maximum depth of about 150 m.

6.2.2 Field Methods

Data were collected using a compact towed video array designed specifically for the survey. The general arrangement follows the design principles of Barker *et al.* (1999), but much reduced in size and complexity. The array was towed on a 10 m tether behind a 20 kg drop weight suspended beneath the survey vessel approximately 2 m above the substrate. The array was slightly positively buoyant and “flew” a constant and adjustable distance above the substrate by using the trailing chain method, which allowed the array to self adjust to irregularities on the bottom. This arrangement can be used on rough substrates and is smaller (0.5 m x 0.5 m x 0.3 m) and lighter (<10 kg) than comparable sled-based equipment. The array was successfully deployed to a maximum depth of 52 m.

The sensor was a high resolution (480 lines) colour “lipstick” camera mounted in a PVC housing at a 45° angle to the substrate. The unit was powered, and the video signal returned to the surface, via a 3-core cable. The video signal was recorded on a SONY Digital 8 ‘handycam’., which doubled as a video monitor with its 6 cm LCD screen. Two laser diodes mounted parallel to each other projected dots onto the bottom a constant 0.5 m apart, allowing calibration of the video images and checking for correct orientation and elevation of the array.

Sample sites were set out in a staggered 5 km spaced array covering the central, eastern, and southern parts of the bay, and offshore waters to the 50 m isobath (Figure 3.1). The 5 km spacing was chosen to facilitate construction of polygons of relative similarity at the local (10 km) scale. For logistical reasons offshore components at the northern and southern ends of the marine park were not surveyed. The western portions of the bay

and the constricted waterways in the south were not surveyed because they were generally too turbid for video based survey.

The sampling design was a single 500 m transect at each site. Preliminary studies showed that this gave equivalent results to multiple replicate transects and had substantial practical advantages for boat based survey. Transect start and finish points were located using GPS, which gave sufficient positional accuracy (about 15 m) compared to the target mapping scale (10 km). Implicit in the sampling design is that habitat elements with linear dimensions less than 5 km may not be captured, and that variability at the 500 m scale is treated as patchiness within habitats.

6.2.3 Data extraction

Digital video was captured at 1 frame every 2-5 s, the frame rate giving maximum coverage without frame overlap. The resultant frame series was stored as a Quicktime movie file, and digital image enhancement carried out where necessary to enhance clarity and contrast.

Overlay layers were added to the Quicktime movies to facilitate data extraction. A calibrated 1 m² frame was overlaid, within which all solitary or discrete colonial organisms were counted, as well as a 9 point array for calculating % cover. For each frame, the taxa present at each of the 9 points were recorded, as was the number of individuals of each taxon in the whole frame. Presence and abundance of bioturbating organisms was quantified by scoring variables for occurrence of biogenically worked sediment surfaces, and counts of burrows or holes in 3 size classes.

Data were pooled for all frames in a transect. Percent cover was calculated from point data, and density calculated from count data and bioturbation indicators. A uniform standardisation technique was used to scale cover, count and bioturbation indicator data into the same range, so that they could be analysed as a single dataset.

6.2.4 Classification and mapping

The data matrix (species by sites) was analysed using multivariate techniques.

Similarity matrices were constructed using Bray Curtis similarity, selected because it does not derive similarity from conjoint absences (Clark and Warwick 1994).

Relationships between sites were visualised using non-parametric multidimensional scaling (MDS) ordination supplemented with cluster analysis and pairwise inter-group similarity using the SIMPER module in the PRIMER package. Significance of derived groups was determined using ANOSIM.

Preliminary analyses compared classifications from the untransformed dataset to those from $\log(x+1)$, 4th root and presence / absence transformed datasets. The results were broadly similar, and the 4th root transformation was selected for subsequent analyses as the best balance between emphases on rare and abundant taxa.

Habitat maps were constructed by spatial agglomeration, that is, allocating sites into groups of relative similarity, based on consistently occurring core groups of sites. A few very depauperate sites (only 1 or 2 taxa and very low densities) had consistently low Bray Curtis similarities and therefore tended not to associate with any group or with each other. This was resolved by conducting a subsequent analysis using a non-zero constant, which aided in determining the group to which they were most similar.

Effect of taxonomic resolution

Taxa were aggregated into groups at 3 levels on the basis of lifeform, biotic groups and phyla (based on the AIMS analytical methodology, Christie *et al.* 1996). Between-site similarity matrices using the aggregated datasets were then compared with the original (morphospecies) similarity matrix using correlation analysis (RELATE routine in the PRIMER package) to determine the effects of taxonomic resolution in the classification. Habitat maps derived from the aggregated data were plotted and group composition compared with the original (morphospecies level) habitat map.

Influence of biotic groups on the classification

Separate between-site similarity matrices based on subsets of the dataset by biotic group were compared to the overall classification using correlation (RELATE routine in the PRIMER package) and comparative MDS (2-stage process in PRIMER) analyses to determine if any biotic groups, singly or in combination, appeared to be driving the classification.

6.2.5 Representation in the existing MPA

The study area characterises about 2,400 km² (outer boundary based on a 2.5 km buffer around each sample site) and constitutes approximately 60% of the marine park. For analysis of representation in the MPA, habitat polygons were constructed using Voroni tessellation, a technique that draws polygons whose boundaries define the area that is closest to each point relative to all other points (Watson and Philip 1984).

Representation of the derived habitat types within the parts of the marine park covered by the study area was assessed by spatially overlaying the derived habitat groups on the digital zoning plan. The analysis was conducted using both point and polygon habitat

data to address biases inherent to both. Point data assumes no spatial extrapolation of the habitat information from a single point in space (in this case the transect centroid) and therefore underestimates representation in smaller zones. On the other hand, polygons derived from Voroni tessellation assume a habitat boundary at the midpoint between sites in different groups and assume homogeneity between sites within a group, and may therefore overestimate representation in small zones. Considering both types of analysis together gives a more balanced assessment of representation.

6.3 Results

6.3.1 Description of dataset

A total of 78 sites was surveyed between September and December 2002. Over 40 km of video transect was recorded, and 16,373 individual frames were analysed. Mean frame number per transect was 202 (range 53 – 435). Relative abundances (as percent cover or density) of 114 morphospecies were recorded, as well as 4 indicators of bioturbation. To allow comparison of cover with density data, relative abundance was derived from a uniform standardisation technique, in which each data type was standardised to the range 0 – 1.

Table 6.1: Taxa contributing more than 10% to total standardised abundance

% frequency is the number of sites in which the taxon occurs, as a percentage of the total number of sites. Number of sites = 78, number of frames = 16,373

Taxon	% total abundance	% frequency
<i>Anemone</i> sp. 7	14.5	17
<i>Halophila spinulosa</i>	12.9	19
<i>Zostera capricorni</i>	12.0	6
Anemone family Cerianthidae	11.9	17
Encrusting algae (multiple species)	10.0	6

Of the 114 morphospecies, 24 occurred in only one site, 64 contributed less than 0.1% to total standardised abundance, and 101 contributed less than 1%. Five taxa (Table 6.1) were very common, each contributing more than 10% to total standardised abundance, and in total represented over 61%. These common taxa were not widespread over the study area, and none occurred in more than 20% of sites. No taxon was ubiquitous. The most frequently occurring species (the acorn worm *Balanoglossus carnosus*) occurred in just under 50% of sites, but contributed only 0.4% to total standardised abundance.

Bioturbation was common, with small burrows (>3 cm diameter) occurring in 55% of sites. Biogenic working of surface sediments was evident in 47% of sites.

6.3.2 Derived Habitat Classification

Several core groups formed consistently across differently weighted MDS analyses (4th root shown in Figure 6.1). Stress levels in MDS plots were high (0.20) so group composition was not determined purely from the MDS plots, but groups agreed well with corresponding cluster analyses. Sites within these groups (Figure 6.2) were aggregated, and pairwise SIMPER analysis was used to determine the similarity between the remaining single points and the core groups.

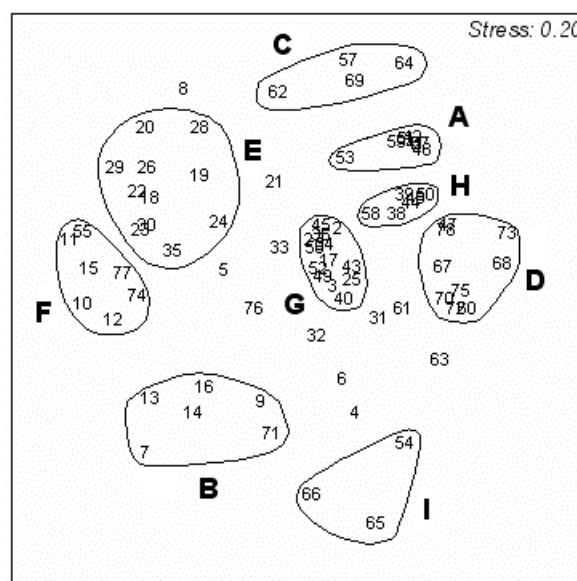


Figure 6.1: MDS ordination plot of all sites with selection of core groups

On the first pass, single sites with similarities of 40% or above were allocated to the group with which they were most similar. Examination of the raw data showed that the 3 sites left after this pass (4, 5, and 76) had consistently low Bray Curtis similarities because they were depauperate, rather than because they had multi-species assemblages very different to the remainder of sites. A parallel analysis using a very small (10^{-10})

constant term improved Bray Curtis values without changing the overall relationships or composition of the core groups, and clarified the groups to which these sites should be allocated (Figure 6.2). ANOSIM analysis verified that the derived groups were significantly different from each other (Global $R = 0.84$, $p = 0.001$, pairwise tests all significant $p \geq 0.018$).

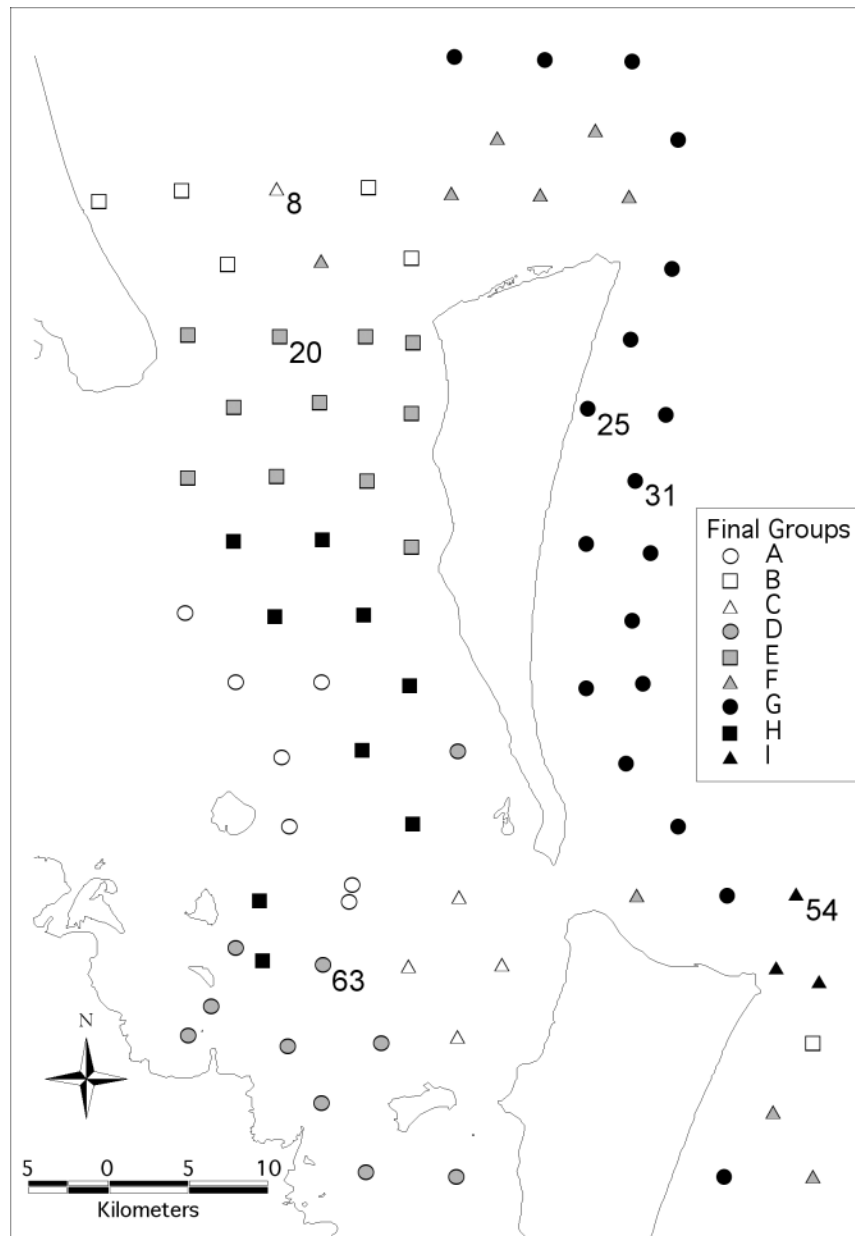


Figure 6.2: Study area showing derived habitat groups
Numbers denote sites referred to in the text

6.3.2.1 Description of Groups

Two groups (Table 6.2) stood out as being species-rich; D (42 taxa) and G (28 taxa). These groups were at opposite ends of the estuarine – oceanic continuum. Group D covered ten sites in the southern portion of Moreton Bay, where it begins to narrow into a maze of mangrove-lined waterways. Macrobenthos of group D was dominated by algae and sponges but was very diverse, with significant contributions from solitary ascidians, anemones and seagrass. Of the 42 taxa, 19 (45%) contributed more than 1% to the total similarity within the group. Group G was the largest group, covering 18 sites that were essentially oceanic. Most sites were deeper than 30 m. Although very diverse, with 10 of the 28 taxa (36%) contributing more than 1% to the total similarity within the group, abundances were generally low, with little cover (except at site 31, see below) and most taxa sparsely distributed. Occasional clumps of the seagrass *Halophila spinulosa* were found at about 25 m depth in several sites.

At the other extreme in terms of species richness were groups A and F. These two groups also represented a contrast of inshore and offshore environments. Group A was a muddy inshore environment dominated by bioturbators, whilst F was offshore, sandy, and depauperate with sparse populations of the acorn worm *Balanoglossus carnosus* responsible for 83% of the overall similarity within the group.

Of the remaining groups, C and I were both cover dominated. Group C sites were seagrass beds, and notably the group included site 8, where seagrass beds have not previously been mapped. Group I was the only reefal group in the classification, dominated by encrusting algae, soft corals and sponges.

Table 6.2: Composition and features of derived groups

CTGS = Contribution to Total Group Similarity, derived from SIMPER analysis. CTGS for each dominant taxon is given in parentheses

Group	No. sites	No. taxa	Dominant taxa (>10% CTGS)	No. taxa >5% CTGS	No. taxa >1% CTGS
A	7	5	Small burrows (54%) Med burrows (35%)	3	3
B	6	8	Bivalve sp. 2 (36%) Sponge sp.1 (28%) Echinoid sp. 4 (14%)	5	8
C	5	19	<i>Halophila ovalis</i> (33%) <i>Halophila spinulosa</i> (17%) <i>Zostera capricorni</i> (13%)	5	9
D	10	42	Worked sediment (16%) Brown alga sp. 13 (11%) Sponge sp. 2 (11%)	7	19
E	11	18	Anemone fam. Cerianthidae (33%) <i>Balanoglossus carnosus</i> (23%) Echinoid sp.4 (10%)	5	8
F	9	4	<i>Balanoglossus carnosus</i> (83%)	3	4
G	18	28	Worked sediment (39%) Small burrows (27%)	4	10
H	9	19	Worked sediment (39%) Small burrows (20%) Anemone sp. 7 (12%) Medium burrows (11%)	5	8
I	3	17	Encrusting algae (20%) Digitate soft coral sp. 2 (16%) Macroalgae unid. (15%) Fan-forming soft coral sp. 7 (11%) White ridge sponge cf. <i>Callyspongia. manus</i> (10%)	5	17

Group E highlighted an assemblage which had not previously been documented in Moreton Bay, dominated by very high density patches (transect maximum 0.85 ind.m⁻², frame maximum 125 ind.m⁻²) of cerianthid anemones. Group H was similar to group G in that it was dominated by bioturbators, but was clearly distinguished by having fewer species, and supporting an array of taxa not found in group G including the seagrass *Halophila ovalis*, and an unidentified sand anemone occurring in high density patches

(transect maximum 0.1 ind.m⁻², frame maximum 38 ind.m⁻²). Group B was a relatively depauperate site characterised by low densities of mobile macroinvertebrates such as echinoids, crinoids, bivalves, and occasional sponges and soft corals attached to patches of rubbly substrate.

6.3.2.2 Exceptional or unusual features

Several sites contained features of unusual diversity or abundance (site numbers shown in figure 6.2) whilst still grouping with one of the core groups on the second pass.

At site 31 and to a lesser extent 25, part of the transect covered a macroalgal reef on boulder outcrops. Cover was dominated by several species of macroalgae, including large brown algae such as *Ecklonia sp.* and *Sargassum sp.* The remainder of the transect was quite depauperate, so overall abundance was not sufficiently high to prevent this site from falling within Group G.

Site 54 contained an unusual deepwater (48 – 52 m) reef assemblage dominated by encrusting algae, soft corals, seawhips, sponges and crinoids. Examination of the SIMPER tables showed that this site was included with Group I on the second pass on the basis of encrusting algal cover and soft coral. It is likely that these were actually different species, but because of the deepwater location, samples were unable to be recovered, so the dominant taxa had to be assigned to general categories. This resulted in the site being allocated to group I, with which it was most similar, as the only reefal group.

Site 63 contained the only significant stands of soft coral reef observed inside the bay but was included within group D on the basis of associated sponge and macroalgae taxa. This location is well known to local anglers as supporting reef fish.

6.3.2.3 Effects of taxonomic resolution

The classification derived from higher taxonomic levels proved to be quite similar to that from the morphospecies level. Spearman's rank correlation between the lifeform and morphospecies classifications was high ($\rho = 0.87, p = 0.001$). The biotic group and phylum classifications were only slightly less highly correlated with the morphospecies classification ($\rho = 0.79$ and 0.77 respectively, $p = 0.001$ in both cases). When the derived groups from the lifeform classification were compared to those from the morphospecies level, it was apparent that there was some difference, with 8 of the 78 sites grouped inconsistently. The core groups were essentially intact. The major inconsistency was that the lifeform level classification combined within bay (parts of Group D) and offshore (Group I) sites that were both dominated by sponges and algae but separated at the morphospecies level on the basis of different species.

6.3.2.4 Influence of biotic groups

Similarity matrices constructed separately from subsets of the dataset by biotic groups were compared to that from the entire dataset by Spearman's rank correlation (Table 6.3). The relationship between similarity matrices was visualised using a 2-stage MDS (Figure 6.3). No single group correlates well with the overall dataset. Bioturbators correlated with the overall classification clearly better than other biotic groups, which would suggest that they had more influence on the overall classification. The remainder of the biotic groups were remarkably consistent in their contribution to the overall

classification. All except ascidians have correlation values between 0.10 and 0.25.

Clearly, no single taxonomic group was driving the classification.

Table 6.3: Spearman’s rank correlation of similarity matrices between biotic groups and the entire dataset

Significance estimated by Monte Carlo randomisation. All correlations significant ($p < 0.05$) except where indicated in parentheses

Biotic Group	Correlation (ρ) with whole dataset
Annelids	0.22
Anthozoans	0.16
Ascidians	0.07 (<i>0.112</i>)
Bivalves	0.20
Bioturbators	0.58
Echinoderms	0.25
Hard Corals	0.10 (<i>0.075</i>)
Macroalgae	0.23
Soft Coral	0.14
Seagrass	0.11
Sponges	0.21

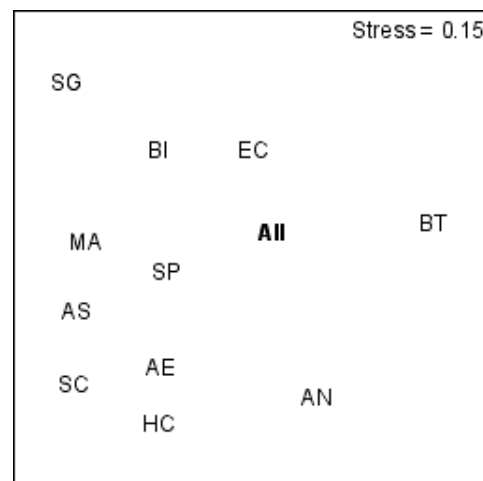


Figure 6.3: 2-Stage MDS illustrating relationship of similarity matrices for individual biotic groups to that from the whole dataset

All = whole dataset, AE = annelids, AN = anthozoans, AS = ascidians, BI = bivalves, BT = bioturbators, EC = echinoderms, HC = hard corals, MA = macroalgae, SC = soft corals, SG = seagrasses, SP = sponges

The 2-stage MDS (Figure 6.3) shows that while echinoderms were the closest group in multidimensional space, the groups were quite evenly spaced over the plot. In contrast to the correlation analyses, bioturbators were more distant than several biotic groups, and clearly influenced the overall classification from a different direction than most biotic groups. No group was nearly co-incident with either the whole dataset or any other group. The MDS plot reinforced the conclusion that the contribution of the various biotic groups to the overall classification was quite even. No single group or subset of groups drove the classification.

6.3.3 Representation in existing MPA

Representation was assessed using both point (Figure 6.4) and polygon (Figure 6.5) analyses. The polygon maps were constructed for the analysis of representation only, and should be interpreted with caution. Voroni tessellation places polygon boundaries at the midpoint between adjacent sites belonging to different habitat groups. In reality, the boundary can lie anywhere between the two sites, and in most cases is unlikely to be very clearly defined.

In each type of analysis the habitat information was overlaid on the Moreton Bay Marine Park zoning plan to derive the % frequency (points – Figure 6.4) or % area (polygons – Figure 6.5) of occurrence of each habitat type in each zone. The information is also presented in terms of IUCN protected area categories (IUCN 1994).

The results of point (Table 6.4) and polygon area (Table 6.5) analyses are comparable. The points analysis showed that none of the habitat types is represented within a highly protected (no-take: IUCN Cat II or below) zone. Four of the nine habitat types are not

represented in a zone managed for protection of the habitat or particular values (IUCN Cat IV or below).

The polygon area analysis concluded that only two of the nine habitat types are represented within a highly protected (no-take) zone, and of these less than 3% is represented. All habitat types had some representation in a zone managed for protection of the habitat or particular values, and in three of the nine habitat types less than 10% of the area is represented.

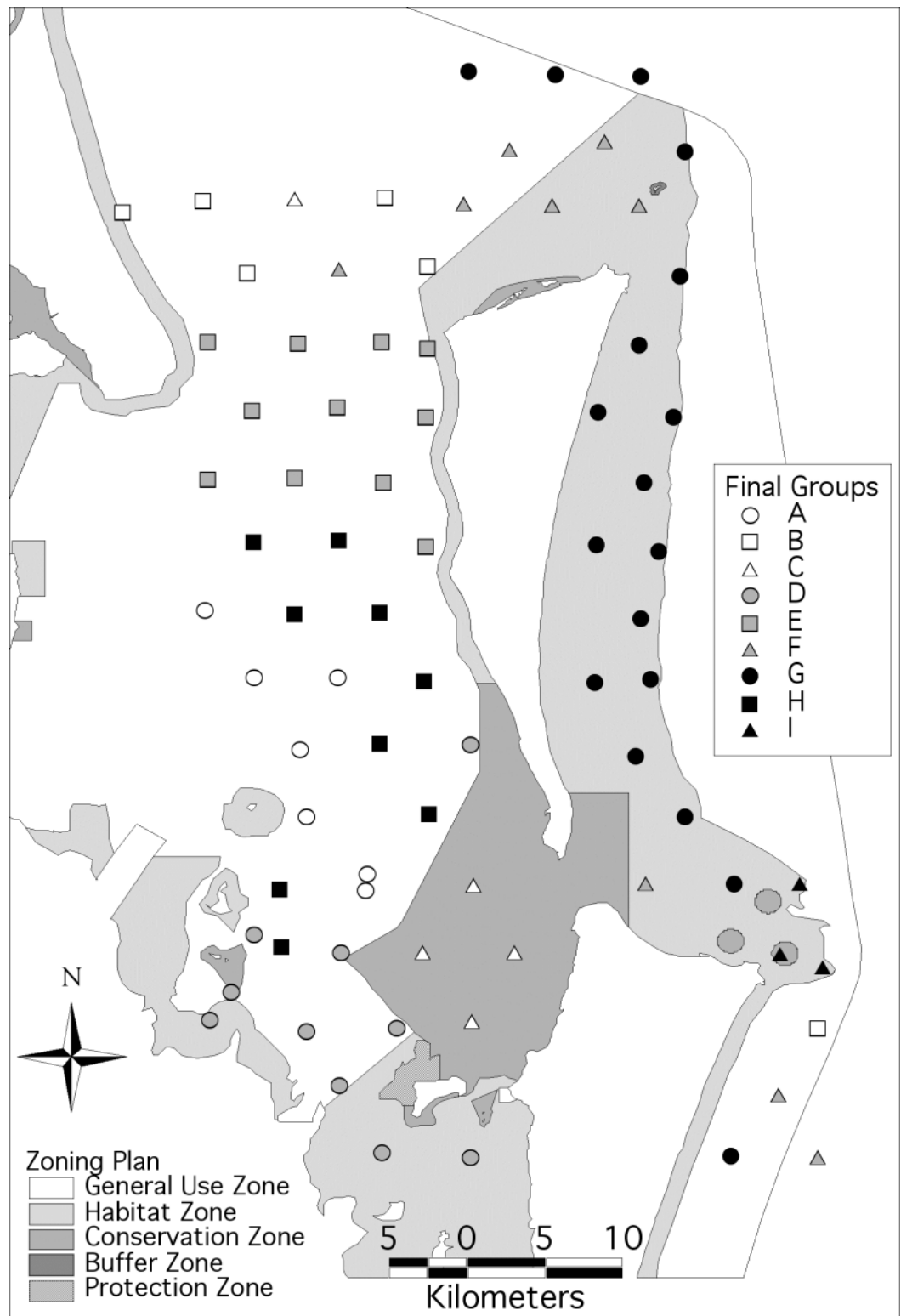


Figure 6.4: Habitat group points superimposed on the Moreton Bay Marine Park zoning plan

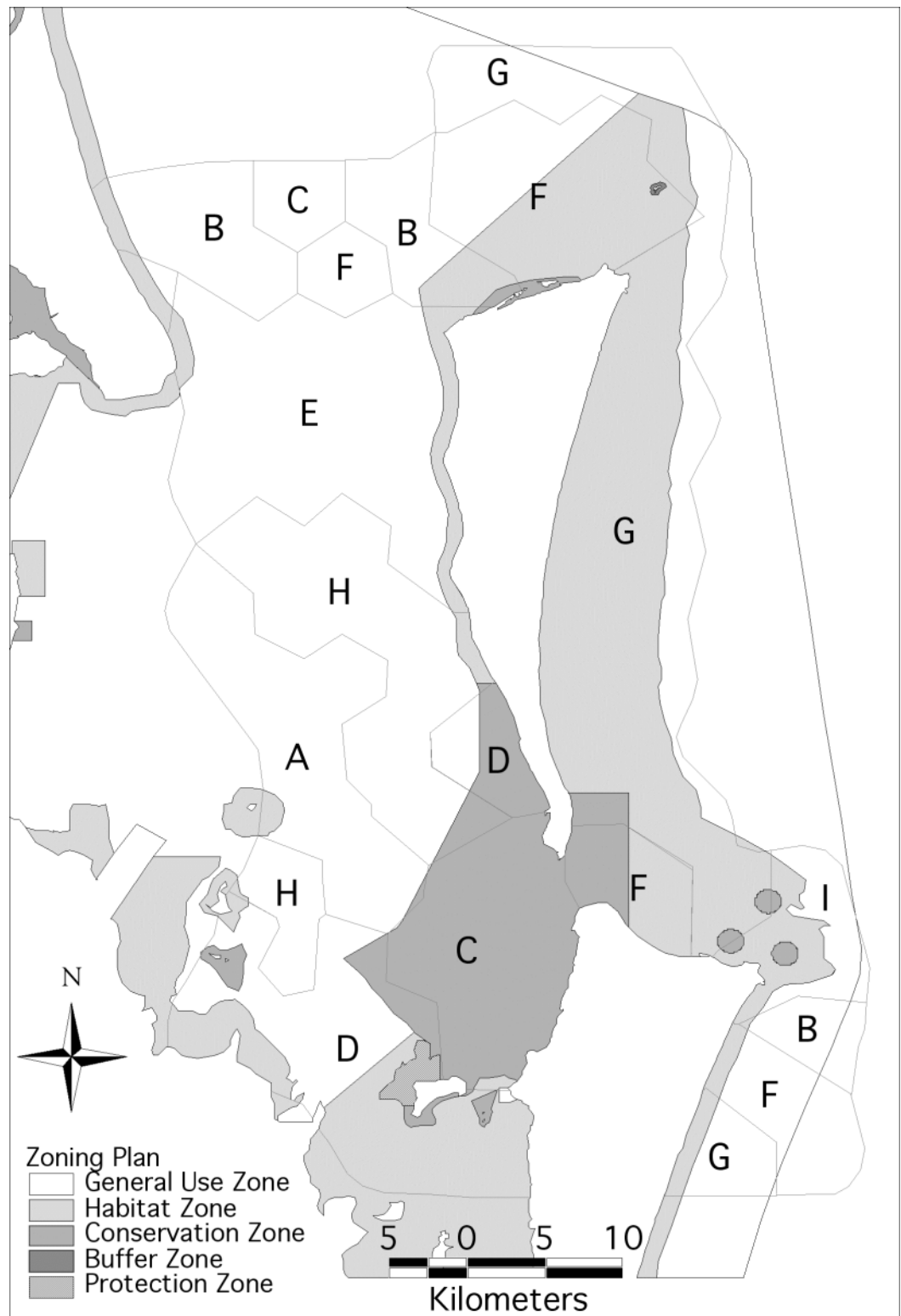


Figure 6.5: Habitat group polygons derived from Voroni tessellation superimposed on the Moreton Bay Marine Park zoning plan

Table 6.4: Representation by points

Number of points of each habitat type in each zone or category divided by the total number of points of each habitat, expressed as %. IUCN categories corresponding to each zone are given in parentheses below the zone name

Habitat Group	Zone and IUCN Category					
	General Use (VI)	Habitat (IV)	Conservation (IV)	Buffer (IV)	Subtotal IV	Protection (II)
A	100					
B	100					
C	20		80		80	
D	70	30			30	
E	100					
F	50	50			50	
G	18	82			82	
H	100					
I		67	33		100	
Overall	63	30	7	0	37	0

Table 6.5: Representation by polygon area

Area of each habitat type within each zone or category, divided by total area of each habitat type, expressed as %. IUCN categories corresponding to each zone are given in parentheses below the zone name

Habitat Group	Zone and IUCN Category					
	General Use (VI)	Habitat (IV)	Conservation (IV)	Buffer (IV)	Subtotal IV	Protection (II)
A	98.29	1.31	0.40		1.71	
B	86.59	12.42	0.99		13.41	
C	17.04	1.01	81.95		82.96	
D	39.16	39.93	18.24		58.17	2.67
E	90.39	9.60	0.01		9.61	
F	45.26	46.20	8.32	0.18	54.70	0.04
G	34.00	63.94	2.07		66.00	
H	93.70	2.43	3.86		6.30	
I	49.65	44.37	5.98		50.35	
Overall	58.55	29.50	11.59	0.02	41.11	0.34

6.4 Discussion

The derived habitat groups illustrate consistently occurring associations of sites at Bray Curtis similarities of 40% or above, plus the three very depauperate sites. Nine habitat types are recognised as a basis for assessment of representation. Analyses of representation show that virtually none of the habitat types derived are included within highly protective zones (IUCN Category II). While about 40% of the existing marine park is not covered by the study, there are no offshore or open water highly protected areas outside the study area (Anon 1997), so representation of habitat types in IUCN Category II areas would not be improved by considering the entire marine park. The proportion of each habitat type that should be included in highly protected zones is contingent on the reserve philosophy, the ecology of the benthic assemblages, and the degree and likelihood of threat to each habitat type. Nonetheless, any rezoning of the park that included representation as a criterion should include substantially expanded highly protected areas to include samples of each of these habitat types, even at the lowest sampling resolution (5 km).

The derived habitat classification proved to be quite robust to decreasing taxonomic resolution, and not driven primarily by any one biotic group. The role of bioturbators is clearly important, and provides a link within this classification, which is otherwise based on epibenthic components, to infaunal elements such as previously surveyed by Stephenson *et al.* (1970). Whilst there was some loss of accuracy with decreasing taxonomic resolution, the core groups remained essentially intact, and this has implications for the wider use of this technique. In training observers to extract data from video images, it is clearly easier (and quicker) to assign taxa to lifeform categories or biotic groups than to individual morphospecies. It does not necessarily follow, however, that studies in other regions will show the same resilience to taxonomic

resolution. Vanderklift *et al.* (1998) examined the effect of differing taxonomic levels on selecting areas for biodiversity conservation. The findings showed that the effect varied enormously depending on the high-level group (plants, invertebrates, fish) considered. The proportion of biodiversity captured is also strongly affected by the scale of the area surveyed (Ward *et al.* 1999). The use of any higher taxonomic level to extract data for habitat classification would therefore need to be carefully evaluated by field trials in the subject region before being adopted for a broad scale survey.

Within the plethora of planning and summary documents produced in recent years that are relevant to Moreton Bay or south-east Queensland more generally (e.g. Department of Environment and Conservation 1989, Brisbane River Management Group 1996, Dennison and Abal 1999, to name a few), subtidal habitats other than seagrass beds and coral reefs have received scant attention. Habitat maps in such documents typically illustrate mangroves, salt marshes, seagrass beds and coral reefs and leave the rest blank (e.g. Brisbane River Management Group 1996). Yet the combined area of these high profile habitats within Moreton Bay Marine Park is less than 10% (<380 km²) of the total marine park area (data from Brisbane River Management Group 1996, Hyland *et al.* 1989, Dennison and Abal 1999). The current study has used an inclusive approach, at a management-relevant scale, to “fill in the blanks”. All the subtidal environments within the study area were classified into habitat types on the basis of biological information, rather than just highlighting high profile habitat types. The habitat types are derived from a quantitative and consistent survey methodology and provide a robust basis for the analysis of representation in the existing MPA, and for incorporation of representation in any future revised zoning plan. This is consistent with contemporary approaches to marine resource management which make it clear that all habitat types

have an intrinsic conservation value and should be represented in reserve systems (Agardy 1995, 2000, Stevens 2002, Marine Reserves Working Group 2002).

This is the most spatially comprehensive survey yet carried out in Moreton Bay. Several studies through the 1970s and 1980s (Hailstone 1976, Young and Wadley 1976, Poiner 1977, Stephenson and Cook 1977, Stephenson *et al.* 1978, Stephenson 1980, Poiner and Kennedy 1984) characterised parts of Moreton Bay, principally Bramble Bay in the west and Middle Banks in the east, on the basis of epifauna and infauna from grab samples. Different benthic communities were apparent with some general east-west trends across the bay. Stephenson *et al.* (1970) defined eight benthic habitat types in the bay on the basis of infauna from 400 dredge samples. However no previous study has attempted to characterise the greater part of the bay including the dynamic sand bank systems in the northern part, and no previous study has examined benthic communities offshore. Other recent surveys in Moreton Bay have focussed on mapping seagrass beds and quantifying changes in their extent over time (Hyland *et al.* 1989, Dennison and Abal 1999).

This survey has brought to light previously unreported aspects of the macrobenthic communities of Moreton Bay and associated offshore areas. Of particular interest is the dominance of cerianthid anemones in the northern part of bay, at maximum densities in a single frame of over 100 ind.m⁻². Given the nature of the local environment, with mobile sand substrates in high to moderate current flows, the diversity of this habitat group is surprising. The dynamic sand bank systems of the northern bay (e.g. Pattiaratchi and Harris 2002) have long been assumed, in the absence of quantitative information (e.g. Dennison and Abal 1999), to be quite depauperate. This study shows that this is not the case. Eighteen macrobenthic taxa (with eight contributing more than

1% to total group similarity) were recorded from the area including the high densities of cerianthid anemones previously mentioned, but also seagrasses and mobile taxa, particularly echinoderms. Seagrasses have also been noted in previously unmapped locations, particularly on the sand banks outside the northern entrance, and sparsely offshore to about 25 m depth.

The inclusive approach to habitat survey and mapping used in this study has also located examples of deep water algal reefs (site 31) and soft coral reefs (site 54) not previously recorded in this area. The scale of the survey program, dictated by the target scale of the classification, did not permit finer scale investigation to determine the boundaries of these habitat types. Subsequent surveys using a stratified sampling arrangement would probably locate further examples, and perhaps other habitat types not found in this study.

Chapter 4 reported on the poor correlation between abiotic surrogates and biological distributions within Moreton Bay. The results of this study indicate that this may also apply in offshore waters. The offshore area south of Point Lookout is quite flat, sandy, and between 35 and 45 m deep. Yet within this area, 5 sample sites within 20 km are classified into 4 different habitat groups on the basis of biological information, representing a clear error of false homogeneity as defined in Chapter 4. Although less marked, similar failure of abiotic data to predict clear differences in biological similarity is apparent in the offshore sites in the north-eastern part of the study area.

Because of the scale at which the survey was conducted, it is certainly possible that habitat elements smaller than the site spacing have been overlooked. A subsequent survey program could be devised using stratified or randomised placement between the

sample sites used in this study to determine the likelihood of this. The study also takes no account of temporal variation, representing in effect a snapshot in time of the macrobenthic biota of the region. Again, this could be the subject of subsequent studies, although most of the taxa recorded are not seasonal or very mobile.

The use of MPAs as a management tool is increasing around the world, and with it the need for robust and objective methods of characterising the habitats encompassed. The method used for this study is characterised by: a) an inclusive approach to habitat characterisation, b) the use of biological information rather than abiotic surrogates, and c) a cost-effective and quantitative survey technique. It therefore has potentially broad application for the design of MPAs both in south-east Queensland and in other parts of the world.

This study has provided a major increase in the information available on the distribution of habitat types on a bay-wide scale. The fact that this study has located examples of habitat types not previously described in Moreton Bay, a relatively well known and intensively studied system (e.g. Crimp 1992, Tibbetts *et al.* 1998), adds urgency to the need to carry out habitat mapping at this scale more generally, before we are reduced, as Stachowitsch (2003) suggests, to studying only impacted marine environments. There is clearly a risk that we may lose habitats before we even realise they are there.

Chapter 7 General Discussion

7.1 Summary of Findings

This study has found that there are detectable and statistically distinct patterns in soft-bottom macrobenthic communities at the local scale within and adjacent to Moreton Bay. Nine habitat types are recognised in the bay, of which only one is on hard substrate.

Commonly used methods of delineating marine habitat types over reasonably large areas are based (wholly or partly) on abiotic surrogates such as depth, sediment composition and current stress. An MPA designed to include representative samples of all habitats, but based on this approach, would fail to recognise and represent the diversity of habitat types present.

It was valid to classify sites into habitat groups by spatial agglomeration, since sites closer together were clearly more similar than those far apart. Moreover, there was little loss of similarity at scales up to, and beyond, the nominal site spacing.

The existing Moreton Bay Marine Park zoning under-represents all the derived habitat types in highly protected (IUCN category I or II) zones. Only two of the habitats were represented at all in highly protected zones, and of these representation is less than 3%. Although this is based on a survey encompassing 60% of the marine park, a habitat classification of the entire park would be unlikely to increase representation, since there are no more highly protected areas in the parts of the park that could be covered by future surveys. It is certainly possible that additional habitat types may be found in the remaining unsurveyed parts of the marine park.

The video survey method used was inclusive in nature, aiming to place all parts of the study area into habitat types, rather than concentrating on high profile or productive habitat types. The habitat classification was based exclusively on biological information, rather than abiotic surrogates. The video method proved to be rapid and cost-effective but still data-rich in comparison to other survey techniques.

7.2 Implications

7.2.1 Habitat Survey and Classification

Studies seeking to characterise benthic habitats at scales similar to the current study have generally used grab samples, dredges, corers and trawls, individually or in combination (e.g. Hensley 1996, Tselepides *et al.* 2000), often as an adjunct to acoustic characterisation (e.g. Brown *et al.* 2002). Habitat mapping of Port Philip Bay (south-eastern Australia), with an area of about 1,900 km², has been derived from grab sampling (Wilson *et al.* 1998, Currie and Parry 1999) and diver operated sleds (Cohen *et al.* 2000). Video sampling has been used as an adjunct to grab or trawl sampling (Cailliet *et al.* 1999, Kiyko and Pogrebov 1997), acoustic characterisation (Bax *et al.* 2000) or laser swath mapping (Carey *et al.* 2003) but is not frequently used as the primary or exclusive device for habitat classification.

Benthic habitats in Jervis Bay, on Australia's south-east coast, were characterised by intensive video survey using a large video sled deployed from an 18 m vessel (CSIRO 1994). Five habitat types were defined in Jervis Bay on the basis of biological and abiotic features, although at 102 km² the area of the CSIRO study is less than one twentieth the area covered by the current study. Other studies have used video at much

smaller scales for impact assessment or monitoring purposes (Christie *et al.* 1996, Sweatman 1997). A contrasting example is the use of video from a Remotely Operated Vehicle (ROV) to characterise benthic habitats of arctic and antarctic shelf systems from 30 – 550 m depth by Starmans *et al.* (1999). Although the total area encapsulated by the video imagery (c. 20,000 m²) was about half that of the current study, it was used to characterise habitats within areas of 100,000s of km² at opposite ends of the globe.

To construct a habitat classification from a broad scale survey obviously entails extrapolation from the areas sampled into adjacent areas, since no survey can in practical terms be comprehensive. To maximise the validity of that extrapolation, the area sampled should be as large as is practically possible in relation to the total area studied. Additionally, the relationship between similarity and distance should be established to give some indication of the distance from the sampled point for which extrapolation is valid.

In this study, it was established (Chapter 5) that between-site similarity diminishes very little at distances up to 3.5 km (mean Bray Curtis similarity > 60%), and relatively little at distances up to 6 km (mean Bray Curtis similarity > 40%), beyond which it falls quite rapidly. Therefore extrapolating habitat groups between sample sites approximately 5 km apart is demonstrably valid. Clearly, however, precision in locating habitat boundaries would be improved by a smaller site spacing, but little would be gained in terms of between-site similarity at spacings less than 2.5 km.

Table 7.1: Comparison of selected studies to characterise marine benthic habitats
 Ratio = Total area sampled / area characterised. Methods key: v = video, b = beam trawl, g = grab, c = bottom corer, p = photographic, di = diver, dr = dredge

Reference	Method	Study Area (km ²)	Area Sampled (m ²)	Ratio
Stevens (this study)	v	2,400	39,000	1.6 x 10 ⁻⁵
Brown <i>et al.</i> 2002	g	336	4.3	1.3 x 10 ⁻⁸
Brown <i>et al.</i> 2002	b	336	4,320	1.3 x 10 ⁻⁵
Cohen 2000	di	1,938	9,000	4.6 x 10 ⁻⁶
Tselepides <i>et al.</i> 2000	c	1,624	44	2.7 x 10 ⁻⁸
Kiyko and Pogrebov 1997	c	2,200,000	55	2.5 x 10 ⁻¹¹
Kiyko and Pogrebov 1997	p	2,200,000	1,000	4.5 x 10 ⁻¹⁰
Hensley 1996	g	15,000	4.8	3.2 x 10 ⁻¹⁰
CSIRO 1994	v	102	105,600	1.0 x 10 ⁻³
Poore <i>et al.</i> 1975	g	1,938	43	2.2 x 10 ⁻⁸
Stephenson <i>et al.</i> 1970	dr	1,500	11,000	7.3 x 10 ⁻⁶

The ratio between the area sampled and the total area characterised by that sampling in this study is higher than most comparable studies (Table 7.1), in some cases by several orders of magnitude. Indeed, of those presented, only one study, the intensive CSIRO (1994) inventory of Jervis Bay, has sampled a greater area, irrespective of the area under study. This gives added confidence in the utility of the derived habitat groups for assessments of representation. It is principally possible because of the ability of video sampling to collect a continuous stream of information over a comparatively large area for little effort, once the camera is in position. There is obviously a cost in terms of lost information compared to diver-based studies, because recognition from video is limited to objects larger than about 3 cm (CSIRO, 1994) and because samples are not retrieved for taxonomic verification (Carleton and Done 1995). In the present application, broad scale survey for habitat classification at a scale relevant to MPA design, this is offset by its ability to sample extensively in a cost effective manner. Whilst species level taxonomy is clearly very important in many contexts, it was demonstrated in Chapter 6

that the habitat classification derived at lower taxonomic resolutions is very similar to that at the morphospecies level, although this may not necessarily apply in other regions.

Video-based surveys clearly sample different components of biodiversity than grab samples, dredges, corers or trawls, and should therefore not be seen as a replacement for such methods. It has advantages over all these methods in terms of its low environmental impact, ease of use, rapid acquisition of quantitative data, and the provision of in-situ information. Caillet *et al.* (1999) compared quantitative sampling from trawl, video sled and submersible and reported that video sampling gear was less subject to bias from gear avoidance and provided consistently higher “and perhaps better” (p. 579) estimates of density. The “flying” video arrays used in this study and others (Barker *et al.* 2000) have the additional advantage of being usable on virtually any substrate. The compact, lightweight array used in this study provides, perhaps for the first time, the capacity to conduct quantitative and broad scale surveys of macrobenthos quite inexpensively. Since it can be deployed from very small craft, the range of habitats accessible is limited only by turbidity (> c. 3 m visibility) and the depth limitations of the camera housing. The ability to deploy it from a small vessel dramatically reduces field costs, and the capital cost of the equipment is low. Estimated costs, based on equipment and vessel costs, person-days in the field and in the laboratory (Chapter 3) are an order of magnitude less than comparable diver-based (Cohen *et al.* 2000), video-sled (CSIRO 1994) or ROV-based methods (Parry *et al.* 2003).

7.2.2 *Designing MPAs for representation*

The survey and classification method used for this survey approximates the BIORAP methodology formulated by Ward *et al.* (1998). It provides a robust layer of information for incorporation into quantitative reserve design processes (e.g. Nicholls and Margules 1993), particularly optimisation techniques such as those recently used in California (MRWG 2002), Cuba (Possingham, pers comm), the Great Barrier Reef (GBRMPA 2003) and other locations (Possingham *et al.* 2000). The utility of such methods depends in part on the sophisticated algorithms used and the expert selection of parameters in the analysis, but more fundamentally on the quality and relevance of the source information (e.g. Pressey *et al.* 1999).

Virtually all published methods for reserve selection and / or design have as an essential early step the need for a map of the habitats encompassed (e.g. Purdie 1987, Nicholls and Margules 1993, Ward *et al.* 1998) at the scale of management. Whilst even observed and measured biological distributions are themselves surrogates for biodiversity at scales from genes to ecosystems, they have the significant advantage of also being direct elements of biodiversity, as well as surrogates (Ward *et al.* 1998). Logically, there is a greater likelihood that habitat mapping based on observed biological distributions will have measurable conservation benefits when applied to MPA design than the use of abiotic surrogates not of direct conservation relevance. This was demonstrated by O'Hara (2001), who compared the performance of a biological (dominant vegetation) and abiotic (lithology, depth, exposure, region) surrogates in predicting patterns of similarity in temperate subtidal rocky reef biota. Whilst the scale at which similarity was assessed was greater than the current study (10s to 100s of km), and within-habitat variation was high, dominant vegetation was the best single predictor of biological similarity. The best prediction was a combination of dominant vegetation

and region. The regions used were from the Interim Marine and Coastal Regionalisation of Australia (IMCRA), a bioregional classification of all Australian waters (IMCRA Technical Group 1998), so that the regional variable in O'Hara's analysis contains in fact some biological component. Whilst not directly comparable to the current study (different scales and substrate emphases), O'Hara's results support the conclusions of the current study. Similarly, at a smaller scale, Benedetti-Cecchi *et al.* (2003) demonstrated that MPAs in the Tuscan Archipelago fail to represent patterns of between-shore variability in intertidal assemblages.

In assessing and planning for representativeness in MPA design, the use of a hierarchy of scales is well accepted. The drawing of MPA boundaries occurs at site and local scales (Stevens 2002, Chapter 1) and can be demonstrably based on habitat maps based on real biological distributions (Chapter 6). MPAs at this scale are nested within regional scale (e.g. Harper *et al.* 1993, IMCRA Technical Group 1998) and continental scale (Kelleher *et al.* 1995) classifications based on biogeographic (e.g. Turpie *et al.* 2000, Awad *et al.* 2002) and biophysical information.

Nonetheless, contemporary examples of reserve design for representation (e.g. MRWG 2002, GBRMPA 2003) commonly use as their basis (wholly or in part) abiotically derived habitat definitions, assuming that this encompasses the range of biodiversity to be represented. Chapter 4 demonstrated that in the area of this study, that assumption would entail errors of false homogeneity of up to 62%, resulting in habitat boundaries that were inaccurate and misleading. In such a case, the measurable benefits to conservation of a reserve system designed on that basis would in all likelihood be negligible.

Community expectations of scientific robustness and procedural transparency in marine conservation planning are high (e.g. Fogarty 1999, White *et al.* 2002). MPAs are a major, although by no means complete (Boersma and Parrish 1999), tool for conservation and management of marine biodiversity. There is an obligation placed on MPA planning and conservation-oriented research alike to use the most rigorous and relevant methods and information available, or be open to significant, and warranted, criticism (e.g. Jameson *et al.* 2002, Pearce 2002). Agardy (1995) spelled out the priorities for marine conservation, chief among which was, and remains, the definition of true ecological boundaries of marine systems. The difficulty in doing so has been a lack of habitat mapping at the requisite scale based on real biological distributions (Solan *et al.* 2003), and the single greatest reason behind that lack has been that it costs too much to do. This study has demonstrated that that need no longer be the case.

Finally, a note of warning. Even the best information base will not prevent inappropriate decision-making, for a host of reasons. In the terrestrial situation, where the information base is generally orders of magnitude better than in marine areas, “*Ad hoc* approaches to reservation persist despite clearly stated representation goals, improving databases, and systematic techniques for reserve collection” (Pressey 1994, p. 662). Information needs not only to be gained, but interpreted, disseminated, discussed and applied at all levels of scientific and management organisations.

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