Designing Marine Protected Area Networks in the Dover Strait

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Thesis submitted for the degree of
Doctor of Philosophy
Durrell Institute of Conservation and Ecology
University of Kent at Canterbury
April 2002



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Table of Contents

LIS LIS AB AC	T OF I T OF I STRA KNOV	OF CONTENTS	I V X XI XII
CH	APTE	ER 1: GENERAL INTRODUCTION	1
1.1	Introd	duction	1
			1
			3
1.4			6
		1 0	8
			10
			12
1.6	Conse		15
			15
		•	16 17
			18
		ÿ	19
	. Thesi		1)
CH	APTE		21
2.1	Introd	luction	21
			23
			25
	2.4 Biodiversity		
2.5	Bathy	metry	27
2.6			28
			29
			30
	2.6.3		31
			31
			32
			32
			33
		TO A CONTROL OF THE PARTY AND A STAR STAR STAR STAR STAR STAR STAR ST	33 34
27			34 34
			3 4 36
2.0	Summ	····	50
CH	APTE		37
3.1	Introd	luction	37
			37
			41
			41
			41
3.3			42
			43
	_		44
		Coast coverage	45
			45
			45
	3.5.2		45
			45
		3.5.2.2 Results and discussion	45

	3.5.3	Selection unit coverage
		3.5.3.1 <i>Methods</i>
	254	3.5.3.2 Results and discussion
	3.5.4	Bathymetry coverage
		3.5.4.1 <i>Methods</i>
		3.5.4.3 <i>Discussion</i>
	3.5.5	Environmental coverages.
		3.5.4.1 <i>Methods</i>
		3.5.4.2 <i>Results</i>
		3.5.4.3 Discussion.
3.6	Sumn	nary
CH	ADTE	R 4: ICHTHYOPLANKTON DISTRIBUTION COVERAGES: MODELLING
CH	IAPIE	TECHNIQUES
		TECHNIQUES
4.1	Introd	uction
4.2	Interp	olation of ichthyoplankton abundance and distribution
		Methods
		Results
		Discussion
4.3		ring abundance coverages for inclusion in the GIS database
		Results
		Discussion
4.4		eting abundance values within the selection unit grid from distribution coverages
		Methods
		Results and discussion
4.5		nary
		R: 5 IDENTIFYING MPA NETWORKS USING THE HOTSPOT APPROACH uction
		fying hotspots using presence / absence data
		Methods
	5.2.2	Results
		Discussion
5.3		fying hotspots using proportional richness
		Methods
		Results
5 1		Discussion
J. 4		Methods
		Results
		Discussion
5.5		ot method comparisons
		Methods
		Results
		Discussion
5.6		etion provided by hotspot methods
		Methods
		Discussion
5.7		nary
CH	APTE	R 6: SELECTION MPA NETWORKS USING PRESENCE / ABSENCE AND PROPORTIONAL AREA DATA
		uction
6.2		fying minimum sets using presence / absence data
		Methods
		Results
	0.4.3	Discussion

6.3	3 Coverage of ichthyoplankton abundance by presence / absence minimum sets	
	6.3.1 <i>Methods</i>	
	6.3.2 Results	
	6.3.3 Discussion	
	4 'Summed rarity' complimentarity selection algorithm	
6.5	5 Complimentarity networks using proportional area	
	6.5.1 <i>Methods</i>	
	6.5.2 Results	100
	6.5.3 Discussion	
6.6	6 Complimentarity networks using proportional conservation targets	
	6.6.1 <i>Methods</i>	
	6.6.2 Results	
	6.6.3 Discussion	
6.7	7 Coverage provided to ichthyoplankton abundance by MPAs selected using proportional are	
	6.7.1 <i>Methods</i>	
	6.7.2 Results	
	6.7.3 Discussion	
6.8	8 Summary	108
~	WILDERD TO ONE DOWN ON A NOT NOT WORK ON A STATE OF THE	100
CH	HAPTER 7: SELECTING MPA NETWORKS USING ABUNDANCE DATA	109
		100
	1 Introduction	
1.2	2 Complimentary networks using abundance data	
	7.2.1 <i>Methods</i>	
	7.2.2 Results	
7 2	7.2.3 Discussion	
1.3	3 Identifying MPA networks for three conservation targets using abundance data	
	7.3.1 <i>Methods</i>	
	7.3.2 Results	
7.4	7.3.3 Discussion	
7.4	4 Overlap of minimum sets for abundance data at two sampling times	
	7.4.1 Methods. 7.4.2 Results.	
	7.4.2 Results. 7.4.3 Discussion.	
7.5	5 Summary	
1.5	, Summary	117
СН	HAPTER 8: IDENTIFYING MPA NETWORKS IN THE DOVER STRAIT USING	
	ICHTHYOPLANKTON SURROGATES	120
8.1	I Introduction	120
	2 Ichthyoplankton assemblages surrogate	
81=	8.2.1 <i>Methods</i>	
	8.2.2 Results	
	8.2.3 <i>Discussion</i>	
8.3	3 Seascape surrogate	
	8.3.1 <i>Methods</i>	
	8.3.2 <i>Results</i>	
	8.3.3 <i>Discussion</i>	
8.4	4 Higher taxa surrogate	
	8.4.1 <i>Methods</i>	
	8.4.2 <i>Results</i>	132
	8.4.3 Discussion	133
8.5	5 Commercial species surrogate	133
	8.5.1 <i>Methods</i>	133
	8.5.2 Results	
	8.5.3 Discussion	
8.6	5 Effectiveness and efficiency of surrogates to identify MPA networks	134
8.6	Effectiveness and efficiency of surrogates to identify MPA networks	134 134
8.6	6 Effectiveness and efficiency of surrogates to identify MPA networks. 8.6.1 Methods. 8.6.2 Seascape surrogate.	134 134 136
8.6	6 Effectiveness and efficiency of surrogates to identify MPA networks. 8.6.1 Methods. 8.6.2 Seascape surrogate. 8.6.2.1 Results.	134 134 136
8.6	5 Effectiveness and efficiency of surrogates to identify MPA networks. 8.6.1 Methods. 8.6.2 Seascape surrogate. 8.6.2.1 Results. 8.6.2.2 Discussion.	134 136 136 139
8.6	6 Effectiveness and efficiency of surrogates to identify MPA networks. 8.6.1 Methods. 8.6.2 Seascape surrogate. 8.6.2.1 Results. 8.6.2.2 Discussion. 8.6.3 Ichthyoplankton assemblage surrogate.	134 136 136 139 140
8.6	5 Effectiveness and efficiency of surrogates to identify MPA networks. 8.6.1 Methods. 8.6.2 Seascape surrogate. 8.6.2.1 Results. 8.6.2.2 Discussion.	134 134 136 139 140

	8.6.4 Commercial species surrogate	143 143
	8.6.4.2 <i>Discussion</i>	146
	8.6.5 Higher taxa surrogate	147
	8.6.5.1 <i>Results</i>	147
	8.6.5.2 Discussion	150
	8.6.6 Overall surrogate results and discussion	151
8.7	Summary	153
СНА	PTER 9: SELECTING MPA NETWORKS WITH A PREFERENCE FOR ADJACENT	
CIM	SITES	154
9.1	Introduction.	154
9.2	Incorporating adjacency into the selection of units for a PA network	155
	9.2.1 <i>Methods</i>	156
	9.2.2 <i>Results</i>	156
	9.2.2 <i>Discussion</i>	162
9.3	Summary	163
CHA	PTER 10: SELECTING MPA NETWORKS USING IRREAPLACEABILITY	164
10.1	Introduction	164
10.2	Site irreplaceability and summed irreplaceability scores	165
	10.2.1 <i>Methods</i>	165
	10.2.2 <i>Results</i>	164
	10.2.3 Discussion	170
10.3	Minimum sets required for proportional conservation targets using site and summed	171
	irreplaceability	171
	10.3.1 <i>Methods</i>	171
	10.3.2 <i>Results</i>	171
	10.3.3 Discussion	175
10.4	Comparing MPA networks identified using three algorithms	175
	10.4.1 <i>Methods</i>	175
	10.4.2 <i>Results</i>	176
10.5	10.4.3 Discussion	177
10.5	Summary	178
CHA	PTER 11: CONCLUDING DISCUSSION	179
11.1	Introduction	179
11.2	Improvements to the methods	180
11.3	Applicability of the methods	180
11.4	Scale and biodiversity surrogates	182
11.5	Facilitating a wider adoption of selection algorithms into conservation planning	183
REFI	ERENCES	186
		200
APPI	ENDIX	206

List of Figures

Figure 2.1 The Dover Strait	21
Figure 2.2 Ichthyoplankton survey positions in the Dover Strait	23
Figure 2.3 Bathymetry of the study area	28
Figure 3.1 The differences between rasters and vectors	38
Figure 3.2 Representation of a polygon by vector and raster models	39
Figure 3.3 Raster and vector lines	39
Figure 3.4 Political boundaries and rivers; data suited to vector representation	40
Figure 3.5 Elevation; data suited to raster representation.	40
Figure 3.6 Sampling points within the three surveys available for analysis	46
Figure 3.7 Survey one stations to be included in the study	48
Figure 3.8 Survey two sampling points to be included in the study	48
Figure 3.9 Survey three sampling points included in the study	49
Figure 3.10 Surveys one and two selection unit grid system	50
Figure 3.11 Survey three selection unit grid system	50
Figure 3.12 Bathymetry interpolated using krigging	54
Figure 3.13 Bathymetry interpolated using splining	55
Figure 3.14 S2 Surface water salinity	57
Figure 3.15 S2 Bottom water salinity	57
Figure 3.16 S2 Surface water temperature	57
Figure 3.17 S2 Bottom water temperature	57
Figure 3.18 S1 Surface Water Density	58
Figure 3.19 S1 Bottom Water Density	58
Figure 4.1 Errors produced by splining and krigging against sample size	
Figure 4.2 An example of an abundance coverage	
Figure 4.3 Summed abundance values for each selection unit	69
Figure 5.1 S1 Presence richness	
Figure 5.2 S1 Presence richness hotspots	
Figure 5.3 S2 Presence richness	
Figure 5.4 S2 Presence richness hotspots	
Figure 5.5 S3 Presence richness	
Figure 5.6 S3 Presence richness hotspots	
Figure 5.7 An example of an area of distribution coverage (zoomed in for display)	
Figure 5.8 S1 Proportional richness	
Figure 5.9 S1 Proportional hotspots	
Figure 5.10 S2 Proportional richness	78

Figure 5.11 S2 Proportional hotspots	78
Figure 5.12 S3 Proportional richness	79
Figure 5.13 S3 Proportional hotspots	79
Figure 5.14 S1 Abundance	80
Figure 5.15 S1 Abundance hotspots	80
Figure 5.16 S2 Abundance	81
Figure 5.17 S2 Abundance hotspots	81
Figure 5.18 S3 Abundance	81
Figure 5.19 S3 Abundance hotspots	81
Figure 5.20 S1 Coincidence between abundance and proportional hotspots	83
Figure 5.21 S1 Coincidence between proportional and presence hotspots	83
Figure 5.22 S1 Coincidence between presence and abundance hotspots	83
Figure 5.23 S2 Coincidence between abundance and proportional hotspots	84
Figure 5.24 S2 Coincidence between proportional and presence hotspots	84
Figure 5.25 S2 Coincidence between presence and abundance hotspots	84
Figure 5.26 S3 Coincidence between abundance and proportional hotspots	85
Figure 5.27 S3 Coincidence between proportional and presence hotspots	85
Figure 5.28 S3 Coincidence between presence and abundance hotspots	85
Figure 5.29 Mean and standard error of the protection provided by hotspot methods	89
Figure 6.1 S1 and S2 minimum sets for 1 representation.	95
Figure 6.2 S1 and S2 minimum sets for 6 representations	95
Figure 6.3 S3 minimum set for 1 representation	95
Figure 6.4 S3 minimum set for 6 representations	95
Figure 6.5 S2 10% highest complimentarity networks	100
Figure 6.6 S3 10% highest complimentarity networks	101
Figure 6.7 S1 Minimum sets for 10%, 20% and 50% of area conservation targets	102
Figure 6.8 S2 Minimum sets for 10%, 20% and 50% of area conservation targets	103
Figure 6.9 S3 Minimum sets for 10%, 20% and 50% of area conservation targets	103
Figure 6.10 S1 Protection provided to all ichthyoplankton by 10% area	107
Figure 6.11 S2 Protection provided to all ichthyoplankton by 10% area	107
Figure 6.12 S3 Protection provided to all ichthyoplankton by 10% area	107
Figure 7.1 S1 & S2 Highest ranking 10% complimentarity units using abundance data	
Figure 7.2 S3 Highest ranking 10% complimentarity units using abundance data	
Figure 7.3 S1 Minimum sets for three proportional abundance conservation targets	113
Figure 7.4 S2 Minimum sets for three proportional abundance conservation targets	114
Figure 7.5 S3 Minimum sets for three proportional abundance conservation targets	
Figure 7.6 S1 Frequency of protection levels for all ichthyoplankton based on 10% abundance target	
Figure 7.7 S2 Frequency of protection levels for all ichthyoplankton based on 10% abundance target	
Figure 7.8 S3 Frequency of protection levels for all ichthyoplankton based on 10% abundance target	
Figure 7.9 Coincidence between 10% minimum sets for surveys one and two	119

Figure 8.2 S1 Distribution of abundance of assemblage C	25 25 25
Figure 8.4 S2 Distribution of abundance of assemblage D1	25 25
Figure 8.5 S2 Distribution of abundance of assemblage D2	25
Figure 8.6 S2 Distribution of abundance of assemblage E1	
Figure 8.7 S2 Distribution of abundance of assemblage E2	~
Figure 8.8 S2 Distribution of abundance of assemblage E3	.26
Figure 8.9 S1 PCA Component 1	.26
Figure 8.10 S2 PCA Component 1	.26
Figure 8.11 S3 PCA Component 1	.30
Figure 8.12 S1 Natural breaks seascape categories. Figure 8.13 S2 Natural breaks seascape categories. Figure 8.14 S3 Natural breaks seascape categories. Figure 8.15 S1 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.16 S2 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.17 S3 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.18 S1 Percentage of each ichthyoplankton protected based on 10% target of seascapes. Figure 8.19 S2 Percentage of each ichthyoplankton protected based on 10% target of seascapes.	.30
Figure 8.13 S2 Natural breaks seascape categories. Figure 8.14 S3 Natural breaks seascape categories. Figure 8.15 S1 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.16 S2 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.17 S3 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.18 S1 Percentage of each ichthyoplankton protected based on 10% target of seascapes. Figure 8.19 S2 Percentage of each ichthyoplankton protected based on 10% target of seascapes.	.30
Figure 8.14 S3 Natural breaks seascape categories. Figure 8.15 S1 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.16 S2 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.17 S3 Minimum sets for three conservation targets of seascape biodiversity surrogate. Figure 8.18 S1 Percentage of each ichthyoplankton protected based on 10% target of seascapes. Figure 8.19 S2 Percentage of each ichthyoplankton protected based on 10% target of seascapes.	.31
Figure 8.15 S1 Minimum sets for three conservation targets of seascape biodiversity surrogate	.31
Figure 8.16 S2 Minimum sets for three conservation targets of seascape biodiversity surrogate	31
Figure 8.17 S3 Minimum sets for three conservation targets of seascape biodiversity surrogate	.37
Figure 8.18 S1 Percentage of each ichthyoplankton protected based on 10% target of seascapes	.37
Figure 8.19 S2 Percentage of each ichthyoplankton protected based on 10% target of seascapes	.37
	38
Figure 8.20 S3 Percentage of each ichthyoplankton protected based on 10% target of seascapes	38
	38
Figure 8.21 S1 Frequency of protection provided to abundance by seascapes	39
Figure 8.22 S2 Frequency of protection provided to abundance by seascapes	39
Figure 8.23 S3 Frequency of protection provided to abundance by seascapes	39
Figure 8.24 S1 Minimum sets for three conservation targets using assemblage surrogate	41
Figure 8.25 S2 Minimum sets for three conservation targets using assemblage surrogate	41
Figure 8.26 S1 Percentage of each ichthyoplankton protected, based on 10% assemblage target	41
Figure 8.27 S2 Percentage of each ichthyoplankton protected, based on 10% assemblages target	41
Figure 8.28 S1 Frequency of protection levels based on 10% assemblage target	42
Figure 8.29 S2 Frequency of protection levels based on 10% target of assemblages	42
Figure 8.30 S1 Minimum sets for three conservation targets based on commercial fish surrogate	44
Figure 8.31 S2 Minimum sets for three conservation targets based on commercial fish surrogate	44
Figure 8.32 S3 Minimum sets based on three conservation targets for commercial fish surrogate1	44
Figure 8.33 S1 Percentage of each ichthyoplankton protected, based on 10% commercial target	45
Figure 8.34 S2 Percentage of each ichthyoplankton protected, based on 10% commercial target	45
Figure 8.35 S3 Percentage of each ichthyoplankton protected, based on 10% commercial target	45
Figure 8.36 S1 Frequency of protection levels provided to abundance by commercial species	46
Figure 8.37 S2 Frequency of protection levels provided to abundance by commercial species	46
Figure 8.38 S3 Frequency of protection levels provided to abundance by commercial species	46
Figure 8.39 S1 Minimum sets for three conservation targets based on higher taxon surrogate	
Figure 8.40 S2 Minimum sets for three conservation targets based on higher taxon surrogate	48
Figure 8.41 S3 Minimum sets for three conservation targets based on higher taxon surrogate1	

Figure 8.42 S1 Percentage of each ichthyoplankton protected, based on 10% higher taxon target	149
Figure 8.43 S2 Percentage of each ichthyoplankton protected, based on 10% higher taxon target	149
Figure 8.44 S3 Percentage of each ichthyoplankton protected, based on 10% higher taxon target	149
Figure 8.45 S1 Frequency of protection provided by higher taxon surrogate to ichthyoplanktor	1
abundance	150
Figure 8.46 S2 Frequency of protection provided by higher taxon surrogate to ichthyoplanktor	1
abundance	150
Figure 8.47 S3 Frequency of protection provided by higher taxon surrogate to ichthyoplanktor	1
abundance	150
Figure 8.48 Mean number of units required for minimum sets using surrogates (adjusted for target)	151
Figure 8.49 Mean number of units required for minimum sets for three conservation targets (adjusted for	r
surrogate)	152
Figure 9.1 S1 10% Conservation target with the use of different levels of adjacency co-efficient	
Figure 9.2 S2 10% Conservation target with the use of different levels of adjacency co-efficient	
Figure 9.3 S3 10% Conservation target with the use of different levels of adjacency coefficient	
Figure 9.4 Effect of adjacency coefficient on efficiency	162
Figure 10.1 S1 Summed irreplaceability 10% target	166
Figure 10.2 S1 Site irreplaceability 10% target	166
Figure 10.3 S1 Summed irreplaceability 20% target	166
Figure 10.4 S1 Site irreplaceability 20% target	166
Figure 10.5 S1 Summed irreplaceability 50% target	167
Figure 10.6 S1 Site irreplaceability 50% target	167
Figure 10.7 S2 summed irreplaceability 10% target	167
Figure 10.8 S2 Site irreplaceability 10% target	167
Figure 10.9 S2 summed irreplaceability 20% target	168
Figure 10.10 S2 Site irreplaceability 20% target	168
Figure 10.11 S2 Summed irreplaceability 50% target	168
Figure 10.12 S2 Site irreplaceability 50% target	168
Figure 10.13 S3 Summed irreplaceability 10 target	169
Figure 10.14 S3 Site irreplaceability 10% target	169
Figure 10.15 S3 Summed irreplaceability 20% target	169
Figure 10.16 S3 Site irreplaceability 20% target	169
Figure 10.17 S3 Summed irreplaceability 50% target	170
Figure 10.18 S3 Site irreplaceability 50% target	170
Figure 10.19 S1 Minimum sets identified using algorithms 1 &2, 10% target	172
Figure 10.20 S2 Minimum sets identified using algorithms 1&2, 10% target	172
Figure 10.21 S3 Minimum sets identified using algorithms 1 &2, 10% target	173
Figure 10.22 S1 Minimum sets identified using algorithms 1 &2, 20% target	173
Figure 10.23 S2 Minimum sets identified using algorithms 1 & 2, 20% target	173
Figure 10.24 S3 Minimum sets identified using algorithms 1 & 2, 20% target	173

Figure	10.25	S1 Minimum sets identified using algorithms 1 & 2, 50% target1	74
Figure	10.26	S2 Minimum sets identified using algorithms 1 & 2, 50% target1	74
Figure	10.27	S3 Minimum sets identified using algorithms 1 & 2, 50% target1	75
Figure	10.28	S1 Selection units identified by three selection algorithms1	76
Figure	10.29	S2 Selection units identified by three selection algorithms	77
Figure	10.30	S3 Selection units identified by three selection algorithms1	77

List of Tables

Table 3.1 Errors associated with two methods to interpolate bathymetry	53
Table 4.1 Accuracy of interpolation methods to predict abundance	64
Table 5.1 Spatial coincidence between hotspot methods	80
Table 5.2 Number of hotspots and ichthyoplankton protected by three hotspot methods	87
Table 5.3 Representation of area of distribution by hotspot methods	8
Table 5.4 Representation of abundance by hotspot methods	88
Table 6.1 Efficiency of presence / absence complimentarity networks	94
Table 6.2 Representations of abundance by presence / absence complimentarity networks	97
Table 6.3 Number of units necessary for three proportional conservation targets	102
Table 6.4 Protection provided to ichthyoplankton elements based on 10% area conservation target	102
Table 6.5 Coverage of abundance levels provided by area data	104
Table 7.1 Numbers of study grid cells needed to satisfy different conservation targets	113
Table 8.1 Environmental variation explained by PCA analysis	129
Table 8.2 Reduction in the dataset to lower taxonomic resolution	133
Table 8.3 Reduction in the dataset by removing non-commercial species	133
Table 8.4 Coverage of abundance levels provided by seascape surrogate	136
Table 8.5 Coverage of abundance levels provided by assemblage surrogate	140
Table 8.6 Coverage of abundance levels provided by commercial species surrogate	143
Table 8.7 Coverage of abundance levels provided by higher taxa (species level)	144
Table 9.1 Efficiency of algorithm using different adjacency coefficients	161
Table 10.1 Efficiency of irreplaceability algorithms	17

Abstract

Heightening world-wide concern about the Earth's marine ecosystems is directed towards the problems of habitat degradation, pollution and heavy exploitation of living resources. Whilst protection of biodiversity requires a suite of management strategies, the creation of reserves or restricted access areas is increasingly identified as one of the solutions to problems of intense pressure from exploitative uses. This research utilised a unique marine dataset to explore conservation planning methods and identify priority areas to protect early life stages of marine fish in the Dover Strait. These methods, mainly tested and utilised in terrestrial environments, have the potential to identify efficient and effective networks of marine protected areas (MPAs).

The Dover Strait and adjacent waters contain spawning and nursery grounds important to species commercially fished in nearby waters. These habitats are vital for the survival of fish stocks and consequently the fishing industry and local communities. The study area was divided into 4 km² selection units. Surveyed data of marine ichthyoplankton abundances and environmental variables were mapped. It was found that the 'hotspot' approach to identify MPA networks provided a wide range of protection to both ichthyoplankton distribution and abundance, and was consequently considered to be less efficient and reliable than 'complimentarity' methods tested using 10%, 20% and 50% conservation targets. Proportional area was found to be more effective than presence / absence data in identifying MPA networks to protect abundance. A 'summed rarity' complimentarity algorithm identified 9.7% to 9.9% of the 4 km² selection units (in three surveys) required to protect 10% of ichthyoplankton distribution. 7.03% to 7.94% of the selection units were required to protect 10% of ichthyoplankton abundance. Two algorithms using 'irreplaceability' were found to identify similar networks for proportional abundance targets with similar efficiencies to those identified by the 'summed rarity' algorithm. A 'site irreplaceability' algorithm identified 7.03% to 7.73% of the selection units required to protect 10% of ichthyoplankton abundance and a 'summed irreplaceability' algorithm identified 7.03% to 7.62% of the units required for the same target.

Several surrogates for ichthyoplankton diversity were tested using three proportional conservation targets and found to protect 36% to 87% of ichthyoplankton elements to the required target. The protection provided by each surrogate varied between ichthyoplankton elements and between sampling surveys. Using a 10% conservation target, 'seascapes' protected 44.5% to 67% of the ichthyoplankton elements to the target, 'commercial species' protected 81% to 86%, 'higher taxa' protected 36% to 75% and 'assemblages' protected 42% to 64% of the ichthyoplankton elements to the 10% target.

It was found that incorporating measures to force the selection of clustered networks using 'summed rarity' produced MPA networks that were well connected. This technique may provide an opportunity to increase persistence of populations with little loss in efficiency. Increased publicity and awareness of softwares to enable the use of these techniques and incorporation of socio-political, economic and biological factors, is necessary to facilitate the wider knowledge, acceptance and use of the approaches advocated in this research, in both marine and terrestrial environments.

Acknowledgments

Sincere gratitude is expressed to the Kent / Nord-Pas De Calais INTERREG II Programme for supporting this research (GOSE 97/C8/03) and to the research team at Université du Littoral for data collection and help (Philippe Koubbi, Alain Grioche, Xavier Harlay and Gwen Cotonnec). Many thanks to my supervisor, Mike Walkey, for help and encouragement.

Many thanks to Mike Fischer (University of Kent) for writing and adapting the selection software, Paul Williams (Natural History Museum) for providing a customised version of WORLDMAP software, Paul Eastwood (Christchurch College University) for digitising the bathymetry and coastline. Thanks for kind permission of The Controller of Her Majesty's Stationery Office, the Port of London Authority, and the hydrographic offices of Belgium, France, the Netherlands and the United Kingdom, to use the bathymetry data. Thanks to Christine Eagle, Joan England, Shelly Roffey and Nicola Kerry-Yoxall at UKC for kind help. Thanks to the C-Plan team (CISCO) for kind permission to use the C-Plan software. Thanks to E.S.R.I. and the Society for Conservation GIS for scholarships to attend conferences and training in the United States, and to E.S.R.I. for allowing me to beta test ArcGIS.

Particular thanks are owed to Bob Smith for writing the selection algorithm, help and encouragement. Thanks also to both Bob Smith and Matt Walpole for many inspiring discussions! Thanks to Jo Leech, Ian Rickards, Stuart Piertney, Pete Esteban, Fiona Carlston, Robin Moore, Rosemary Godfrey, Tom Oldfield and Sam Lish for their support. A million thanks to Karl for absolutely everything.

Finally I would like to thank my parents and Jonathan for all their loving support and encouragement.

Chapter 1: General Introduction

1.1 Introduction

Every natural ecosystem on the Earth has been altered by humanity, some to the point of collapse (Meffe & Carroll, 1994). Rates of species extinction have led to the belief that a mass extinction is underway and efficient methods are urgently needed to guide conservation efforts (Soulé, 1991; Ehrlich and Wilson, 1991; Myers, 1993).

Many processes are responsible for the biodiversity loss. The main causes have been identified as habitat loss and fragmentation, introduced species, unsustainable harvesting and chains of extinction (Diamond, 1984; 1989; Pimm & Raven, 2000). Measures to protect species and habitats have been developed in an attempt to conserve biodiversity, as it is now regarded as having both inherent and utilitarian value (Ehrlich & Ehrlich, 1992; Wilson, 1989; 1992; Daily *et al.*, 2000). International legislation, governmental and non-governmental organisations (NGOs) have been created to achieve this goal. The measures used are wide ranging and are designed to restore habitats, prevent further habitat loss, reduce pollution, stop destructive trade, reduce introduced species or their effects and increase sustainable use of biodiversity.

The designation of protected areas (PAs) has become one of the most widespread strategies to conserve biodiversity (Flather *et al.*, 1997), being the cornerstone of most national, regional and local conservation strategies (Soulé, 1991). PA design has undergone a considerable evolution, originally often intended to protect scenic beauty or natural areas (Leader-Williams *et al.*, 1990). Today, biodiversity conservation is an active strategy strongly underpinned by the concept of protection integrated with sustainable use by local communities.

1.2 Marine biodiversity

Heightening world-wide concern about the Earth's marine ecosystems is especially directed towards the problems of habitat degradation, marine pollution and heavy exploitation of living marine resources. Despite (and because of) their economic importance (Rose, 2000), overexploitation of marine fisheries has become a serious problem worldwide, even for those that have been intensively managed by coastal nations (Lauck *et al.*, 1998). During the 18th and 19th centuries it was believed that the seas were an inexhaustible source of food and wealth (Roberts & Hawkins, 1999) and that humans could not have a significant impact upon the marine environment as a whole (Cushing, 1988). It is now agreed that policy makers should shift towards fishery management systems based on the 'precautionary principle' (Essington, 2001).

It is difficult to quantify the human induced changes in the marine ecosystem in many heavily utilised areas because little baseline data are available (Fogarty, 1999). The effects of anthropogenic changes in environmental quality on fish populations have therefore remained elusive and controversial (Rose, 2000). Changes in the catch per unit effort can, however, indicate changes in fish abundance since records have been kept. A comparison between 1906-1909 and 1990-1995 in the North Sea indicates large reductions in stock densities of several species. A rise in fish yields were seen, however, when fishing activities stopped during the world wars and the stocks were allowed to recover (FSBI, 2000).

Collapsed fisheries are now commonplace (Powles et al., 2000). In the northwest Atlantic, cod (Gadus morhua), haddock (Melanogrammus aeglefinus) and halibut (Hippoglossus stenolepis) fisheries have collapsed, resulting in the loss of 40,000 jobs in Newfoundland (Tyler, 1994). It is also beginning to be appreciated that the impacts of fishing extend far beyond the targeted species (Roberts & Hawkins, 1999), as disruption to the marine food web causes indirect affects to other species including seabirds and mammals (Jennings et al., 1999). There is a consensus that fisheries need better management if they are to continue to make a major contribution to world food supplies, livelihoods of people, human health and the economy, and if marine biodiversity, ecosystems and the ecological services they provide are to be maintained (Williams, 1998a).

In the past, many locations could act as refuges for marine life because they were inaccessible to fishing techniques and gears. In modern times, fishers have become so successful, with technologically advanced gear and increased knowledge about fish location, that there are now few places that are not fished (Roberts, 2002). Pollution and habitat destruction have also extended to a much larger proportion of the seas. Many measures have been put into place to try to remedy the depletion of marine biodiversity, but these have not been fully successful. The Fisheries Society of Britain (FSBI, 2000) lists the reasons for the failure of management to stop severe fishing down of stocks in the North Sea to include harvest overcapacity combined with habitat damage, inappropriate fishing techniques, lack of proper enforcement of regulations, the inability of management to react in a timely way to changing stocks, technological advancement in fishing and difficulties in addressing allocation issues.

The North Sea and the English Channel are home to a wide range of fish species, the North Sea being one of the most productive areas in the north east Atlantic (FSBI, 2001). Species taken include cod, haddock, plaice (*Pleuronectes platessa*), whiting (*Merlangius merlangus*), saithe (*Pollachius virens*), herring (*Clupea harengus*), mackerel (*Scomber scombrus*) and sole (*Solea solea*) for human consumption and sandeel (*Ammodytidae spp*), Norway pout (*Trisopterus esmarki*), blue whiting (*Micromesistius spp*) and sprat (*Sprattus sprattus*) processed for fish meal and oil.

The total range of fish species can be large, but spawning and nursery grounds necessary for breeding can be small and predictable. Without substantial climate change or stock collapse, they can remain stable for several decades (Pawson & Robson, 1993) and so protection could be provided in a small but vital part of the lifetime range. The study area for the current research, in the Dover Strait and adjacent waters, has been documented to include important spawning and nursery grounds for target species (see Grioche & Koubbi, 1997). The long term persistence of these habitats is therefore important for the survival of the fisheries. Whilst protection of biodiversity requires a suite of management strategies, the creation of reserves or closed areas to protect marine biodiversity is increasingly identified as one of the solutions to the problems of intense pressure from exploitative uses (Sumaila *et al.*, 2000; Roberts & Hawkins, 2000).

The following section describes the use of marine protected areas (MPAs) to protect marine biodiversity, including the legal framework that includes provisions for their designation. Section 1.4 provides a description of the techniques and methods that have been used to identify the areas best suited for designation as PAs. Section 1.5 is a description of the need to plan PAs capable of sustaining viable populations of the species they are designed to protect. Section 1.6 outlines conservation targets. Section 1.7 is an overview of the practicalities of PA designation after suitable areas have been identified. Section 1.8 contains a review of the suite of complimentary measures necessary for MPAs to be successful in providing protection to marine biodiversity. Section 1.9 outlines data availability and scale. The aims of the current study are outlined in section 1.10, and the structure of this thesis is explained in section 1.11.

1.3 Protected areas in the marine environment

IUCN, The World Conservation Union, defines a Marine Protected Area (MPA) as "any area of intertidal or subtidal terrain, together with its overlying water and associated flora, fauna and cultural features, that has been reserved by law or other effective means to protect part of all of the enclosed environment" (Kelleher & Kenchington, 1991).

The legal framework for environmental protection has developed extensively over the past 20 years (QSR, 2000) and provides the potential for the development of a system of MPAs in the north east Atlantic that could conserve marine biodiversity including fish stocks and their spawning and nursery grounds. It includes the International Conferences on the Protection of the North Sea (North Sea Conferences), the Convention for the Protection of the Marine Environment of the North-East Atlantic (OSPAR Convention 1992; formerly Oslo Convention on dumping at sea and the Paris Convention on pollution from land-based sources), the Bonn agreement, initiatives within the International Maritime Organisation (IMO) and the Convention on the Conservation of European Wildlife and Natural Habitats (the Bern Convention). The Convention on Biological

Diversity (CBD) and the European Union (EU) Habitats Directive also contain obligations for the member countries to protect their marine ecosystems.

The International Conferences on the Protection of the North Sea are political events for a broad and comprehensive assessment of the measures needed to protect the North Sea environment (North Sea Conferences, 2002). The OSPAR convention sets out obligations with respect to MPAs including "the protection of the maritime area against the adverse effects of human activities..., to develop strategies ... for the conservation and sustainable use of biological diversity... and the need to establish a network of marine protected areas" (Christiansen, 2000). The Bonn Agreement is an international agreement by North Sea coastal states together with the European Community (EC) to prevent pollution. The IMO is concerned with maritime safety, efficiency of navigation and prevention and control of marine pollution from ships.

The CBD commits governments to protect the Earth's biological resources within the framework of sustainable development. A set of actions have been agreed that aim to protect coastal and marine environments including establishing (or consolidating) representative reserve systems of marine and coastal protected areas (Christiansen, 2000). The United Nations Convention on the Law of the Sea (UNCLOS) imposes obligations on all nations to protect and preserve the marine environment (Gjerde, 2001). The EU habitats directive implements the conservation of natural habitats and species of wildlife that are rare, endangered or vulnerable in the European Community through a network of areas known as the Natura 2000. The network includes 'Special Areas of Conservation' (SAC) and 'Special Protection Areas' (SPA) and where the area includes sea or seashore it is described as a European marine site (Gubbay & Knapman, 1999). In the UK, both Habitats and Birds Directives are implemented through the Wildlife and Countryside Act (1981) and the Conservation (Natural Habitats) Regulation.

Several other pieces of European Union (EU) legislation are of relevance to the study area. The Maastricht Treaty requires that all EU fisheries policies, including the Common Fisheries Policy (CFP), must comply with the precautionary principle. The Convention on the Conservation of Migratory Species of Wild Animals (Bonn Convention, 1979) obliges Parties to conserve and restore important habitats, remove obstacles to migration, control or eliminate alien species, and prevent or control harmful activities (Gjerde, 2001). The Convention on Wetlands of International Importance (or Ramsar Convention, 1971) obliges Parties to designate and protect wetlands of international importance, and includes marine waters up to six meters deep (Gjerde, 2001).

MPAs are designated under many regimes and levels of protection. Many include zones permitting varying levels of use. The IUCN categorisation attempts to clarify applications and use of the term PA (IUCN, 1994). The categories range from I to VI, with category I affording the highest level of protection, and least consumptive use. The term PA will be used here to identify a protected area

that may be located either in the marine or terrestrial environments and MPA to define a protected area that is purely marine.

The objectives of MPA designation can be wide ranging and include habitat restoration, protection of target and non-target species, development of recreational and educational activities and promotion of scientific understanding. MPAs presently cover less than half a percent of the world's oceans (Roberts & Hawkins, 2000), 71% of which were reported to have no active management in 1994 (Kelleher *et al.*, 1994). Most of the existing MPAs around the world have been reported to be under-resourced, poorly managed and offer little protection (Roberts & Hawkins, 2000; Jamieson & Levings, 2001). There is an urgent need for improvements to the present system, and more reserves (Roberts & Hawkins, 2000; Cole-King, 1995), designed efficiently and managed effectively in order to address the developing crisis in the oceans.

Motivation to close areas of the sea to some or all consumptive uses is difficult for local communities and fishers when short-term effects may appear to be devastating to livelihoods. Issues of over-fishing, pollutants and habitat destruction, however, are concerns of the fisher as much as the conservationist. In July 2000 the World Wide Fund for Nature (WWF) estimated that there would be 15,000 full-time and 3,500 part-time fishers in the UK whose jobs would be jeopardised by the commercial extinction of fish (WWF, 2000). Recent scientific evidence suggests that the creation of reserves are not only powerful strategies for conservation but can also provide much needed support for fisheries (Lauck et al., 1998; Roberts, 1995; Guenette & Pitcher, 1999; Roberts & Hawkins, 2000). In several regions, fish stocks have increased rapidly following MPA establishment, and have enhanced catches in adjacent areas (Kelleher, 1999; Roberts et al., 2001). A synthesis by Mosquera et al. (2000) of marine reserve research demonstrate that overall abundance of fish inside reserves is on average 3.7 times higher than outside reserve boundaries. These fish were mostly target species as non-target species were equally abundant on both sides of the boundary. One study found a 8-fold increase in total biomass after a four year fishing ban off Sicily, with the individual species increases ranging from 1.2 fold to 497-fold, with a decrease found in only one species (Pipitone et al., 2000).

Some studies have highlighted the effects on inter-specific interactions when fisheries target species begin to recover, which can cause non-target species to show a decrease in abundance or biomass when the area is protected from fishing (Planes *et al.*, 2000). MPAs are often designed to provide protection from other factors in addition to fishing. It is hoped that they can provide fish larvae for stock recruitment in neighbouring areas, which may enhance the likelihood of their success by benefiting the local fishing communities. Mixed results, however, have been found from studies researching larval export into surrounding populations (Planes *et al.*, 2000). Protection of vulnerable species is only likely to be successful if networks of reserves are established throughout species ranges to link larval supply and nursery areas (Roberts, 1995). The

design of a MPA is therefore crucial in maximising the likelihood of its success. The following section describes the methods designed to select the best areas to conserve biodiversity in an effective and efficient manner.

1.4 Selecting protected area networks

From the perspective of conservation alone, the largest possible PA network (a group of protected areas, either designated independently or together and integrated by management) should offer the best protection. Available resources combined with social and political pressures, however, force decisions to be made concerning the positioning of limited numbers (and size) of PAs to best protect biodiversity. Both in the marine and terrestrial environments, selection has historically been opportunistic (Leader-Williams *et al.*, 1990; Pressey, 1994; Brunckhorst & Bridgewater, 1994; Pressey *et al.*, 1996; Roberts, 2000), and largely remains so (Pressey & McNeill, 1996). Most reserves originally having been selected not for their biological value but for their scenic beauty, cultural significance, lack of economic value or to protect a few charismatic flagship species (Pressey *et al.*, 1993; Pressey, 1994; Simberloff, 1997; Andelman & Flagan, 2000; Williams *et al.*, 2000). They were usually the easiest, politically and economically to protect and had the least need for strict reservation (Pressey & Tully, 1994). These 'lands that nobody wanted' included those that are high and infertile, inaccessible, or had other problems such as those in Zambia that were infested with tsetse fly (Leader-Williams *et al.*, 1990; Pressey, 1994, Pressey *et al.*, 1996).

The view that PAs existed for the pleasure of those visiting began to diminish with the recognition that their designation should aim to reduce biodiversity loss. This led to a re-evaluation of the existing PAs. It was shown that poorly planned or *ad hoc* reserve networks are less effective in protecting biodiversity (Pressey, 1994), hence most PAs whether terrestrial, coastal or marine do not adequately represent the diversity of ecosystems (Brunckhorst & Bridgewater, 1994). This has led to duplication in the protection of some habitats and species and inadequate protection of others (McNeill, 1994; Pressey & Tully, 1994), including the most threatened (Pressey *et al.*, 1993; Rodrigues *et al.*, 1999).

It has also led to the evolution, over the past twenty years, of systematic techniques to select new PAs with clear, efficient procedures driven by quantitative reservation goals that provide defensible and flexible decision support. The aim of selection methods is to result in maximum representation of biodiversity elements in PAs (Pressey *et al*, 1993; 1997), that will allow persistence of populations, through the choice of sites (or selection units) in an region (Margules *et al.*, 1988), whilst minimising cost (often in the form of area). The biodiversity elements are surrogates for biodiversity, such as species abundances or habitat distribution. Biodiversity can be measured according to a wide range of characteristics, from the molecular to the land or seascape level.

Surrogates (Chapter 8) are chosen to represent as much of the variation in biodiversity as is possible given the limited resources, knowledge available and difficulty of measuring and mapping the distribution of all species and the diversity of characters within populations for the foreseeable future. The most common surrogates are a sub-set of the species in the area under consideration.

The use of surrogates and related PA selection methods have mainly been created and tested in the Some researchers had considered the land-based theories to be terrestrial environment. inappropriate for marine systems (Kenchington, 1990), as large differences between the two environments seem to exist, both physically and biologically. Systematic methodologies have developed for MPA design (eg Kenchington, 1996; Kelleher et al., 1994; Salm et al., 2000), but mostly do not include selection algorithms, relying instead on selection criteria when considering selection units (those sites under consideration) in turn, and candidate sites proposed in response to specific threats (eg Hooker et al., 1999). There are two fundamental similarities in terms of conservation planning between the marine and terrestrial environments. There is, firstly, the need for definitions of biodiversity as a basis for decisions on the location of Pas, and secondly, the need to deal with spatial relationships when allocating PAs. The research carried out on terrestrial ecosystems has also found that the techniques are highly transportable and can be applied to any consistent database at national, regional or local scales in virtually any part of the world's land surface (Pressey & McNeill, 1996). Factors leading to the dismissal of land based selection procedures for use in MPA selection include the less static nature of less well defined marine ecological boundaries. The system of currents, waves and tides, combined with the dispersive larval phase of many marine organisms, makes the marine environment possess a greater degree of connectivity than terrestrial systems (Pressey & McNeill, 1996). As a result of greater connectivity, endemism was thought to be rare. It was also once thought that habitats are rarely critically restricted (Kelleher, 1999) and that marine species are resilient to extinction because of their large geographic ranges (Roberts & Hawkins, 1999). These views are now being questioned. Despite the high level of connectivity, isolated areas and species do occur in marine environments, some areas are remote so few larvae reach them and some species have relatively restricted larval range. Some invertebrates and fish species produce few large eggs which can be attached to the seabed or in some cases guarded by the parent, producing small dispersal distances (Kelleher et al., 1994). A recent analysis of coral reef species (Roberts et al., 2002) found that 7% to 53.6% of reef fish, coral, snail and lobster taxa have highly restricted ranges and are clustered into centres of endemism rendering them vulnerable to extinction. Some centres of endemism occur in unexpected areas, such as those that appear to be highly connected with other regions. This accords with growing evidence that species with pelagic larval stages do not always disperse widely (Barber et al., 2000 see Roberts et al., 2002). The natural processes and methods of implementation differ between the marine and terrestrial environments but the fundamental issues for planning are the same (Pressey & McNeill, 1996).

Due to the inefficient protection provided to the features least threatened when PAs are allocated opportunistically (Pressey *et al.*, 1993; Pressey & Tully, 1994; Brunckhorst & Bridgewater, 1994; Rodrigues *et al.*, 1999), effective protection is more expensive and difficult to achieve. PAs should instead be chosen with clear, explicit systematic procedures driven by quantitative reservation goals. The selection techniques applied to marine ecosystems can be adapted to take account of the variability and connectivity. This may require the use of flexible management approaches that can respond to changing ecological conditions. Many PA management techniques include off reserve strategies that can also be adopted by marine conservation planners. These advantages, and the flexibility of iterative reserve selection methodologies allows them to be adaptable for application to the identification of networks of MPAs within a holistic bioregional planning framework (Brunckhorst & Bridgewater 1994). The potential to apply well-tested approaches for terrestrial conservation should therefore be more fully investigated for marine areas.

Due to the slow adoption of systematic selection techniques (Pressey & McNeill, 1996; Beck & Odaya, 2001), a system incorporating a larger series of stages necessary for PA designation and implementation has evolved. The first step is to measure and map biodiversity in the area, the second to identify the conservation goals for the planning region. Step three involves reviewing existing reserves. Selecting additional reserves forms the fourth step. The fifth step is the implementation of conservation actions on the ground, and the final step is to manage and monitor the reserves (Margules & Pressey, 2000). The selection techniques should therefore be a vital process in a larger system of conservation planning.

The selection techniques have followed the following methods; hotspots and scoring or evaluation methods, gap analysis, and iterative reserve selection algorithms. The methodologies provide the efficiency and scientifically defensible decision support required for future proposals for new reserves (Brunckhorst & Bridgewater, 1994), and are described in the following sections.

1.4.1 Hotspots and scoring evaluation methods

Many marine conservation planning situations have used a type of scoring method (Jamison & Levings, 2001). Values are assigned to different components of biodiversity such as species diversity or educational value score, by a panel of experts, and then weighted through a statistical process. This is designed to reflect the relative importance of the qualities a site possesses and the degree to which is possesses them (Usher, 1986; Bedward *et al.*, 1991). The approach has been criticised because it is highly subjective and the method of combining the scores has no theoretical basis. Also, the process is not transparent, and it makes the results difficult to understand and defend (Williams, 1998b). Scores are also based on subjective weightings given to each category, providing equally justified differences in scores to the same locations based on different

preferences. The outcome of the procedure may produce results that are surprising to those involved in the process and do not reflect their original values, due to score combinations.

Hotspots are areas that rate highly on a value scale. The type of scale can be one of many value systems. The term has become popular following the initial influential analysis by Myers (1990; 1998), who identified areas on a worldwide scale that rated highly on a combination of high species richness, endemism and threat. The term has since become popular to describe areas scoring highly either on a similar combination of value scales, or on only one scale (Rebelo & Siegfried, 1992; Prendergast *et al.*, 1993; Curnutt *et al.*, 1994; Lombard *et al.*, 1995; Williams *et al.*, 1996; Freitag *et al.*, 1996; Dobson *et al.*, 1997; Freitag & van Jaarsveld, 1997; Troumbis & Dimitrakopoulos, 1998; Virolainen *et al.*, 1999; Myers *et al.*, 2000).

If hotspots for different taxa coincide, there would advantages for the selection of sites for conservation, because reserve selection based on an indicator taxonomic group (Gaston, 1996; Williams & Gaston, 1998) would protect species from other taxonomic groups. If one or two indicator taxa could be used, the efficiency of biodiversity surveys designed for collecting data to be used in priority set selections could be improved (Lombard et al., 1995; Dobson et al., 1997). When studies tested the effectiveness of hotspots across taxa, several showed that their hotspots do not coincide, especially when larger numbers of taxa are considered (Prendergast et al., 1993; Pressey et al., 1993; Williams et al., 1996; Howard et al., 1998). This is possibly not surprising, as the distribution of diversity in one group of organisms does not necessarily indicate the distribution of diversity in others (Ryti, 1992; Prendergast et al., 1993), particularly where the groups are associated with different habitats. It was also found that for some combinations of taxa, hotspots of one taxa often coincide with coldspots of others (Virolainen, 2000). Hotspots can be identified on different scales, from global and national to local (Myers, 1988). Most analyses have been carried out at a scale at least an order of magnitude larger than most reserve sites, and the effectiveness of this method may well be scale dependant. Curnutt et al. (1994) used 100 km² cells to analyse data on bird species in Australia, and found that more rare species were protected under species richness hotspots than had been found by Prendergast et al., (1993) using a spatial resolution of 1km². Both sets of authors suggest the results are also dependant on the degree of fragmentation of the landscape.

The hotspot approach does not have the ability to incorporate the size, location or species protected within existing PAs, so that gaps can be identified. The approach also does not permit inclusion of conservation potential and threat of areas (Dinerstein & Wikramanayake, 1993). Techniques of 'gap analysis' were developed to overcome this problem, and have been widely used in the United States Gap Analysis Project (Scott *et al.*, 1993; Strittholt & Boerner, 1995; Mann, 1995; Thompson *et al.*, 1996; Davis *et al.*, 1998; Redmond *et al.*, 1998; Merrill *et al.*, 1996; Stoms, 2000; Jennings, 2000) and elsewhere including India (Ramesh *et al.*, 1997). The techniques use the

distribution of another easily mapped factor such as land cover to map the distribution of species (Scott *et al*, 1993). The technique originally identified hotspots of species under-represented in the PA system. The hotspot approach, however, also does not consider patterns of between-site complimentarity that greatly increase the representation of all mapped species (Mace *et al.*, 2000; Margules & Pressey, 2000; Pressey *et al.*, 1993; Faith & Walker, 1996; Williams, 1998b). The GAP project therefore adopted techniques based on complimentarity to replace those previously based on the hotspot approach (Kiester *et al.*, 1996). The techniques offer protection to a larger number of species at a greater level of occurrence in a much more efficient manner. This approach is described in section 1.4.2 below.

1.4.2 Complimentarity: iterative reserve selection algorithms

The concept of complimentarity was first applied by Kirkpatrick (1983), and formalised by Vane-Wright *et al* (1991). Complimentarity is defined as the degree to which an area contributes biodiversity elements that are otherwise unrepresented in other sets of areas. These new ideas initiated the development of powerful decision-support tools that have started to change the way conservation planning is undertaken in many parts of the world.

Iterative (stepwise), or 'minimum set complimentarity algorithm' methods select sites of optimal representation while attempting to minimise the total area or number of all selection units (Pressey et al., 1993; Nicholls & Margules, 1993). The selection algorithms can identify networks of selection units to answer two identification problems. The first, 'minimum area', is to identify the minimum number of units that would represent all biodiversity elements to a conservation target. The conservation target is either a proportion of the biodiversity elements distribution or abundance, or a set area of the biodiversity elements distribution or abundance. The second is that of 'maximum coverage', to identify which selection units will maximise the representation of biodiversity elements in a given area (Williams, 1998b; Cabeza & Moilanen, 2001).

Identification of the optimal or absolute minimum set of sites can be achieved by using an integer linear program and techniques such as branch-and-bound (Underhill, 1994; Willis *et al.*, 1996). These techniques, however, are computationally intensive and have been reported to be unable to solve some complex selection goals and to require long computational times for large problems. They also do not offer flexibility, making them unrealistic in interactive planning scenarios with decision makers (Pressey *et al.*, 1996; Margules & Pressey, 2000), although have recently improved dramatically (Rodrigues & Gaston, 2002a). Heuristic techniques have been designed which offer much faster and only slightly less efficient solutions (Williams, 1998b). These techniques provide flexibility and accountable transparency, essential components of practical conservation planning that are often more desirable than maximum efficiency (Pressey *et al.*, 1995). It is desirable for conservation planners to be able to investigate alternative configurations

Chapter 1: Introduction 10

of selected units to maximise other factors in addition to biological representation. These can include land suitability (Bedward *et al.*, 1992), social, political and economic factors. The near-minimum set (hereafter called minimum set or selected network) is often one of many possible combinations of selection units, so flexibility is required to investigate the alternatives (Pressey *et al.*, 1994; Rebelo & Seigfried, 1992).

Many variations of algorithms have been produced, the effectiveness and efficiency of which vary and are influenced by the data being used (Cusuti et al., 1997; Pressey et al., 1999). 'Greedy richness' algorithms first choose the most species rich areas and then choose areas that add the most number of biodiversity elements to those first selected (Rebelo & Seighfried, 1992; Saetersdal et al., 1993; Dobson et al., 1997). These algorithms are relatively inefficient (Underhill, 1994; Csuti et al., 1997) although fast to execute. 'Rarity based' algorithms first choose the areas with more restricted range species. They use either a continuous range size rarity measure (Rebelo & Seighfried, 1992; Kirkpatrick & Brown, 1991; Williams et al., 1996; Williams, 2001; Csuti et al., 1997; Hacker et al., 1998; Fjeldsa & Rahbek, 1998), or by first choosing those under a threshold range size. Such algorithms are known as 'progressive rarity' algorithms (Margules et al., 1988; Margules et al., 1991; Pressey & Nicholls, 1991; Bedward et al., 1992; Ryti, 1992; Saetersdal et al., 1993; Margules et al., 1994; Freitag et al., 1996; Williams et al., 1996; Williams, 2001) and are more efficient than greedy richness algorithms (Csuti et al., 1997). 'Simulated annealing' algorithms generate a completely random selection and iteratively explore trial solutions by making sequential random changes and test for improved solutions (Csuti et al., 1997; Possingham et al., 2000a). Some algorithms can check and remove within-set redundant choices after the initial selection (Williams et al., 1996).

Complimentarity algorithms available in Worldmap software (Williams, 2001) provide information on irreplaceable and flexible selection units to achieve the conservation target in use. Other complimentarity algorithms, however, do not indicate the relative contribution of each unit This is one of the reasons for the development of the principle of towards the goal. 'irreplaceability' (Pressey, 1999b). Irreplaceability is defined both as the potential contribution of any site to a reservation goal and the extent to which the options for a representative reserve are lost if that site is lost (Pressey, 1999b) and fully incorporates the principle of unit flexibility. Irreplaceability allows managers and conservation planners to fully explore alternative ways of achieving goals. The individual contribution of selection units can be important in practical planning situations at fine scales where choices need to be made between large numbers of selection units. Using a geographic information system (GIS), maps of the irreplaceability scores of selection units can show which units have no replacement units and must be included in each set to achieve the goal and which areas have varying numbers of replacements (Pressey 1999b). If an irreplaceable selection unit were to be lost it would prevent one or more conservation targets from becoming achievable (Ferrier et al., 2000). Areas of high irreplaceability can become nodes

around which other areas are preferentially chosen (Pressey *et al.*, 1994; Rebelo, 1994). This encourages the clustering of selected units. The calculation of the exact irreplaceability for all selection units in the area under consideration is currently intractable for most realistic datasets and conservation targets. Application therefore relies on prediction of values (Ferrier *et al.*, 2000) which can make the process less transparent (Williams, 1998b). In some planning situations there may be many selection units that are irreplaceable, but contain a varying number of unique species that would be lost if the area was destroyed. To resolve this problem, an index known as summed irreplaceability is used. This is the sum of the irreplaceability of each element calculated separately (Pressey, 1998 see Ferrier *et al.*, 2000). If a measure of vulnerability or threat is also available for the selection units it can be combined with irreplaceability to map the scheduling of conservation action (Pressey & Taffs, 2001; Araujo & Williams, 2000; McCarthy & Thompson, 2001).

A newly developed algorithm based on 'summed rarity' is currently being tested (Smith, 2001). This provides a measurement of the contribution of each selection unit to the conservation target. It is based on the proportion of the biodiversity elements, within the whole area under planning consideration, that exists within each selection unit (proportional area or abundance). The contribution of each selection unit can be mapped. This provides a method for prioritising units within the network and offers substitutes for units should they become unavailable for designation.

Many factors, in addition to minimising the area and maximising the biodiversity representation, require consideration when selecting reserve networks. These aim to improve the probability that the populations of species for which the PA network was designated persists through time. These are outlined below.

1.5 Ensuring viability and the persistence of populations

PA selection algorithms are designed to represent biodiversity efficiently, but little is known about the performance of these networks to protect biodiversity in the long-term, such as their success in maintaining the persistence of viable populations and communities (e.g. Margules *et al.*, 1994). The success of PA networks depends on the planning process that selects their location and spatial arrangement (Virolainen *et al.*, 1999). Two studies have found that the minimum set of sites did not perform well for long term persistence. Rodrigues *et al.* (2000a) tested selection methods for efficiency and effectiveness to prevent species loss, finding the most efficient network (the smallest proportion of selection units necessary to satisfy the chosen conservation target) suffered the most species loss. Margules *et al.* (1994) found that a minimum set of sites was not adequate eleven years later, due to a high turnover in species composition. PA networks identified from a snapshot in time may not serve the purpose of their declaration for prolonged periods. These studies highlight the necessity to include concerns about the long term maintenance of the biodiversity elements within the selection process (Rodrigues *et al.*, 2000a; 2000b). Measures to increase the

likelihood of persistence of processes that sustain ecosystem structure and functioning may be one method to increase persistence, and so are necessary to include in the selection process (Noss, 1996). Quantifying these measures, however, remains difficult.

Island biogeography (MacArthur & Wilson, 1963) and metapopulation theory (Hanski, 1999) provide information about possible means to achieve persistence of populations within PA networks in the design process. The theory of island biogeography implies that connected or close PAs are better than unconnected ones and that larger PAs are better than smaller ones. The implications of this were debated by researchers. It concerned whether 'single large or several small' (SLOSS) PAs of the same area could best achieve the targets of PA planners. The effect of habitat fragmentation on species was researched with the aim of identifying 'minimum viable populations' (Shafer, 1981, see Meffe & Carroll 1994; Wielgus, 2002), which implies the minimum reserve area needed for the target species. 'Minimum habitat size' has also been researched, but mostly for single species (Beier, 1993; Fahrig, 2001). Defining values for minimum size for ecosystems has proven even more elusive (Powell *et al.*, 2000). There are no accepted methods for calculating minimum sizes (Caughley, 1994), it is recognised that it is best to maximise the size as far as possible.

A large MPA would intuitively seem to offer higher effectiveness in terms of fisheries production and conservation of biodiversity, and would be more likely to provide suitable breeding areas (King & Faasili, 1998). Larger populations in larger reserves are more likely to survive stochastic events and disturbances that small populations in small reserves may not survive, although less influential in marine reserves with permeable boundaries, especially if a series of small reserves could provide habitat in areas away from a nearby stochastic event. Widely fluctuating populations may also need larger areas depending on their behaviour. The persistence of more sedentary species depends on regular recolonisation from where they have disappeared and such sources are more likely to exist in large reserves (Roberts & Hawkins, 2000).

These reasons tend to indicate the favouring of large MPAs. An area made up from a series of smaller units, however, may be beneficial as they cause less disruption to existing human activities and may incorporate a wider range of habitats and ecological conditions (Roberts & Hawkins, 2000). The combined larval production from many small MPAs is likely to be greater than that from a smaller number of large ones. The interconnections between larval sources and settlement areas, however, are only poorly understood (King & Faasili, 1998). A series of small reserves have a longer boundary compared to their area than one large reserve, although this has less influence as the boundaries are permeable. Fauna and flora are free to move across the boundaries although 'edge effects' (e.g. Woodruff & Ginsberg, 1998) can still be influential despite the transversal boundaries. An example is the phenomenon of fishers 'fishing

Chapter 1: Introduction 13

the line' a term used to describe the concentration of fishing along the boundary of an MPA (Ramos-Espla & McNeill, 1994; Roberts & Hawkins, 2000).

As most MPAs around the world have historically been of a small size, it has been difficult to empirically determine the effect of size on reserve performance (Roberts & Hawkins, 2000). Recently, however, more reserves of different sizes have become established, allowing a better understanding of the contribution of size as a factor in contributing to the success of a reserve. A review by Halpern (in press) found that abundance, biomass, size and diversity of organisms increased inside MPAs in almost every case, and the magnitude of these effects was independent of reserve size.

Principles from metapopulation (Hanski, 1999) can be employed to increase the probability that a population will persist in PAs. These include measures to decrease local extinction rates, increase between patch colonization rates, increase the number of suitable patches and increase the number of occupied patches (Hanski, 1999; Possingham et al., 2000b). To reduce edge length of the selected PA network, selection algorithms have been designed to choose areas that are closer together (Nicholls & Margules, 1993; Lombard et al., 1997; Briers, 2002). Reducing the distance between PAs can also increase dispersal and recolonisation rates, as can the restoration and protection of areas that can be used as corridors between patches (e.g. Ranta et al., 1998; Danielson & Hubbard, 2000; Sieving et al., 2000; Beier & Noss, 1998). Again, the effects of isolated patches of habitat are often (although not always) reduced in a highly connected marine environment with strong currents and a high degree of mixing. Increasing connectivity often has the effect of increasing the effective size of reserves (Taylor et al., 1993). Increased recolonisation also increases the possibilities for survival of populations through predicted climate change, as will designing a system of PAs that spans environmental gradients (Fairbanks et al., 2001). Close and well connected PAs are disadvantageous if the spatial arrangement increases correlations among reserves in environmental variation, or the likelihood that climatic change will affect all the PAs. Disadvantages attributed to close well connected PAs also include increased chances of disease, exotic species or disturbance events spreading from one PA to another (see Possingham et al., 2000b). The aim, however, is often to join patches of habitat that were once contiguous, so these issues should not discourage connectivity.

Opinions concerning the SLOSS debate still differ. The design of some MPAs now favours a mix of the two (one large and several small) strategies (Kelleher & Recchia, 1998). Large areas are often managed for multiple use, including areas of strict protection and areas allowing sustainable consumptive use, through a system of zoning. This is considered by some to be more effective than small isolated highly protected areas (Pressey & McNeill, 2000).

Other suggestions for the selection process to increase the chances of persistence include simply selecting a large number of selection units, thereby including a larger number of populations and a higher chance of protecting resilient populations. This is an expensive alternative and reduces the efficiency of the selection process. Rodrigues *et al.*, (2000a) suggest that selection methods based on species abundances rather than presence / absence data may be more likely to select areas with robust populations. Other suggestions include the representation of species throughout their geographic range. This would capture potential genetic and ecological variation within species (e.g. Scott *et al.*, 2001). This may also be an expensive strategy in terms of area. The capture of genetic variability between species has also been suggested as a conservation target, but requires complex data which may not be available (e.g. Vane-Wright, 1996a; 1996b; Polasky *et al.*, 2001).

1.6 Conservation targets

The IUCN has recommended that at least 10% of each nation or of each ecosystem should be protected to ensure the persistence of the biodiversity within them (IUCN, 1992). This figure is based on that agreed at the Third World Congress on National Parks and Protected Areas to be an appropriate and practical target for each of the world's major ecosystems (McNeely & Miller 1984 see Green et al., 1999). This figure has gained authority from repetition. Ecological theory has little advise to resolve what is an adequate proportion of each element (Nicholls, 1998). Some have voiced concerns that the 10% figure is too low, or may become a ceiling of protection levels. Many studies in marine ecosystems suggest that reserves may need to cover at least 20% of the area or abundance of the biodiversity elements (Roberts & Hawkins, 2000; Beck & Odaya, 2001). A study concentrating on the coastal region suggests that a system of reserves that encompass nearly 30% of the South African coast would be necessary to represent all known fish species in the area (Turpie et al., 2000). Ward et al. (1999) indicated that at least 40% of Jervis Bay in Australia would require protection to represent most of the marine taxa. A target of 50% has been suggested as a level which may be more likely to represent more biodiversity elements including wide ranging species (Soulé & Sanjayan, 1998). These values may be unrealistic for practical conservation, but can provide patterns of priority.

The planning process includes a complex variety of considerations to identify the best solution for a particular area at a particular time. Some of the practicalities involved in the process are outlined below.

1.7 Practicalities of MPA design and implementation

The selection of areas by site selection algorithms forms a small part in the MPA design process (Laffoley *et al.*, 1994). Many additional challenges exist for managers, conservation scientists (biologists, ecologists and social scientists) and economists during this process and in the

implementation and evaluation of MPA networks (Carr, 2000). Many factors involved are not part of the biodiversity dataset. These include available funding, the agreement of the stakeholders, conflicting use of the areas, practicalities of management, socio-cultural impacts on the surrounding communities and enforcement of protection (Badalamenti *et al.*, 2000).

The specific objectives of any proposed MPA must be agreed amongst a diverse group of stakeholders if they are to be successfully achieved. The objectives of different stakeholders may vary significantly to the extent of direct opposition. MPA objectives can include ecosystem conservation, fisheries enhancement and ecotourism. These objectives can all lead to differences in the parameters of the MPA such as size, positioning, and the activities permitted (Carr, 2000). Another important challenge of utmost importance in the design of such a PA or PA network, is the enforcement of protection. Sustained enforcement needs to be structured and should include involvement of the stakeholders (Carr, 2000). Dissemination of information to involved parties and in many situations to the wider public may be an important aspect of gaining support and increasing the likelihood of success. Due to the high influence of the stakeholders on the likelihood of success, candidate PAs that enjoy strong local support may contribute less to the conservation target but could require modest amounts of personnel, time and money to manage and have a higher chance of success (Salm *et al.*, 2000). These areas can be useful for conservation planners to consider when flexible selection units are under consideration.

Unfortunately gaps exist between the scientists and the management, between the theory and the application (Roberts, 1997). PA selection algorithms and gap analysis approaches are not widely used for conservation planning, despite their benefits. This may be due to some planners having been largely unaware of the existence of the methods. Inadequate funding, lack of understanding and general antipathy towards what might be viewed as a prescriptive approach to conservation are also blamed (Prendergast *et al.*, 1999). Unfortunately some of these are included in the many misconceptions that exist about the use of selection algorithms (Pressey & Cowling, 2001). Selection algorithms can help conservation planners to combine the highly complex set of social, economic, political and biological factors into part of an explicit, defensible planning process. Some of the misconceptions should be addressed with wider publication and communication through media such as the internet so that the process can also involve a wider range of experts.

1.8 Complimentary measures

MPAs are not a panacea for all the problems facing the seas and oceans. They form only part of a suite of complimentary fisheries management and ecosystem management measures (e.g. Jennings *et al.*, 1996; Allison *et al.*, 1998). The influence of management practices in the marine and in the terrestrial environments can be far-reaching and need to be considered when managing the marine ecosystem. The boundaries of a MPA can be traversed by alien species, chemicals and particles

within the water. In coastal areas these will be added to by river waters and runoff from the land. These are distributed in the water masses by currents and tides, thereby causing areas to be strongly influenced by the effects of activities in distant areas (Chapter Two).

Integrated management regimes need to operate at large enough scales to encompass the effects of these far reaching influences (Bronckhorst & Bridgewater, 1994; Kelleher & Recchia, 1998). Several approaches have emerged to deliver these needs. Bioregional planning, integrated coastal management and integrated ecosystem management are examples. These approaches all cover large areas and take a holistic approach that treats the land and sea as a single integrated system. Integrated management is difficult and requires a system of prioritisation to deal with problems (Kelleher, 1999). Some threats to the ecosystem may require management at an even larger scale dependent on national or international policy.

The monitoring and evaluation of the effects of the management is imperative and should be adaptive i.e. periodically reviewed and revised. This process is of utmost importance, but costly to implement. Resources for monitoring programmes should be a precursor to designing management strategies, to enable planning of achievable protection. To provide meaningful outcomes of monitoring in terms of management, the natural sciences are needed to understand the functioning of the ecosystem, and the social sciences are needed to understand the human-induced problems and how they can be solved (Kelleher, 1999). If possible, sustainable utilisation of the natural resources within PAs can help achieve funding and stakeholder goals. The management of PAs should include information for stakeholders on the management aims and goals (Laffoley *et al.*, 1994).

1.9 Data availability and scale

There is a lack of good quality data at appropriate scales for national and local scale conservation area prioritisation (Bronckhorst & Bridgewater, 1994). When available, information on species distributions may be incomplete or exist only as incidence probabilities (Cocks & Baird, 1989; Margules & Stein, 1989; Polasky *et al.* 2000; Polasky & Solow, 2001). The marine environment also suffers from increased survey costs and, although utilised to some extent, techniques such as volunteer data collection are less frequently available for marine ecosystems, especially sub-littoral (eg see JNCC, 2002).

Appropriate scale of analysis for realistic conservation planning is debated (Erasmus *et al.*, 1999), but should depend on the purpose of the analysis in addition to the data available. As mentioned, information is often only available at broad scales, so has been the scale of most reserve selection exercises. The aim of a reserve selection exercise is often to advance the theoretical aspects of conservation planning and those carrying out the work are mostly conservation organisations and

academic departments. These tend to be poorly funded and so unable to conduct surveys to collect fine scale data. Analyses often use data collected for other purposes. These may be affected by its age and sampling bias (Freitag *et al.*, 1998). It is advisable to try to reduce the influence of errors in datasets if at all possible by recognising their source.

Coarse scale analyses often select broad areas where conservation efforts could be applied (priority areas). Whilst very important and useful on international scales, the priority areas are often an order of magnitude larger than economic and social constraints allow for PAs. When a priority area is thus allocated, the PA network that needs to be designed must able to protect all the biodiversity elements for which the larger area was identified. There is a risk that this may not be possible, as the size of the priority area means it may include human settlements or other unsuitable habitat. Local finer scale data and analyses are therefore needed to identify the appropriate areas that can incorporate all the elements leading to its initial identification as a priority site.

This study utilised a local fine scale dataset on the abundance of marine ichthyoplankton. It was collected during three surveys in Spring 1995 and 1999 by the Ichthyology Department of the University of Littoral, Calais, France. Data were available on the spatial location, abundance and developmental stage of all the ichthyoplankton species found in the survey area. This quality of data is rarely available and provides a unique opportunity to test MPA selection methods. Efficiency, effectiveness and selected network patterns identified using different data types and different selection algorithms were identified. It is unknown, however, to what extent the ichthyoplankton can be an effective surrogate for other marine taxa, even within the study area. The methods are therefore emphasised rather than the particular areas identified. It is hoped that the methodologies can also be applied to situations where biodiversity surrogates are representative of a wider range of biodiversity both in the marine and terrestrial environments. The type of PA network developed in this thesis is a potential approach that could be used to protect the transitional and changing biodiversity resources in the Dover Strait. The habitats necessary for specific parts of the life cycle, such as spawning and nursery areas are essential for the survival of the species and to replenish the fish stocks so necessary for the continuation of the fishing industry that is economically and socially vital to so many communities surrounding the area.

1.10 Aims and objectives

This research aims to incorporate the ichthyoplankton database available for the Dover Strait into a GIS database to test protected area selection methods with 'presence / absence' data, 'area' data, 'abundance' data and ichthyoplankton 'surrogates'. The PA selection methods include the 'hotspot' approach, a 'progressive rarity' algorithm, a 'summed rarity' algorithm and two 'irreplaceability' algorithms.

The specific objectives therefore are to:

- Incorporate all available and appropriate environmental, cartographic, species and bathymetric data into a GIS database of the area.
- Test and identify an accurate method to interpolate point bathymetric data. Use the resultant method to interpolate bathymetry across the Dover Strait and surrounding waters.
- Test and identify an accurate method for modelling ichthyoplankton abundance and distribution data. Use the resultant method to model the distribution of all species of ichthyoplankton found by sampling surveys within the Dover Strait and surrounding waters in Spring 1995 and 1999.
- Test methods to identify PA networks using the 'hotspot' approach with 'presence /
 absence' data, 'proportional area' and 'abundance' data reflecting the effects of the data
 type.
- Test methods to identify PA networks using a 'progressive rarity' algorithm with 'presence / absence' data.
- Test methods to identify PA networks using a 'summed rarity' algorithm with three proportional conservation targets using 'proportional area' data and 'abundance' data.
- Identify ichthyoplankton surrogates and test their performance in PA network selection using a 'summed rarity' algorithm with proportional conservation targets.
- Test methods to identify PA networks using a 'summed rarity' algorithm that includes
 measures to encourage the selection of adjacent selection units, and two algorithms using
 'irreplaceability'.

1.11 Thesis structure

Chapter one examines the need for protection of ichthyoplankton and the methods by which MPAs can be selected. Chapter two presents an overview of the study area, its hydrography and the threats to ichthyoplankton species. Chapter three describes the creation of a GIS database necessary for the analysis. It details the testing and use of the modelling procedures to map species distributions, bathymetry and environmental data. Chapter four describes the assessment of

procedures to model the distribution and abundance of ichthyoplankton samples. Chapter five describes the identification of MPA networks in the Dover Strait using three 'hotspot' approaches. Chapter six presents the use of a 'progressive rarity' algorithm to analyse presence / absence data to identify minimum sets of selection units for MPA networks for two conservation targets. A 'summed rarity' algorithm is used to analyse proportional area data to identify minimum sets for three proportional conservation targets. Chapter seven describes the selection procedure using the 'summed rarity' algorithm with abundance data for three proportional conservation targets. Chapter eight describes the identification, mapping and use of surrogates to identify near minimum sets and an analysis of their effectiveness at protecting ichthyoplankton abundance. Chapter nine examines the effect of including the provision for encouraging adjacency in the 'summed rarity' selection algorithm, and chapter ten presents the selection procedures using the 'irreplaceability' concept. The conclusions of the study are presented in chapter eleven.

Chapter 2: A Description of the Dover Strait

2.1 Introduction

The Dover Strait is situated between England and France with the North Sea to the east and the English Channel to the west (Figure 2.1). These areas form one of the worlds most extensive shelf areas (Huthnance, 1991) and thus one of the major fish producing ecosystems in the world (FSBI, 2001).

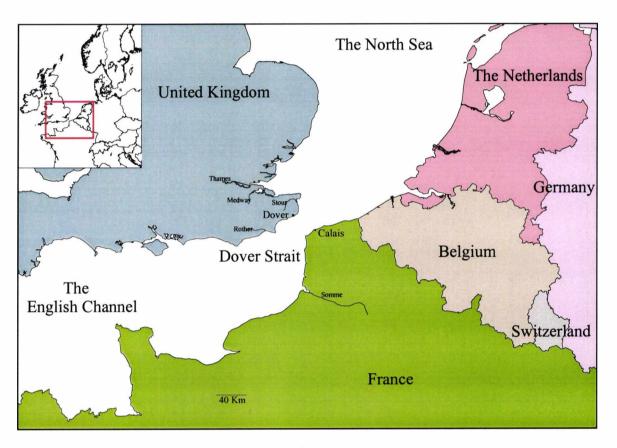


Figure 2.1 The Dover Strait

The productivity and fish catches of the North sea result in total annual landings of around 2.5 million tons (North Sea Conferences, 1992). The productivity of the greater North Sea is associated with its comparatively shallow depth and the existence of mixing mechanisms transporting nutrients from the nutrient rich bottom layer to the upper layers of the water column (FSBI, 2001). The Dover Strait and surrounding waters are thought to provide important areas for some larval stages of species targeted by commercial fisheries (Grioche & Koubbi 1997).

The North Sea and English Channel are surrounded by densely populated, highly industrialized countries and consequently the waters and biodiversity within them are subject to a large number of anthropogenic pressures. These include pressure from some of the busiest shipping routes in the

Chapter 2: Study Area 21

world, waste disposal, coastal zone recreation, dredging, extraction, offshore gas and oil production, commercial fishing, pollution by hazardous substances and chemicals, all of which can all pose threats to the areas various species and their habitats.

The Convention on the Law of the Sea recognizes three classes of marine area. The territorial sea is subject to coastal state jurisdiction and extends 12 nautical miles (nm) offshore. The exclusive economic zone extends 200nm (350 including the continental shelf). Within this zone the coastal state has exclusive right of exploitation of resources, including fisheries, and is responsible for regulating pollution. The open sea beyond is not subject to national jurisdiction. Responsibility for the management of the North Sea and the English Channel is taken by the surrounding countries. The North Sea European Union (EU) member states have transferred most of their exclusive rights to fisheries to the European Commission. The area supports multiple use by many nations, but there is now recognition of a need to achieve sustainabilility in its use.

The EU (and member states) have adopted measures to reduce environmental stress. These include regulations to reduce emissions, discharges and losses of hazardous substances, radioactive substances and nutrients. These address specific sources such as industries (land and offshore) or treatment plants, and those as diverse as agriculture. To lower the risk of accidents, navigational controls have been imposed. In an aim to achieve sustainable fisheries, measures such as net size regulation and catch quotas have been introduced (QSR, 2000). These measures are vital as the study area (Figure 2.2) is of great importance to the larval stages of many commercial target and non-target species.

The ichthyoplankton surveys used in this research are located along the French coast to the Dover Strait and across the English Channel to the English coast including the mouth of the Thames Estuary (Figure 2.2).

Chapter 2: Study Area

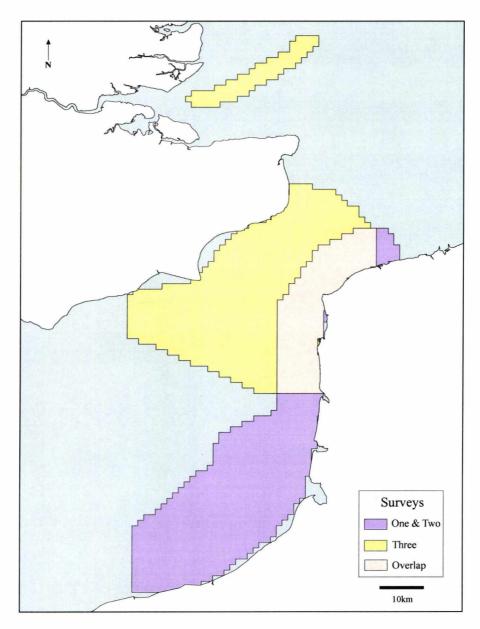


Figure 2.2 Ichthyoplankton survey positions in the Dover Strait

The following section is a description of the hydrographic features of the study area, and section 2.3 is an account of its climate. Biodiversity found in the Dover Strait is described in section 2.4 and section 2.5 is a depiction of the bathymetry. Human activities that may influence the marine ecosystem of the area are outlined in section 2.6 and section 2.7 is an illustration of the measures to protect biodiversity in the greater North Sea. The chapter is summarised in section 2.8.

2.2 Hydrographic features

The Dover Strait is characterised by highly variable hydrography typical of shallow depths. Tidal currents are the most energetic feature in the area, stirring the entire water column in most of the southern North Sea and the English Channel. The shelf areas of northwest Europe are believed to dissipate one-eighth of the world's tidal energy (Mann & Lazier, 1991). Tidal waters enter the area

through the northern boundary in the North sea and through the English Channel. The predominant north-easterly flow of water through the strait from the English Channel to the North Sea generates a pattern of currents, which is modified by the residual circulation of waters in the North Sea and further by outflows from estuaries. These combine to generate complex and highly variable hydrographic conditions.

The central English Channel waters are predominantly of Atlantic origin and the coastal waters originate from the estuaries along both coasts. The coastal water mass parallel to the French coast is well separated from the central waters by a tidally influenced frontal zone (Brylinski & Lagadeuc 1990), which is caused in part by alternating currents parallel to the coast (Grioche & Koubbi, 1997), but which disappears during low water. In contrast, waters in the English coastal areas are not separated. Dutch, Belgian and French river waters entering the North Sea have moderating effects. Significant although localised effects are seen from rivers entering the area from the south-eastern English coasts, the rivers Alde, Deben, Orwell, Rother, Colne, Blackwater, Crouch, Thames, Medway (and Swale) and Stour. The greater North Sea (which includes the English Channel) has an annual input of fresh water from river systems is in the order of 300Km³ (QSR, 2000).

Predominant North Sea circulation patterns are regularly disrupted by minor events such as winds and saline fronts. The general conclusion about controlling factors is that physical, chemical and biological parameters and processes in the North Sea are significantly influenced by climatic variability and unusual events, to variable extents (QSR, 2000). All these forces affect planktonic assemblages in the southern North Sea, the Dover Strait and the Eastern English Channel.

Thus the hydrography of the eastern English Channel and southern North Sea is under a number of prevailing weather, tidal and topographic influences. The major determinants may be summarised as: a) Atlantic currents flowing in a north-easterly direction through the English Channel and Dover Strait, b) diluting effects of fresh water entering the system through English, French and Dutch rivers and c) residual coastal currents in the southern North Sea. The area is generally categorised as "well-mixed" throughout the year (QSR, 1993) although frontal zones, marking the boundaries between different water masses are important in restricting horizontal dispersion and enhancing local biological activities.

Hydrological studies in the area show that average temperature is higher and salinity lower in the French coastal waters than in the English ones. Mean surface temperature and salinity in the region also vary depending on season, the temperature between 5-17°C and salinity between 34-35g/kg (Edwards & John 1993). Decreasing coastal to offshore nutrient gradients have been reported for SPM (Suspended Matter), POM (Particulate Organic Matter) and plankton (Brunet *et al.*, 1992;

Chapter 2: Study Area 24

QSR, 2000). The concentrations of SPM and phytoplankton biomass are greater in the French coastal waters, with maxima during the spring due to the biological productivity.

Temperature, salinity and density of the study area are mapped in the current research and described in Chapter Three.

2.3 Climate

Larger climatic effects influence the local influences of the hydrography. The waters at this temperate latitude are strongly affected by the inflow of oceanic water from the Atlantic Ocean and also by the large scale westerly air circulation which frequently contains low pressure systems. The extent of this influence varies. The winter North Atlantic Oscillation (NAO) index, a pressure gradient between Iceland and the Azores, governs the strength and persistence of westerly winds. The area has a high level of cloud cover and high precipitation. Rainfall averages 425 mm per year, although the Norwegian coast receives about 1000 mm annually as a result of wind-forced uplift of moist air against high, steep mountain ranges. A balance is roughly achieved between direct rainfall and evaporation (QSR, 2000).

Climatic effects can produce anomalies in the normal hydrographic conditions. During 1985 to 1992 the North Sea experienced climatic conditions that were exceptional for this century. Winters were particularly affected, especially over the southern North Sea where the study area is situated. A sequence of very cold winters was followed by exceptionally mild winters from 1988 to 1992. Very low rainfall was also experienced, which, in addition to the influence of the high salinity of the Atlantic water may have contributed to the record high salinity levels in the early 1990s. Storms were also more frequent, with an increase in wind speeds in some locations (QSR 1993).

It is difficult to determine the possible regional effects of climate change. Predictions, however, are that a surface air temperature increase of approximately 1.5° C, a sea level rise of about 0.5m and a general increase in storminess and rainfall will occur by the year 2100. If changes were to occur in global oceanic circulation patterns, the effect on the marine ecosystem and some human activities could be enormous (QSR, 2000). These changing climatic patterns indicate the need to plan protection of biodiversity with flexibility to adapt to change.

2.4 Biodiversity

The pelagic systems of the greater North Sea are influenced greatly by physical factors, particularly stratification due to differences in water density. These are particularly manifested by changes in the structure of plankton food webs, greater matter and energy cycling within the water column (OSR, 2000). The open (stratified) North Sea is dominated by picoplankton and nanoplankton in

contrast to the coastal areas. The phytoplankton is dominated by diatoms and dinoflagellates. Substantial increase in biomass of larger phytoplankton species only occurs during transient phases between lengthy periods of limitation (QSR, 2000). The plankton increase in the study area only occurs in spring and no winter increase is reported as is usual in September in the North Sea (Edwards & John, 1993). In normal conditions, the size-classes of algae involved in blooms are controlled by the grazer community. The algae in picoplankton and nanoplankton size ranges are effectively controlled by their microzooplanktonic grazers. Mesozooplankton show a much slower population response and this lack of control allows for rapid biomass increases in the larger algae. Zooplankton contains representatives of most marine phyla but is dominated by crustaceans, mostly copepods (Edwards & John, 1993). Diatoms and flagellates fluctuate along different annual cycles with particularly large inter-annual fluctuations in summer dinoflagellate stocks (QSR, 2000).

Plankton plays a fundamental role in the food chain of benthic and pelagic organisms. Impacts are seen throughout the ecosystem if environmental stress is imposed on the plankton. Primary production in the study area is lower than in the central North Sea, although the zooplankton biomass in the Dover Strait was found to be high in comparison to other parts of the North Sea (Krause & Martens, 1990).

In the littoral and upper sublittoral zones there are perennial fucoids (e.g. knotted wrack (*Ascophyllum nodosum*), bladder wrack (*Fucus vesicullosus*) and serrated wrack (*Fucus serratus*)), with annual green algae. In deeper water, species of kelp (e.g. *Laminaria hyperborean*) tend to dominate. These can form dense forests and are exploited in several countries surrounding the sea. Numerous (approximately 700) macroalgal species are found in the English Channel area, the most developed communities being found on rocky shores and on hard bottoms in the sub littoral zone down to approximately 15m in southern parts of the North Sea (QSR, 2000).

Approximately 230 species of fish inhabit the greater North Sea, of which thirteen are the main targets of commercial fisheries (cod, haddock, whiting, saithe, plaice, sole, mackerel, herring, Norway Pout, sprat and sandeel) (QSR, 2000). Exploited fish stocks fluctuate, primarily with variability of juvenile fish recruitment (Pawson & Robson, 1993). The causes of the variability are not fully understood. They are thought, however, to be determined by density independent environmental factors at the time of spawning and in the subsequent larval survival, and by sea temperature and currents that affect larval drift to nursery grounds, in addition to density dependant factors such as predation on the eggs and larvae (QSR, 2000). The scale of these fluctuations increases with exploitation of fish stocks (Pawson & Robson, 1993), and can differ by a factor of 5 for plaice, 50 for sole and over 100 for haddock (QSR, 2000). The species in the study are described in the Appendix.

Chapter 2: Study Area 26

The area is very important for a variety of bird life, both breeding and migratory. Coastal areas are used as wintering and migratory staging areas for waterfowl. Approximately 10 million seabirds are present in the North Sea at most times of the year (QSR, 2000). The migrations and seasonal shifts are pronounced. During autumn, many species leave and are replaced by visitors from northern and western waters. There are no endemic species. Some species, however, have over 50% of their world population in the area (QSR, 2000). Many species reached their largest population sizes in the 1990's, possibly caused by improved protection since the 1920's, increase in numbers of small fish prey and increased supply of discards and offal from fisheries. It is thought that human disturbance has decreased the numbers and breeding success of other species.

The North Sea and English Channel support several species of marine mammals, including common seals (*Phoca vitulina*), harbour seals (*Phoca vitulina*), grey seals (*Halichoerus grypus*), harbour porpoises (*Phocoena phocoena*), long finned pilot whales (*Globicephala melas*), common dolphins (*Delphinus delphinis*), while sided dolphins (*Lagenorhynchus actus*), Risso's dolphins (*Grampus griseus*), killer whales (*Orcinus orca*), sperm whales (*Physeter macrocephalus*) and minkie whales (*Balaenoptera acutorostrata*) (QSR, 2000).

2.5 Bathymetry

The bathymetry of the study area is relatively shallow and gently sloping, with a maximum depth of 55m (Figure 2.3). Currents tend to flow along the contours. The channel deepens to about 100m from the Strait of Dover westwards towards the Atlantic Ocean and eastwards towards the North Sea. During glacial periods when the sea level was lower, river valley systems were carved into the seabed (QSR, 2000).

hapter 2: Study Area

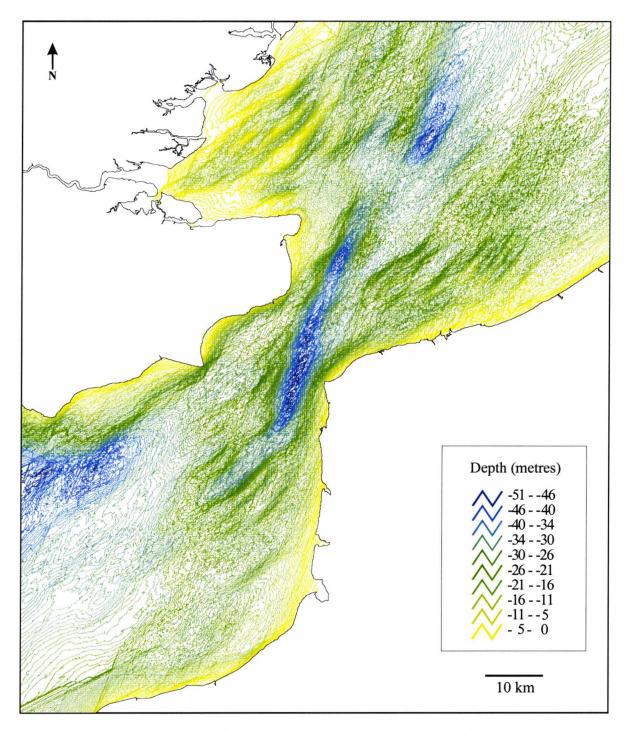


Figure 2.3 Bathymetry of the study area (© Crown Copyright)

2.6 Human activities affecting the marine ecosystem

The EU coastal zones are areas of high biological productivity and intense human pressure (Holdgate, 1994). The traditional sustainable lifestyles of communities surrounding the sea have come under increasing pressure. Changes have occurred in the practices of those not only on the coastal zone, but also inland, and the effects have become unsustainable. The southern North Sea is one of the most heavily industrialised areas of Europe (Swaby & Potts, 1993). The activities of humans which influence the North Sea and English Channel marine ecosystem are described in the following sections.

Chapter 2: Study Area

2.6.1 Commercial Fisheries

Fishing has traditionally been an extremely important activity in all the countries bordering the English Channel and North Sea. Commercial stocks consist of the round-fish (e.g. cod), the flatfish (e.g. flounder) and the pelagic fish (e.g. herring) fished for human consumption, and fish that are processed for fish-meal and oil (e.g. sprat and sandeel). Sustainability of the fishing industry declined with a sharp increase in numbers of ships and the use of larger ships with more powerful engines after the second world war. In 1995 the total fishing effort was approximately 2.25 million hours (Jennings *et al.*, 1999).

Within the waters of the EU member states, management of the North Sea is regulated by the EU Common Fisheries Policy (CFP) and within Norwegian waters by national policy (QSR, 2000). Total allowable catches (TACs) are allocated annually by the Council of Fisheries Ministers for the main commercial stocks (EC Fisheries, 1998) based on scientific information provided by the International Council for the Exploration of the Seas (ICES). The main impacts of fisheries result from the removal of target species (30-40%) of the biomass of commercially exploited fish species is removed every year), seabed disturbance by towed demersal gear and from the discarding and mortality of non-target species (by-catch). These impacts are widespread and ecologically important, but differ according to the type of fishery. Older and larger target individuals are more frequently removed leading to possible changes in the genetic composition of the population. It is thought that fast growing individuals are also often removed causing a smaller size and lower age of maturation (QSR, 2000). Stocks of haddock, whiting, saithe, plaice and herring, are close to or outside Safe Biological Limits, cod and sole are outside them (ICES, 2001). The spawning stock of mackerel has not yet recovered from its collapse in the 1960's (QSR, 2000). The herring fishery was closed in the 1970's, and rebuilt to high levels in 1988. Fishing mortality was too high, however, and the stock declined rapidly to low levels in 1996. Lowering the TAC to half the amount and introducing other measures such as restricted mesh sizes allowed the stock to increase again. Flatfish levels have also declined in the past ten years. Plaice had high recruitment levels in the 1980s but these have now declined with an increase in fish mortality (ICES, 2001).

Certain fishing practices lead to the discarding of more than half of the weight of all fish species caught. Offal from gutting and benthic by-catch are also additionally discarded at sea. Seabirds benefit from some of these discards, but as a consequence their populations have increased to unusually high levels. The whole food web is affected by fisheries. Changes in target species populations reduces available food for predators, and decreases predation pressure on prey (QSR, 2000).

Planton 2. Study Area

Effects of trawling is more widespread than merely effects on target species, and can affect the whole ecosystem. Turbidity is increased by repeated trawling of an area. Light penetration is thus affected and contributes to eutrophication by reducing de-nitrification (QSR, 1993). In addition to immediate effects of trawling on biota the sea bed may be altered in terms of depth and current flow. This can be caused by the change from a relatively well-compacted cohesive sediment into one with a lighter structure more easily eroded by storm action (QSR, 1993). The actual seabed is also affected by towed demersal gears, although the distribution of the frequency of the disturbance is patchy, increasing from the north to the south (Jennings, 1999), and the effects differ between gears. A depth of at least 1-8cm of the seabed is turned over when the gears pass over. The tracks left behind can last as little as a few hours in shallow areas with strong currents and tides, and for years in deeper waters. The composition of species is affected by towed gears, the larger long-lived species are being replaced by smaller opportunistic species (QSR, 2000).

Management measures have been implemented in an effort to conserve stocks of both pelagic and demersal species. These include minimum landing sizes (MLS), minimum mesh regulations and quantitative controls on catches through catch quota management (QM) of the setting of TACs, and delineation of areas where fishing is prohibited at certain times of the year (section 2.7). ICES provides scientific advice on which TACs are based. These are then divided into quotas. The TAC system within the CFP has been highly criticised as it rarely reduces the amount of fish caught, the dead excess being returned to the sea. Misreporting or unreported landings also occur (QSR, 2000).

Recommendations for consideration by the appropriate authorities include the continuation of efforts to reduce fleet capacity and the additional identification and use of closed areas to protect juveniles and benthos. The development of fishing gears which reduce or eliminate catches of non-target organisms and habitat disturbance is also encouraged (QSR, 2000).

2.6.2 Waste inputs

There is a range of human activities which cause waste to be put into the marine ecosystem. Industrial, domestic and agricultural industries all contribute material which is deposited into rivers, estuaries and coastal waters. There are several ways in which waste products and effluents containing contaminants reach the marine environment; sewage, agricultural run off and trade effluents are discharged from outfalls into rivers or directly into the sea, air-borne contaminants reach the sea via winds. Discharge is licensed but accidental release of industrial pollutants also occurs (Bell & Gilbert 1993c). Wastes can include nutrients such as nitrate and phosphate, metals such as copper, zinc, cadmium and mercury and organic compounds (QSR, 1993). Waste can originate from urbanisation and the disposal of untreated sewage in estuaries. Eutrophication can result where a rapid and artificial increase in nutrient levels occurs. Algae grow quickly due to the

hanter 2: Study Area

higher level of nitrates and phosphates and form blooms, some of which are toxic. In turn when the algae die and breakdown, oxygen is used at such a rapid rate that large areas may become oxygen deficient, causing most of the marine life to move away or die. Fish are particularly sensitive to the reduction in dissolved oxygen which results from eutrophication. Fish leave the area or die. Some areas such as the Thames have improved recently and fish are returning (Swaby & Potts, 1993). The dumping of sewage sludge has been banned under OSPAR since the beginning of 1999. The level of treatment of domestic sewage has improved and the EC has succeeded in phasing out the disposal of sewage sludge at sea (QSR, 2000).

2.6.3 Shipping

The study area and the North Sea contain some of the busiest shipping routes in the world, at approximately 420 000 shipping movements per year (QSR, 1993). More than 400 ships pass through, and 600 ships cross the Strait of Dover daily. In 1996, approximately 270 000 ships entered the main 50 ports in the North Sea and English Channel area (QSR, 2000). There are many negative impacts that these shipping activities impose on the marine environment, including cleaning and venting tanks, loss of cargoes containing harmful substances (50% of goods carried at sea can be described as dangerous), discharges of oil and wastes, discharge of ballast water containing species alien to the area and the use of anti-fouling paints containing biocides. New regulations aim to ban the use of harmful ingredients in anti-fouling paint by 2003 and removal of paint from hulls by 2008 (QSR, 2000).

2.6.4 Sand and gravel extractions

Marine gravel and sand are extracted by commercial companies for concrete production, road construction, building, beach replenishment and soft coastal defences. Terrestrial sources are no longer sufficient to meet the demand in Britain (Doody *et al.*, 1993). The marine environment supplies 8% of aggregate production and 2% of sand and gravel production. The east Thames and south coast of Britain provided over 10,000,000 tonnes of marine aggregate in 1995, which represents 44% of the total for Great Britain in that year (Bell & Gilbert, 1993a).

Effects on the marine ecosystem are difficult to assess, and depend on the extraction method, sediment type, bottom topography and bottom current strength. If an overflow system is used, displaced water flows back into the sea forming a turbid plume of suspended sand and silt (de Groot, 1996). Removal of substratum results in the destruction of infaunal and epifaunal biota. Surface mud is disturbed in order to access aggregate underneath which also affects fauna within and can affect flatfish feeding. A stable gravel bank can be replaced by an area of mobile sand (de Groot, 1996). Spawning grounds can be greatly affected if a particular substrate is required by a species (such as herring). Re-deposition of fines from the plumes may smother eggs laid on the bottom in a large area. Wide ranging effects can be seen if sediment deposition and topography are

changed. Uneven bottom profile can reduce current strength and may result in the deposition of finer sediment (de Groot, 1996). Recolonisation of areas by opportunistic species can be fast (van Dalfsen *et al.*, 2000), altering the species composition. Species richness restored along the French coast of the English Channel 16 months after extraction was accompanied by reduced densities and biomass after 28 months. A different community structure was in place corresponding to the new type of sediment in place (Desprez, 2000). The effects, however, are unlikely to be permanent if the remnant substrate is identical to the superficial sediments (Bell & Gilbert 1993a), sites tested in the North sea took two to four years to recover, although areas which have a less dynamic hydrographic regime are estimated to take longer (van Dalfsen *et al.*, 2000).

2.6.5 Dredging and disposal of dredged materials

The marine environment is also affected by dredging of materials from the sea bed, both for capital and maintenance dredging. Maintenance is regularly carried out and capital dredging is one off removal of sediment, mostly for deepening shipping channels and constructing new docks. The sediment is mostly deposited at sea, although some is used for land claim and beach recharge (Bell & Gilbert 1993a).

Short-term localised effects can be the removal of material and organisms, but it is difficult to assess long term effects. It is especially difficult to determine which effects are the result of dredging and which are due to other factors (Doody *et al.*, 1993). The disposal of dredged materials at sea also affects the marine ecosystem, including blanketing the seabed. If deposition is greater than the natural sedimentation rate, benthic flora and fauna may be killed through suffocation and starvation. Particle size can also change, which can change the faunal and floral composition, thereby affecting the whole food chain (Bell & Gilbert 1993a), in a similar manner to those described in section 2.6.4. Temporarily elevated levels of suspended particulate matter can occur as a result of both dredging and disposal of material. Light penetration and therefore primary productivity may be affected in addition to processes such as fish migration (Bell & Gilbert, 1993a). The characteristics of spawning and nursery areas may also be altered by both dredging and disposal, making them unsuitable for the species concerned. Dredged material often have high levels of contaminants (QSR, 1993). Part of the trace metal component often present is of natural origin, so the material is relocated rather than being fresh input into the environment.

2.6.6 Infrastructure

Fish spawning and nursery areas are vulnerable to the development of infrastructure such as pipelines, gas and oil exploration, building on the coast and wind farms. Reasons are those mentioned under sections 2.6.4 and 2.6.5. In addition, large structures can effect tidal and current regimes that can alter the seabed (Pawson & Robson, 1993).

Oil and gas structures release hydrocarbons, heavy metals and production chemicals. The UK continental shelf production in 1995 was 220 million tonnes. The number of platforms increased from 300 to 475 between 1990-92 and 1996-98 and oil production almost doubled. Gas is also exploited in the shallower areas of the southern North Sea (QSR, 2000). The length of pipelines is increasing, representing about 9670 km of both rigid and flexible pipes, comprising approximately 1.7 and 2.2 x 10⁶ t of steel and concrete respectively, 5,100 t of tar, 62,000 t of asphalt, 10,000t of aluminium and 6500 t of zinc anodes as protection against corrosion (QSR, 2000). Power stations on the coast can also affect fish, as although modern power stations have 'return systems' they can still trap large numbers in the intake waters (Swaby & Potts 1993).

There are reports of the possible plans to build up to 5,000 giant wind turbines, twice the size of traditional ones, off Germany's north coast. These create concerns about shipping safety in addition to effects on the marine ecosystem (BBC, 2002). Denmark, the United Kingdom, the Netherlands and Sweden also plan to build offshore wind turbines. Turbines are expected to affect the roosting, feeding or migrating of seabirds, to destroy the benthos by construction of foundations and influence hydrology and sedimentation patterns. Small and large scale orientation of fishes and marine mammals could be affected by the artificial magnetic and electronic fields generated by the cable links, in addition to the noise and vibrations produced in the water column through the turbine tower as well as from the shadows or flashes generated by reflections of the turning rotors (BBC, 2002).

2.6.7 Radioactive substances

Artificial radionucletides are discharged into the North Sea from nuclear reprocessing plants, nuclear fuel fabrication and to a lesser extent nuclear power stations (QSR, 1993). The main source is the Cap de la Hague reprocessing plant, although the discharge has been decreasing since 1986. Natural sources of radionucletides are natural processes of weathering and transport (QSR, 1993).

2.6.8 Mariculture

Salmon are farmed in Scotland and Norway, rainbow trout in Norway, Denmark and Scotland, halibut, arctic char, cod, turbot and eel in Norway. Sea trout, cod, halibut and turbot, sea bass and eels are being considered for production elsewhere in the UK. Shellfish are also cultured along the North Sea margins, many species on the Kent coast, including Pacific oysters, native oysters, mussels and Manila clams (Robson, 1993). Oysters are also cultured in the Netherlands, Norway, Normandy and Brittany in France, Germany and Scotland. Blue mussels are cultured in Denmark, the Dutch and German Wadden Sea, the Eastern Scheldt, Brittany in France, Norway, Sweden and the UK (QSR, 2000). Concern has been voiced over the introduction of non-native species for

33

cultivation as the marine ecosystem will be affected if self sustaining populations establish in the area. The Netherlands are introducing new regulations to minimise this risk in Dutch waters.

2.6.9 Other influences

Changes in the outflow caused by damming can cause negative impacts on the productivity of coastal rivers. Coastal defences, land reclamation, power generation and dumping of items such as ships or oil and gas platforms can all cause changes and damage to the marine ecosystem, although the extent is unknown. Dumping of iron/steel vessels is forbidden, and all other ships will be forbidden after 2004. Litter also remains a considerable problem for the marine environment, the sources mostly being shipping (fishing and commercial). This can include drift fishing nets and ropes, but a little is also transported by the wind, currents and rivers. The amount is estimated at 70 000 m³ per year (QSR, 2000). The dumping of litter is prohibited, although little improvement has been seen.

Bewers & Wells (1992) consider progress made in the protection of the marine environment during the past 40 years, concluding that the present approach has limited effectiveness and is overdue for replacement by a comprehensive strategy for social development and environmental protection. Recent changes to regulations provide hope that many negative effects are being reduced, although many are still damaging the ecosystem.

2.7 Protecting fish in the Eastern English Channel and the North Sea

Many methods have been employed in recent years to protect marine biodiversity and fisheries in the UK. These include the establishment of protected areas and regulations through the CFP concerning fishing gears and quotas. Mesh size, gear configuration, minimum landing sizes, vessel licences, engine sizes, effort control such as kW-days at sea (Horwood, 2002) are all regulated. There are several forms of protected areas including MPAs, voluntary protected areas, 'no-take' or closed areas and fishery exclusion zones (Rogers, 1997).

Many measures have received mixed reception from the fishing communities. The CFP has been highly criticised and is due for review in 2002. Fishers claim that subsidies and catch quotas are not effective at protecting both the fishing industry and fish stocks (WWF, 2002). There are also significant problems in the past with developing statutory marine nature reserves due to public opposition. It is hoped that with new methods, a balance can be achieved between top down legislative and bottom-up community involvement approaches to management (Laffoley *et al*, 1994). There are now three marine nature reserves in UK waters; Lundy Island in the Bristol Channel, Skomer Island off the Pembrokeshire coast and Strangford Lough. There are no marine reserves in the French waters of the English Channel, although several are proposed (Boncoeur *et*

al., 2002a; 2002b). Britain also has 66 candidate marine SACs (Horwood, 2002), and management plans for twelve of these.

Several EU regulated 'no take zones' designed to protect fisheries target species exist around Britain. The 'plaice box' is an area of 38,000 km² along the Dutch, German and Danish coast partially closed to fishing since 1989 (Pastoors et al., 2000). The aim is to protect juvenile demersal species such as plaice and sole in their main nursery ground. The ban on fishing was introduced gradually, which produced heavy exploitation in the 'open' months and on the edges of the area (FSBI, 2000). The partial ban was extended to the whole year from 1995. The box has produced fishery benefits by reducing mortality of younger fish and hence boosting recruitment to the adult stock. The size composition of commercially exploited species has changed inside the box, larger sizes increasing in number, although the non-target species did not change. Other trends were also discovered both inside and outside the plaice box, including a decrease in the relative abundance of plaice and an increase in species richness due to the influx of southerly species (Piet & Rijnsdorp, 1998). It has been suggested that a total ban would provide greater fisheries benefits (FSBI, 2000).

The 'mackerel box' is positioned off southern Ireland and England and very successfully protects juvenile mackerel, whose mortality has been reduced by 83%, 60% and 20% for ages 0,1 and 2 years (FSBI, 2000). The 'sandeel box' was introduced in 2000 off the east coast of Scotland to protect the sandeels as a food resource for local predators including seabirds. Fishing is banned for three years (Horwood, 2002). 34 areas have been designated as statutory bass nursery areas under the 'Bass Specified Sea Areas Prohibition of Fishing Order', where juvenile bass are abundant and are most easily caught particularly during the summer months (Pawson & Robson, 1993).

North Sea cod, recognised as being at very low levels for over ten years, have only very recently shown signs of recovery (FSBI, 2000). The EU agreed in 1993 that restricting fishing in large areas would not be adequate to protect cod in the North Sea. This decision was based on ICES simulations and was due to high cod mobility. Implications are that even restricting fishing in an area equivalent to a quarter of the North Sea would have little beneficial effect for cod (FSBI 2000, Jennings, 1999). In 2001, however, it was decided by agreement between the EU and Norway that emergency measures were needed. An area closed to fishing, except for pelagic vessels and vessels fishing sandeels, was implemented from 14th February to 30th April. The closure covers the main spawning season for cod and was the first step in a series of measures forming a cod recovery plan. It is designed to protect mature cod and allow them to produce as many eggs as possible in the hope of increasing abundance of young cod (CEFAS, 2001). Emergency measures are also being set up to aid the recovery of Northern hake stock.

A seasonal trawl ban in the Normand-Breton gulf (English Channel) within the 12nm zone of the UK and France has been proposed, and a marine park project has been proposed in West Brittany that would be first park of this type in France (Boncoeur et al., 2002a; 2002b).

'No take' zones are usually large areas, but designed for single species. If areas can be identified which are used by many species, then areas needed for protection might be dramatically reduced. Measures in place to reduce the catch of fish will not protect the actual grounds needed for spawning and nursery, nor the waters. These areas need protecting from physical damage to the substrate, pollution and alien species, in addition to the protection of the adults when spawning. The aims of this study include the testing of methods to identify such areas.

2.8 Summary

- The Dover Strait is situated between the North Sea to the north-east and the English Channel to the south-west and forms part of one of the major fish producing ecosystems in the world. High productivity is associated with its comparatively shallow depth and the existence of mixing mechanisms transporting nutrients from the bottom layer to the upper layers of the water column.
- The Dover Strait and adjacent waters provide important spawning and nursery areas for some larval stages of species targeted by commercial fisheries.
- The area is surrounded by densely populated, highly industrialised countries. The marine ecosystem is consequently subject to a large number of anthropogenic pressures. These include some of the busiest shipping routes in the world, waste disposal, coastal zone recreation, dredging, aggregate extraction, offshore gas and oil production, commercial fishing and pollution by hazardous substances and chemicals. All of these can pose threats to the area's various species and habitats.

Chapter 3: Creation of a GIS Database for the Dover Strait

3.1 Introduction

A geographic information system (GIS) is "a system for capturing, storing, checking, manipulating, analysing and displaying data which are spatially referenced to the Earth" (Burrough & McDonnell, 1998). GIS technology provides powerful tools for the management and analysis of spatial data. Many ecological phenomena contain a spatial element and so areas such as conservation planning and conservation management are increasingly utilising GIS technology.

The role of the GIS as a tool in processing and displaying resource data is extensive. The main strengths of GIS are the common analysis of spatial and associated attribute data (Sarkozy, 1998), the ability to combine or overlay map layers and to conduct spatial analysis and perform queries within one layer or among objects in two or more layers. GIS are also open-ended and can easily be updated by receiving new or integrating old data (Salm *et al.*, 2000). GIS can allow increased speed and accuracy in spatial data calculations, thus facilitating evaluation of proposed management scenarios and informed decision making (Stanbury & Starr, 1999). This is of particular relevance to PA selection.

A GIS was utilised to interpolate ichthyoplankton and environmental data and to carry out much of the analysis in this research. This chapter describes this process. Section 3.2 is a description of GIS systems and spatial analysis using GIS. Section 3.3 contains a review of GIS use in previous studies and its potential to revolutionise the way in which all spatial data is analysed. Section 3.5 is an explanation of the way the data available in the Dover Strait ichthyoplankton spatial database were derived, incorporated into the GIS and manipulated for later analysis. Section 3.6 contains a summary of the chapter.

3.2 Analysing spatial data using GIS

GIS technology enables use of themes or map layers known as coverages. Each theme is a collection of similar geographic features such as roads, water bodies, vegetation, elevation or cities. Many themes can therefore represent different aspects about one area or region. Geo-referenced information is linked to attributes stored in a table, and forms a database. This contains information concerning both the location and the properties of the represented objects and phenomena. This forms the basis for locating and combining field or other thematic data.

The two models of spatial data representation used in a GIS are those of rasters and vectors. The form used affects both the representation of the data and the methods of analysis possible. The choice of method therefore heavily depends on the type of data in use, the type of analysis required and the software available.

Vectors consist of points, lines and polygons representing features in the area of interest (Figure 3.1). A line is produced by joining two or more points, and a polygon is then created when a series of lines joins to form a boundary around a homogeneous entity (Figure 3.1 and Figure 3.2). Arcs, which are lines with information regarding direction, can also be used. These could be useful when representing rivers or roads. Vectors are discrete objects in space, although can form tessellating shapes.

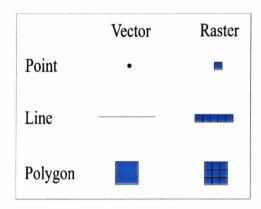


Figure 3.1 The differences between rasters and vectors

Rasters are continuous data representations (Figure 3.2 and Figure 3.5). They are made up of smaller tessellating units, most commonly square, that are often likened to the pixels of a computer screen or electronic image (Figure 3.2 and Figure 3.5). Each pixel contains information concerning the nature of the location in space it represents. This could be a class of phenomena such as vegetation type, or represent a measurement such as elevation or distance from a feature of interest. Rasters are useful for representing data which occur over the whole area of interest or has a high spatial turnover, such as much environmental data, including elevation and vegetation type. A less sharp boundary for instance, such as the transition between two vegetation types, can be represented by a raster with a mix of pixels.

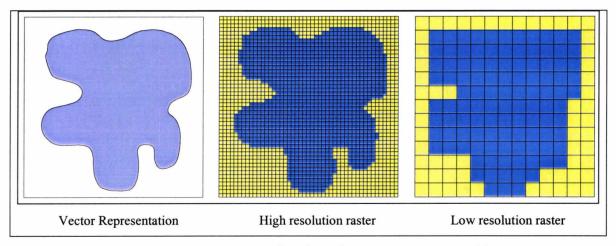


Figure 3.2 Representation of a polygon by vector and raster models

A vector can often look more accurate than a raster (Figure 3.2 and Figure 3.3) but vector data could be inaccurate due to digitising errors. Vectors provide good representation of entity models. They have a compact data structure and co-ordinate transformation is straightforward. Vectors give the same graphic representation at all scales, can show very small features and database query is easy. Data concerning individual features can be easily retrieved for updating or correction. Vector representation, however, has a complex data structure. The polygons are considered to be homogeneous so spatial analysis within them is impossible. The simulation modelling of processes is more difficult as each entity may be of a different size, the representation of high spatial variability is inefficient and initial data capture can be very slow.

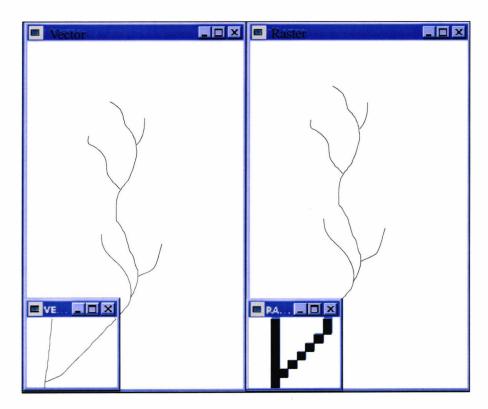


Figure 3.3 Raster and vector lines

Raster data structures also have many advantages and disadvantages. They have a simple data structure. Many kinds of spatial analysis and filtering may be used. Mathematical modelling is easier because all spatial entities have a simple, regular shape. Overlaying and merging is easily performed. Scanning technologies can supply huge quantities of data cheaply. Remote sensing techniques produce data for integration into GIS in a raster format and analysis of continuous data is powerful. Disadvantages, however, include the large memory needed for storing and displaying data and the reduction in spatial resolution and information with the use of large cell sizes. Network analysis is also more difficult.

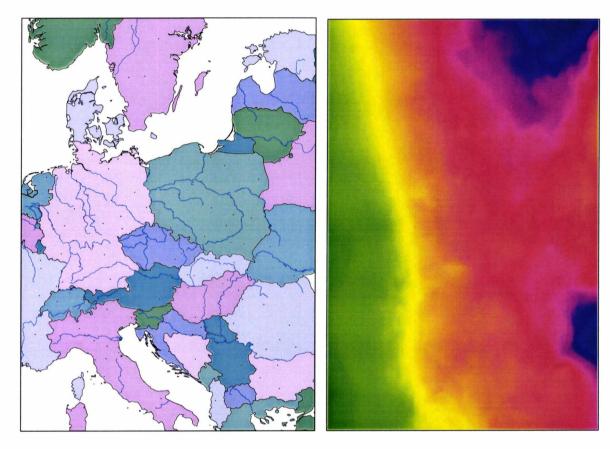


Figure 3.4 Political boundaries and rivers; data suited to vector representation

Figure 3.5 Elevation; data suited to raster representation

Limitations of the two systems are increasingly less important as computer power increases and software is more able to combine the ability to analyse the two data models. Both raster and vector data representation were utilised in this research. Coverages such as the coastal map and the selection unit grid were represented efficiently and accurately using vectors (Figure 3.4). In contrast, distribution of species and the environmental variables were better represented and analysed using rasters (Figure 3.5). For this reason, two groups of software were used. ArcView, ArcInfo and ArcGIS softwares (ESRI, 2002) were used for the vector analysis and some raster analysis. Idrisi software (Clark Labs, 2002) was also used for some raster analysis.

3.2.2 Sources or error

Credibility is often given to results produced by a GIS because the outputs can look accurate and impressive. Unfortunately this may not reflect reality and can hide dubious methods. Errors are often not outlined with the results of the analysis. The effect of errors can be reduced if they are documented and considered when analysing and interpreting results from GIS analysis, although often the actual error cannot be removed. Errors can be introduced to the data from a wide range of sources. Errors that cannot be removed include those incurred from projection transformations and locations recorded by a global positioning system (GPS). The accuracy of the measurement may be known, but the direction of the error unknown. Similarly, when two or more coverages are combined, errors in the original coverages are also combined, producing a less accurate resultant coverage. Other errors include inappropriate projection use, data derived from inappropriate scales and inconsistencies between scales, out of date information or data originating from different times, incomplete or partial coverages, measurement errors during data collection, digitising errors, observer bias, inappropriate data model choice and low density of observations. There are also data entry errors, classification problems, inappropriate interpolation method choice, laboratory analyses errors, data relevance and surrogacy, data format and conversion problems, overlay errors and vector / raster conversion errors. When using interpolation techniques, those that include a measurement of the accuracy of the model can be useful in calculating error. The documentation of all information concerning a dataset is classed as metadata. Its accumulation is essential to minimise the effect of many errors, and is described below.

3.2.3 Metadata

If metadata are documented, many errors can be assessed. Information loss during data exchange, such as among dissimilar computer platforms and between analysts, can be reduced (Stanbury & Starr, 1999). Metadata include data source, projection information, digitising accuracy, data age, data scale and any transformations performed on the coverage. Available datasets in some areas are often second or third generation, or of untraceable origin. These increase the likelihood of inappropriate data use. Following metadata standards and documenting the history of database amendments increases the quality and integrity of spatial data in addition to facilitating its exchange amongst agencies and institutions (Stanbury & Starr, 1999).

3.2.4 Scale and data compatibility

GIS facilitates map viewing at any scale. It is easy to select and visualise data subsets (zoom in to specific areas), especially when using vectors. This, however, can create an apparent accuracy at a larger scale than the source data. This can encourage the use of data at inappropriate scales, and also the combination of data sources originating at different scales. The data utilised in this research were derived from two data sources. These sources are samples georeferenced by GPS

and coverages digitised from UK Hydrographic Office charts. Some data were discarded to enable two survey datasets to be comparable and compatible. This process was necessary to ensure data quality and integrity.

3.3 The use of GIS for conservation

GIS has revolutionised the way in which biodiversity data are stored, manipulated, analysed and displayed. It has allowed fresh insights into spatial relationships, such as those between elements in an ecosystem. In its early years the cost of the technology and training necessary to use GIS was prohibitive to its use within conservation biology to all but large well funded projects. These often concerned charismatic fauna or habitats. The analyses have often been to define favourable habitat for single species, such as buzzard (Buteo buteo) nesting sites in Scotland (Austin et al., 1996), grizzly bear habitat in Western Montana (Mace et al., 1999), and in the Northern Cascades (Agee et al., 1989), Californian condor (Gymnogyps californianus) in western United States (Stoms et al., 1994), moose (Alces alces) in Ontario (Puttock et al., 1996), black bear (Ursus americanas) in Arkansas (Clark et al., 1993), red pandas (Ailurus fulgens) in Nepal (Yonnzon et al., 1991), fisher (Martes pennanti) in the Klamath region, USA (Carroll et al., 1999), black-tailed deer (Odocoileus hemious columbianus) in California (Boroski et al., 1996), reintroduced eastern wild turkey (Meleagris gallopavo sylvestris) habitat in Michigan, USA (Donovan et al., 1987) and black rhinoceros (Diceros bicornis) in South Africa (Huggins, 1996). GIS has also been utilised to predict favourable habitat from the models. These include the marsh-breeding red-winged blackbird (Agelaius phoeniceus L.) in coastal lake Erie wetlands, USA (Özesmi & Mitsch, 1997) and several species of antelope in South Africa (Smith, 1996).

Large scale management projects have utilised GIS for monitoring and predicting ecosystem changes. Examples include the Astrakhanskiy biosphere reserve in Russia (Lychagin *et al.*, 1995) that utilised GIS for management of changing conditions due to fluctuations in the Volga river flow and the Caspian sea level. GIS was used to develop ecological indicators of landscape degradation produced by livestock related activities in subantarctic forest, in Los Alerces National Park, Argentina (Elba de Pietri, 1995), where areas at risk were identified and changes in livestock management could be made. GIS has also been used extensively to study forest fragmentation and destruction (e.g. Skole & Tucker, 1993; Trejo & Dirzo, 2000).

Further applications and uses of the technology became more widespread with decreased cost and increased training opportunities. GIS was used to determine roe deer (Capreolus capreolus) population densities compatible with forest management goals and to assess harvest rates necessary to maintain the desired deer densities in Germany (Radeloff et al., 1999). Boyce & McDonald (1999) describe the use of GIS methods to predict species population sizes. GIS has been used to analyse the effect of disturbance on moose habitat (Rempel et al., 1997), to analyse the effects of

different timber harvesting strategies on pine martin (*Martes americana*) and woodland caribou (*Rangifer tarandus*) in British Columbia (Klisey *et al.*, 1999). The effects of forest management on red squirrels (*Sciurus vulgaris*) was investigated using GIS in the UK (Gurnell *et al.*, 2002). It was used to assess the potential impact of climate change on species richness in mountain forests in Switzerland (Kienast *et al.*, 1998). Other applications have included the analysis of human-elephant (*Loxodonta africana*) conflict in Kenya (Smith & Kasiki, 2000), the identification of factors limiting fecundity and movement patterns of the black rhinoceros (*Diceros bicornis*) in Namibia (Hearn, 1999), to identify a linked reserve system in Florida (Hoctor *et al.*, 2000), to identify priority areas for conservation of several species of lemur in Madagascar (Smith *et al.*, 1997) and using bird data in the UK (Woodhouse *et al.*, 2000). GIS has also been used to identify under-represented ecosystems and species in PAs (e.g. Loomis & Echohawk, 1999).

The multidimensional and strong spatial component of marine and fisheries data is well suited to the use of GIS to visualise, facilitate and understand marine relationships. It has been used to incorporate the spatial component of fisheries data into stock assessment models (Booth, 2000), habitat suitability models (Brown 1997), growth and transport model of mackerel (Bartsch & Coombs, 2001) and habitat assessment with resource management (Stanbury & Starr, 1999).

GIS can enhance analysis and decision support in biodiversity and conservation planning (Brockhorst & Bridgewater 1994). It can provide temporal and spatial flexibility required in the use of protected area design methodologies. These methodologies require units of area that can be considered for inclusion in PA networks, based on their biological or environmental properties. The design of these units is described in the following section.

3.4 Designing PA network selection units

To create the selection units, the study area was subdivided into a series of units that form a selection unit grid. The grid was also used to delineate the study area and reduce the effects of spatial autocorrelation in the data. The selection units can be arbitrary subdivisions of the landscape such as regular grids of squares (Kirkpatrick & Brown, 1991; Belbin 1993; Church *et al.*, 1996; Williams *et al.*, 1996) or other shapes such as hexagons (Csuti *et al.*, 1997). They may be natural units such as catchments (Bedward *et al.*, 1992) or isolated patches of habitat (Margules *et al.*, 1988; Saetersdal *et al.*, 1993) or they can be administrative units such as tenure units or land parcels (Pressey *et al.*, 1994; Pressey & Taffs, 2001b). This research was carried out at a fine scale and in an environment where natural or administrative units were not appropriate or available. A series of tessellating square units of equal area were instead created.

Appropriate scale of analysis for realistic conservation planning is debated. The scale chosen should depend on the purpose of the analysis, in addition to the available data and the methods

used. Information is often only available on broad scales. This has determined the scale at which most reserve selection exercises have been carried out (Chapter One).

The size of the units has important implications for the actual process of selection. This includes the number of units that can be handled by the analysis in a reasonable time. The size of units affects the efficiency of selection algorithms (Schwartz, 1999), small scale selection units appear to be more efficient in terms of the proportion of the considered units identified as necessary for the specific conservation target in use (Pressey & Logan, 1998). The size of the units relative to the scale of the underlying features should also be considered in their design. The map projection can introduce differences in the actual size of the selection units designed to be of equal size, so a size appropriate for the projection system in use is advisable. Convenience of conversion of selection units to management units on the ground is also a consideration (Pressey & Logan, 1998). The current research was able to utilise fine resolution data to identify areas realistic to the scale of conservation within the area. The size of the selection units for this research was chosen with consideration of many of these factors. Important considerations were to allow a realistic size for practical protection and to enable a large enough difference between the resolution of the underlying distribution data and the selection unit. The mean values of abundance and proportional area of species distributions within the selection units were both used in the analyses. The process to create the selection unit grid is described in section 3.5.3 below.

3.5 GIS coverage creation

The GIS database for the study was designed to integrate spatial information from various sources. The spatial extent of the study area was defined to include as many of the predetermined survey sampling stations as possible (section 3.5.3). The resolution of the raster coverages needed to be identical for all data sources. It was also necessary for the vector selection unit grid position to match these raster coverages precisely. The UTM projection was chosen for the database because of its precision at the scale and position of the study area, its use of metric units for distance and its probable compatibility with future research in the area. It uses the WGS84 datum and the Transverse Mercator projection. The zone selected was 31 North as its central meridian is at 3° East. This projection allowed accurate representation with minimum distortion across the study area (Ordinance Survey, 1999).

The following sections describe the creation of the individual coverages used in this research.

3.5.1 Coast coverage

3.5.1.1 Methods

A coverage of the coastal margin was needed for several applications within the research. The study area is adjacent to the coast, so the coastal line was necessary to establish a boundary at the coastal margin. The coastal vectors were digitised from UK Hydrographic Office Charts (nos. 2449 and 2451) at a scale of 1:50,000 (Crown Copyright). The charts were projected using Mercator and referenced to European 1950 datum and Ordnance Survey of Great Britain 1936 datum. Formal acknowledgement is given for kind permission of The Controller of Her Majesty's Stationery Office, the Port of London Authority, and the hydrographic offices of Belgium, France, the Netherlands and the United Kingdom, to use the data. The vectors were reprojected into UTM zone 31 North reference system, using a Transverse Mercator projection referenced to WGS84 datum using Idrisi. This enabled compatibility with the Dover Strait database and accuracy for spatial analysis (Ordinance Survey, 1999).

3.5.1.2 Results and Discussion

The coast coverage is illustrated in Figure 3.6. It was used to define the study area of interest and give context to the coverages of protected area networks identified by later analysis.

3.5.2 Ichthyoplankton abundance distribution coverages

3.5.2.1 Methods

The ichthyoplankton sampling surveys were carried out by the Department of Ichthyology at the University of Littoral. Surveys were conducted during April (Survey One) and May (Survey Two) 1995 off the French coast, and April 1999 (Survey Three) in the Dover Strait and the Thames Estuary (Figure 3.6 and Chapter Two). The positions of the sampling points (Figure 3.6) were designed to include as wide a range of environmental conditions as possible, in accordance with Brunet *et al.* (1996).

Ichthyoplankton was sampled by a 'bongo net' (for full methodological details see Grioche *et al*, 1999). The sampling net had a mesh size of 500 μm. The net was towed from 3 to 5 m above the seabed to the surface. The position of the boat was recorded using a global positioning system (GPS), the error of which was unavailable. The volume of water passing through the net was calculated by a flow meter positioned in the middle of the net frame.

After deployment, the net end-bag was removed and the sample washed into a jar and fixed using buffered 5% formaldehyde solution. Temperature, density and salinity were recorded using a 'Seabird 19' CTD profiler (conductivity, temperature, density) at each sampling point. Readings were taken just above the bottom and just below the surface.

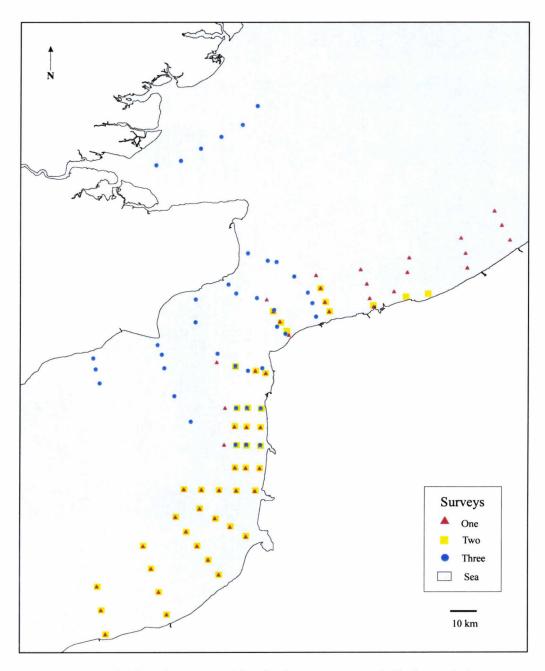


Figure 3.6 Sampling points within the three surveys available for analysis

Ichthyoplankton were sorted and identified at the Ichthyology Laboratory, University of Littoral, Calais. The species present (Appendix) were identified according to Russell (1976 see Grioche *et al.*, 1999) and the stage of development of each fish larvae was identified according to Koubbi (1990, adapted from Ryland, 1966 see Grioche *et al.*, 1999). Stages recorded were the yolk larvae (stage 1), pre-flexion larva (stage 2), flexion larva (stage 3), transition larva with formed fin-rays (stage 4) and Stage 5 in flat fish according to the eye migration (Grioche *et al.*, 1999).

3.5.2.2 Results and Discussion

Ichthyoplankton abundances were expressed as the number of organisms per 100 m³, obtained by using the reading from the flow meter. The abundance of each ichthyoplankton stage was recorded

in a spreadsheet, identified by survey and sampling station. The methods of modelling the distribution and abundance to produce the coverages for inclusion in the GIS database were tested for the most appropriate method. These are described in Chapter Four.

3.5.3 Selection unit coverage.

The selection unit grid (Section 3.4) was necessary to define areas for consideration in PA network identification.

3.5.3.1 Methods

It was necessary to first identify the area of interest for the study from the three surveys. Several factors influenced the boundary position. Data surveys were carried out at a series of sampling points. Those in surveys one and two had a large area of overlap and Survey Three was overlapping but not completely. In order to produce two areas of information that could be compared, and produce a compatible dataset, many of the data points from Survey Two were discarded (Figure 3.7). Several data points in Survey One were also discarded, due to their spatial arrangement. Their data were included during the interpolation of biological and environmental variables to allow a more accurate model. Those portions outside the study area were subsequently removed (Figure 3.7 and Figure 3.8). One selection unit grid was identified for surveys one and two and a spatially distinct, although overlapping, selection unit grid was identified for Survey Three.

A polygon was created to encompass the set of sampling points incorporated in the study using 'animal movement' extension in ArcView. A buffer of 2km was then produced around this polygon using the 'buffer' command in ArcView. The two polygons were joined together using the 'geoprocessing wizard' in ArcView. The resultant polygon encompassed all the sampling points to be included in the study, with a 1km buffer around the outer points.

A series of square vector selection unit polygons was created using the 'planimetry' script, with a cell size of 4km². The polygons were positioned across the complete study area beyond the sampling points. The selection units that were encompassed by the study area polygon were then selected using the 'select by theme' command in ArcView. These selected units were then exported to a separate shapefile (the files utilised by the ArcView software). The selection unit shapefile was further modified by clipping the coastal units to the coastline using the 'geoprocessing wizard' in ArcView. This excluded areas extending on to the land. Any squares unsuitable for inclusion in the analysis (i.e. extremely small or behind barriers such as harbours or outcrops of land) were removed from the selection unit grid system. Each unit within the final grid system was assigned a selection unit number.

3.5.3.2 Results and Discussion

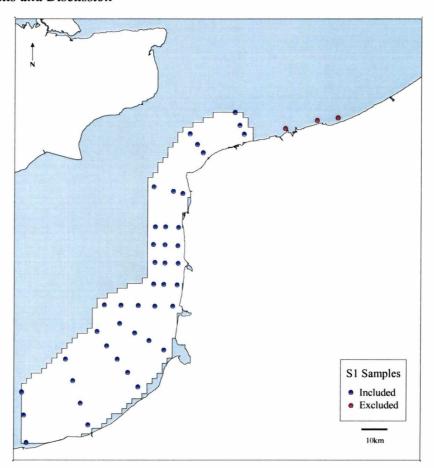


Figure 3.7 Survey One stations included in the study, surrounded by Survey One polygon

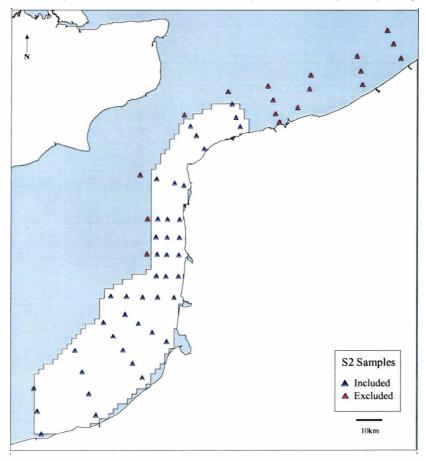


Figure 3.8 Survey Two sampling points to be included in the study, surrounded by Survey Two polygon

Three sample points were excluded from Survey One and 17 sample points were excluded from Survey Two (Figure 3.7 and Figure 3.8).

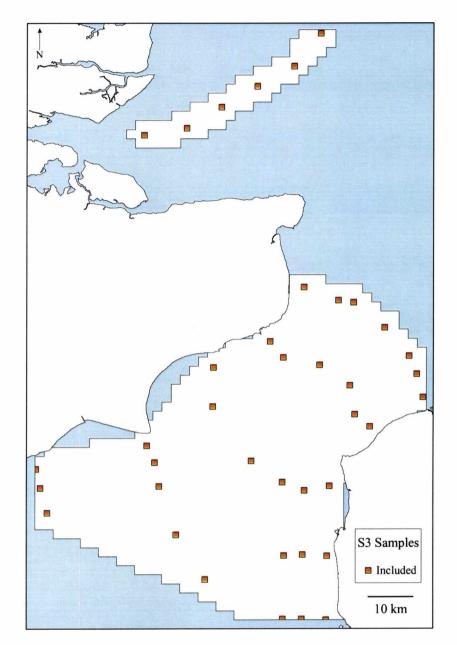


Figure 3.9 Survey Three sampling points included in the study, surrounded by Survey Tthree polygon

All the sample points were included in Survey Three (Figure 3.9).

The selection unit grid for Surveys One and Two contained 919 units, and Survey Three selection unit grid contained 1010 units. The selection unit grids allow calculation of the environmental conditions and abundance of ichthyoplankton within each unit. These values were used in the PA selection methods analyses (Chapters Five to Nine).

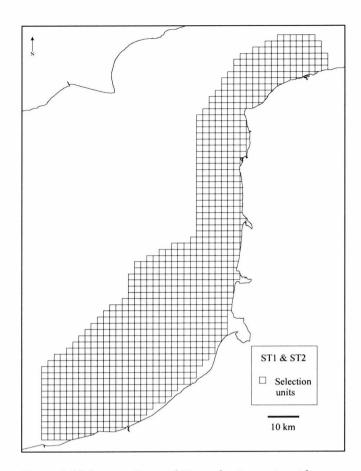


Figure 3.10 Surveys One and Two selection unit grid system

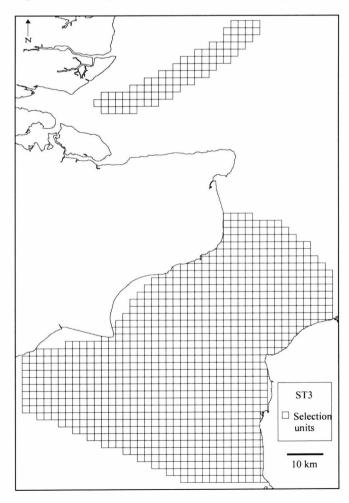


Figure 3.11 Survey Three selection unit grid system

3.5.4 Bathymetry coverage

The selection units were considered for inclusion in a MPA network. The aim of the MPA network is to protect the early life stages of as many marine fish species as possible. A coverage of bathymetry was necessary to consider the depth of water. The abundance values in the database are measured by volume. To identify the number of individuals in the complete water column within each selection unit it was necessary to multiply the abundance values by the depth using a coverage of bathymetry. The bathymetry coverage was also needed to create seascape coverages (Chapter Five).

Bathymetric data was available as point depths (Crown Copyright) reproduced from Admiralty Charts numbers 1406, 1607, 1975, 2449, 2451 and 2656. Formal acknowledgement is given for kind permission of The Controller of Her Majesty's Stationery Office, the Port of London Authority, and the hydrographic offices of Belgium, France, the Netherlands and the United Kingdom, to use the data. It was necessary to interpolate the point data to produce a complete coverage in which a measurement of depth was available across the whole surface of the study area. An interpolation method was required which would most accurately model the depth at unmeasured points throughout the study area.

Two methods were chosen, those of krigging and splining, due to their documented applicability to bathymetric and other environmental data (Kitanidis, 1995; Rosenbaum & Soderstrom, 1996; Collins & Bolstad, 1996; Forney, 2000; ESRI, 2001). Interpolation is based upon the common observation that on average, values at points close together in space are more likely to be more similar than points further apart. The value at locations which have not been measured can therefore be estimated from points which are located in near spatial proximity.

Spline Interpolation: Splining is a local deterministic interpolation technique to represent two dimensional curves on three dimensional surfaces (Collins & Bolstad, 1996). Local interpolators operate within a small zone around the point being interpolated to ensure that estimates are made only from data points in the immediate neighbourhood and the fit is as good as possible. This differs from global interpolators which use all available data to provide predictions for the whole area of interest (Burrough & McDonnell, 1998). The steps involved with this approach are a) defining a search area or neighbourhood around the point to be predicted, b) identifying the data points within the defined neighbourhood, c) choosing a mathematical function to represent the variation over this limited number of points and d) evaluating it for the point on a regular grid. The procedure is repeated until all the points on the grid have been computed (Burrough & McDonnell 1998).

Splining techniques gain their name from the flexible rulers draughtsmen used to fit curves to sets of data points before the widespread use of computers. Spline interpolators are piece-wise functions (Burrough & McDonnell, 1998). That is they are fitted to a small number of data points exactly, while at the same time ensuring that the joins between two parts of the curve are continuous. It is therefore possible to modify one part of the curve without having to recompute the whole. The curve is constrained at defined points but the maximum and minimum computed values may not be within the measured data range. Spline interpolators create visually appealing curves, but no estimates of error are given, and uncertainty may be masked by the smooth surfaces which appear smoother than the underlying reality.

Krigging Interpolation: Krigging is a geostatistical method named after D.L.Krige who used its underlying theory to estimate ore content. The technique is most well known for its application to the mining sector, but can be used "wherever a continuous measure is made on a sample at a particular location in space (or time) and where a sample value is expected to be affected by its position and its relationships with its neighbours" (Clark, 1979).

Geostatistical methods for interpolation recognise the fact that the spatial variation of any continuous attribute is often too irregular to be modelled by a simple, smooth mathematical function. A stochastic surface is instead used to describe the variation (Burrough & McDonnell, 1998). The technique uses a linear combination of weights at known points to estimate the value at an unknown point. The weights change according to the spatial arrangement of samples by the use of a semivariogram, a measure of spatial correlation between points. The semivariogram will indicate how far away points are that make a useful contribution to estimating the value of the attribute. The contribution of points in different directions can be calculated and the search window adjusted according to the amount of correlation between points in different directions. If the variogram is calculated with no directional effects it is known as isotropic. With directional effects, it is termed anistrophic. The position at which the model intersects the y-axis gives a measure of the residual spatially uncorrelated noise, known as the nugget. The interpolated surface passes through the data points and remains within the range of the measured data. Krigging can be especially useful as it calculates an estimation of the error at each point on the resulting coverage. Cross validation can also be carried out. This gives a measurement of the accuracy of the model. The process involves removing one sample point at a time and recalculating the model and then comparing the modelled with the measured value.

3.5.4.1 Methods

Point depth readings were digitised from paper charts (Crown Copyright) using ArcINFO. The point shapefile was reprojected into UTM zone 31N using Idrisi. Depth readings were restricted to the sea, leaving areas of land absent of points. Interpolation methods would be more accurate if readings were included throughout the land indicating a zero depth, especially along the coastline.

Zero depth readings were added along the coastline vector (section 3.5.1) using the 'add points to line' extension to ArcView. Randomly located zero readings were produced throughout the land by using the 'animal movement' extension in ArcView. The coverage containing the zero depth readings was joined to the bathymetry coverage using the 'geoprocessing wizard' in ArcView, to produce one coverage containing 8885 point depth readings throughout the area.

To test the accuracy of the interpolation model at predicting depth in unsampled areas, the data were split into two groups. One set containing 90% of the points was used for building the model using both interpolation methods. The smaller test set contained 10% of the data points to compare the value predicted by interpolation with the actual measured value. The points were allocated into these groups using ArcGIS, which randomly allocates the test and sample data into separate shapefiles. This was repeated 30 times to enable replication of the test.

Ordinary krigging and thin plate spline interpolation were carried out using the 'geostatistical analyst' extension in ArcGIS. During krigging, anisotropy and trends in the data were investigated and if necessary taken into account in the model. Both interpolation methods were used with the 30 sets of model building data producing 60 coverages.

To test the accuracy of the model produced by each method, the corresponding model testing shapefile for each repetition of the test was overlaid on the coverage produced by interpolation. Values at the testing sites were extracted using the 'summarise zones' option in ArcView. These values were exported into an MS Excel spreadsheet and compared to the expected values contained within the model testing point shapefile using a Wilcoxon's signed rank test.

3.5.4.2 Results

Typically variation in the direction of correlation was apparent when variograms were examined during the krigging procedure. The anisotropic nature was incorporated into the model by using a directional search.

Interpolation Method	Mean error (m)	Maximum error (m)	Minimum error (m)
Krigging	4.3	7.9	2.9
Splining	6.5	35.2	2.7

Table 3.1 Errors associated with two methods to interpolate bathymetry

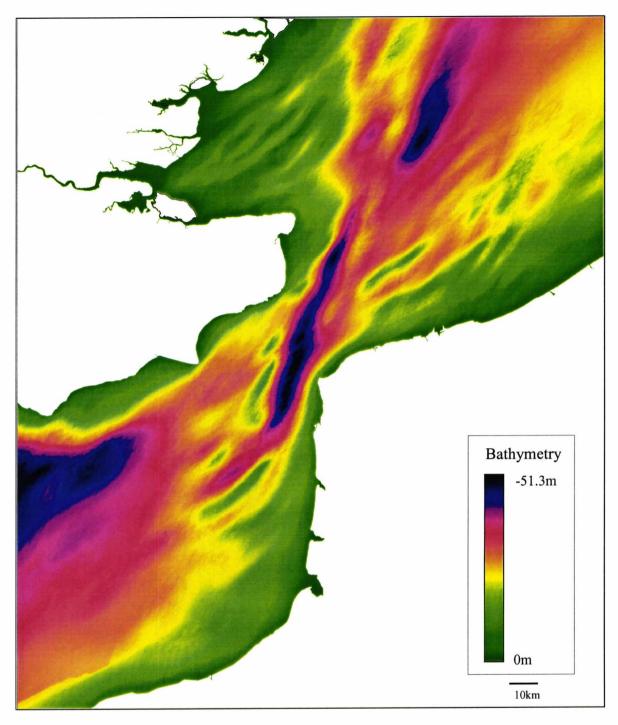


Figure 3.12 Bathymetry interpolated using krigging (© Crown Copyright)

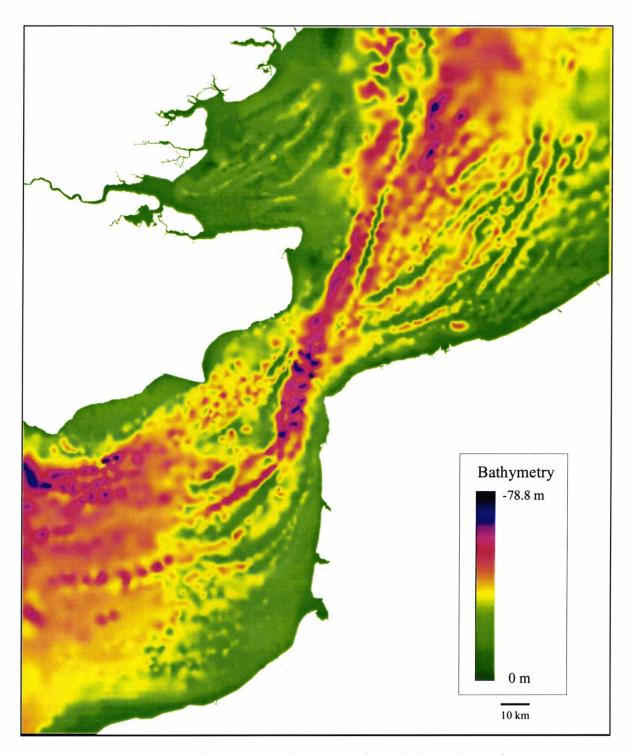


Figure 3.13 Bathymetry interpolated using splining (© Crown Copyright)

Krigging showed significantly lower errors with bathymetric data than splining (Wilcoxon's signed rank test z=-3.754 p=0.000). The mean error for krigging was 4.3m, and for splining was 6.45m.

3.5.4.3 Discussion

Splining produced several areas much deeper than the expected value, and generated less visually realistic patterns. Krigging was found to be more accurate and was therefore used to interpolate the full data set to produce the bathymetry coverage. This coverage was used both in the creation of

seascape types and to create distribution coverages that consider the depth of the water column (Chapters Four and Eight).

3.5.5 Environmental coverages

Coverages of temperature, salinity and density were required to create seascape ichthyoplankton surrogates (Chapter Eight). Several other parameters were measured during Survey Three, but it was not possible to use them due to requirements of consistency across all three surveys. Interpolation was necessary to produce complete coverages of the environmental variables across the study area as they were sampled at the same discrete sample points as ichthyoplankton (section 3.5.2).

Krigging was found to be a better predictor of bathymetry (section 3.5.4). Data to be used in the seascapes are likely to be highly spatially correlated, also making them suitable for interpolation by krigging. Krigging has been recommended for similar data e.g. temperature (Collins & Bolstad, 1996) and radiation levels (ESRI, 2001) and so was used for additional environmental variables.

3.5.5.1 Methods

Krigging was carried out using the 'geostatistical analyst' extension in ArcGIS. The outermost sample points restricted the position of the coverage edge. This influenced the study area extent, as only areas inside the sample points could be used. The resultant coverage contained interpolated values only and no extrapolated values. Cell size was $40,000\text{m}^2$ (0.04km^2), chosen to produce a size able to reflect change across a selection unit (4km^2). This allowed proportional area distribution measurements and a total to be calculated per unit (section 3.4) thereby reducing the effect of spatial autocorrelation. This cell size also matches the size of the ichthyoplankton abundance coverages (Chapter Four).

Separate coverages were produced for the following environmental variables: surface temperature, bottom temperature, surface density, bottom density, surface salinity and bottom density.

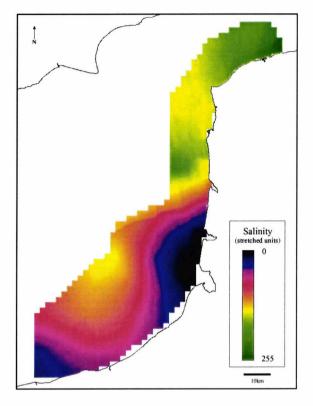


Figure 3.14 S2 Surface water salinity

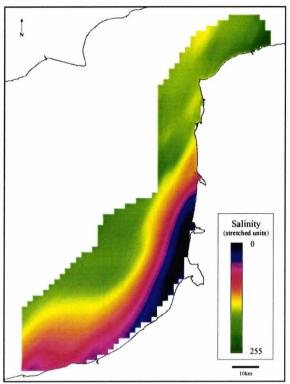


Figure 3.15 S2 Bottom water salinity

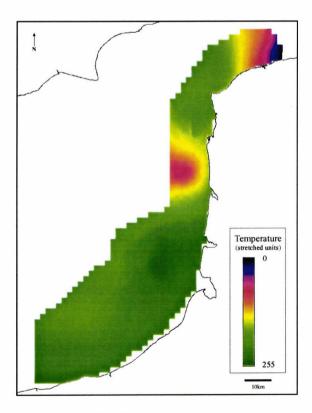


Figure 3.16 S2 Surface water temperature

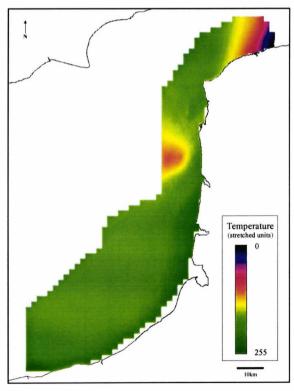
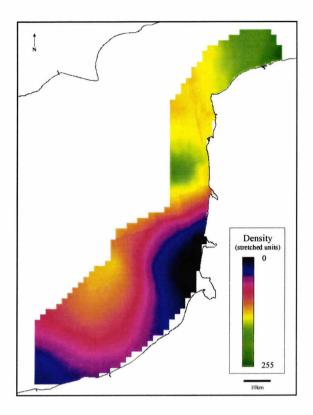


Figure 3.17 S2 Bottom water temperature



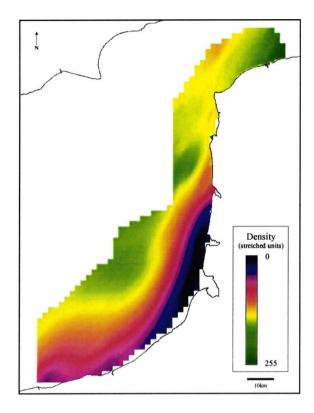


Figure 3.18 S1 Surface water density

Figure 3.19 S1 Bottom water density

* S1 represents Survey One, S2, Survey Two and S3, Survey Three.

3.5.5.3 Discussion

The coverages were used to produce seascapes described in Chapter Eight, which were tested for their effectiveness as a surrogate for ichthyoplankton abundance when designing marine protected area networks.

3.6 Summary

- GIS technology provides powerful tools for the management and analysis of spatial data. This
 is increasingly utilised for conservation research, management and planning.
- GIS coverages were created to describe the study area and for analysis, including a coast coverage and selection unit grid.
- Interpolation techniques were tested on the bathymetry dataset using a series of model building and testing data subsets. Krigging was found to be a more accurate interpolator than spline interpolation for bathymetry. The bathymetry was therefore interpolated using krigging.
- GIS coverages were created from other environmental data by krigging interpolation, sampled during the three surveys at the stations used for ichthyoplankton sampling.

Chapter 4: Ichthyoplankton Distribution Coverages: Modelling Techniques

4.1 Introduction

Protected area planning and reserve selection methods require a database for site evaluation (Margules & Stein, 1989; Bedward *et al.*, 1992). If adequate information were available, the database should contain data on the geographical distribution, abundance and habitat requirements of all species within the region of concern, including measures of taxonomic distinctiveness, to allow protection of the widest genetic diversity (Polasky *et al.*, 2001; Vane-Wright *et al.*, 1996b). These data are very often scarce, incomplete or lacking (Pressey, 1994; Possingham, 2000; Cabeza & Moilanen, 2001). Such fragmented data are often the only type available on which to base selection of reserve sites (Freitag *et al*, 1996) and to form a surrogate for biodiversity of the region. The ichthyoplankton data are used in the current research as surrogates for biodiversity, although it is not known to what extent the species represent other marine species present in the area.

Distributional data are often in the form of discrete samples or sightings from collections made at point locations. If further distribution at non-sampled points is required, it may be possible to utilise modelled probabilistic data (Cocks & Baird, 1989). These reserve selections may be based on the likelihood of a species being present rather than actual sightings or samples (Polasky *et al*, 2000).

Many methods exist for modelling the distribution of species. The choice of appropriate technique depends on the available time, personnel, number of species to be modelled and the type of data available (for example presence/absence or abundance). Modelling is often used to identify the habitat preferences of individual species to aid its management, but is extremely intensive, time consuming and data dependent. For this type of modelling, information on the location of species abundance or presence must be available, in addition to further information concerning the characteristics of the area in question. Characteristics of the area occupied are extracted from the relevant coverages using a GIS. Statistical methods are used to identify which characteristics, of those measured, influence which areas are inhabited. The model can then be used to predict the probability of presence or the abundance of the species, in non sampled locations.

Modelling can use multiple regression if abundance data are available (e.g. Puttock *et al*, 1996; Huggins, 1996; Saveraid *et al.*, 2001; Pearce & Ferrier, 2001), although such data are very rarely available. Logistic regression can be used if presence / absence data are available (Pereira & Itami, 1991; Pausas *et al*, 1995; Özesmi & Mitsch, 1997; Mace *et al.*, 1999; Beard *et al.*, 1999;

Carroll et al., 1999; Gros & Rejmánek, 1999; Pearce & Ferrier, 2000; van den Berg et al., 2001; Fleishman et al., 2001). Information concerning the locations of absence, however, is often missing, as wildlife surveys generally only record faunal species presence. It is difficult to confirm that a mobile species is not present since sites may be utilised when observers are not present. A technique has been adapted which models information on presence-only data, based on the Mahalanobis statistic (Dettmers & Bart, 1999; Dunn & Duncan, 2000). The method relies on defining optimum habitat as a multivariate vector of the means of the habitat variables sampled. This has been utilised for conservation planning in Italy based on wolf distribution (Corsi et al., 1999).

Similar statistical techniques have been used in combination with computer software to aid the modelling process. Some have utilised computer software to link the models to a GIS, or combined several techniques to suit the data (e.g. Garcia & Armbruster, 1997; Lamouroux et al, 1998; McGregor, 1998; Kliskey et al., 1999; Ji & Jeske, 2000; Lenton & Perez del Val, 2000; Boone & Krohn, 2000; Kobler & Adamic, 2000). For example, Augustin et al. (1996) used an autologistic model to predict wildlife distribution, in which the spatial autocorrelation inherent in such data was modelled and used as a factor in the model. Ortigosia et al (2000) developed a program to integrate several types of habitat suitability models into a GIS. Gerrard et al (2001) used field data coupled with expert knowledge to evaluate habitat for the San Joaquin Kit Fox in California, USA. Similar models have also been developed using various techniques in the marine (Horne & Campana, 1989; Swain, 1993; 1997; Perry & Smith, 1994; Swain et al, 1998; Maury & Gascuel, 1999; Chen & Jackson, 2000; Forney, 2000; Bez & Rivoirard, 2000) and freshwater environments (Layer & Maughan, 1985).

A popular method is that of habitat suitability indices (Bain & Bain, 1982; Soniat & Brody, 1988; Terrell & Carpenter, 1997; Monaco & Christenson, 1997; Rempel et al., 1997; Brown et al., 1997; Christensen et al., 1997; Coyne & Christensen, 1997; Rubec et al., 1998; Prosser & Brooks, 1998; Radeloff et al., 1999). These are calculated in several ways, more recently directly from data driven multivariate models, but previously from individual published preference ranges of separate variables which are then combined. Some models have been criticised for the methods by which a preference range is calculated for each factor in isolation, without consideration of other co-varying factors. The factors are then combined, ignoring possible interactions between the variables. Such models have also performed poorly when undergoing field testing (Layer & Maughan, 1985). This may be due to the artificial environment used to acquire the indices and the equal weighting given to each variable in the model. Other modelling techniques include discriminant analysis (Rogers, 1992; Manel et al., 1999), artificial neural networks (Lek & Guegan, 1999; Manel et al., 1999), general linear models (Boroski et al., 1996) and principle component analysis (Zeng et al., 2001).

These data driven models are very data intensive and time consuming to construct. It is difficult to obtain source data of sufficient quality, even in well-mapped countries. For most of the world it is unavailable (Lenton *et al.*, 2000). It is also expensive and time consuming to collect, so any such modelling is often only used on a few, or a single, species. Reserve selection techniques rely on distribution data of a large number of species. For these reasons, data driven statistical techniques for delineating the distribution of every species necessary for a reserve selection database are often impossible and have only been used in a few studies (Tamis & Van t' Zelfde, 1998; Wu & Smeins, 2000; Araujo & Williams, 2000). Li *et al* (1999) designed a habitat suitability model for red crowned crane (*Grus japonensis*) to define the minimum core zone for the Yancheng Biosphere reserve in the Peoples Republic of China. Only one species, however, was involved.

These models rely on clear relationships between the species in question and other variables easier to sample and map. The models can be difficult to develop when the species data are poorly correlated with the variables, or do not hold to assumptions of the mathematical modelling techniques. Other methods, therefore, have been developed to try to overcome these problems.

The alternative methods integrate several types of information. These can include data from the scientific literature, atlases, boundaries around previously collected marginal records for a taxon, and/or expert judgement. All maybe used to delineate distribution (Csuti *et al.*, 1997; Garibaldi & Caddy, 1998; Williams *et al.*, 2000; Peterson *et al.*, 2000). Many such species range maps, however, are small-scale (e.g., >1:10,000,000) and derived primarily from point data for field guides (Smith *et al.*, 1998). They often use expert opinion to counteract incomplete or biased sampling. Many occurrence data sets are difficult to assess for accuracy. They are rarely collected systematically and many are submitted by amateur volunteers on an *ad hoc* basis from places and times usually of their own choosing (Hopkinson, 1999). Many surveys are based on charismatic species such as mammals, birds and butterflies, often from places where collectors anticipate finding them and that are conveniently accessible. Road networks (Margules & Pressey, 2000), for example, or favourite study sites such as field stations or areas close to major universities or museums, are typical (Possingham, 2000).

Other methods developed and widely used in the United States are those used for the 'Gap Analysis Project' (GAP Project). These methods use the distribution of another easily mapped factor to delineate the distribution of species. The project as a whole uses a variety of methods, but they are based on using land-cover to map the distributions of vertebrates. Maps of vegetation are prepared from satellite imagery and verified through field checks and examination of aerial photographs (Scott *et al.*, 1993). To enhance the distribution modelling methods, supplemental information is often also used. This information includes local records, literature searches, range limits, expert knowledge (Brannon, 2000), museum specimens (Smith *et al.*, 1998) and minimum area

requirements of species (Allen *et al.*, 2001) combined with information on the habitat affinities of each species (Scott *et al.*, 1993). Gap Analysis maps are produced at a small scale and are intended for applications at landscape scale (Davis *et al.*, 1998).

In the present study area, however, information concerning the habitat associations of each species of ichthyoplankton was not available. Neither was there information on habitat cover. It was intended that environmental data would be analysed for its associations with the ichthyoplankton elements. Ichthyoplankton distribution would then be modelled statistically from these associations, as isolated sample measurements of abundance were available. Environmental factors used for modelling included data that had been measured during the ichthyoplankton surveys and those derived (including distance to the coast and to rivers) and from other sources (sea surface temperature).

During species identification, each sample was examined for the presence and abundance of all species. Many developmental stages, however, only occurred at a few sample points and were absent at the others. Many sample points therefore yielded zero readings for many of the species. This caused the data to be skewed from a normal distribution. It did not therefore conform to the assumptions of many mathematical modelling techniques. Several methods were tested for their ability to identify relationships within the data, but yielded poor results. It was necessary, therefore, to identify a method that could incorporate this type of data.

An example of a modelling technique used in an effort to identify relationships between the species data and environmental variables is the generalised additive model (GAM) (Hastie & Tibshirani, 1987; 1990; 1996; Beck & Jackman, 1997; Lin, 1999; Marx & Eilers, 1998). This technique can accept a large proportion of zero readings. It is designed to derive non-linear relationships with data containing many zero readings. GAM automatically allows the data to suggest more complex response shapes, rather than assuming an a priori model (Ferrier and Watson, 1996). Thus it does not assume linearity or normality (Swartzman *et al.*, 1992). This method has been especially utilised in fisheries research where these problems of zero counts are common (Borchers *et al.*, 1997; Swartzman, 1997; Swartzman *et al.*, 1992; 1994; 1999; Maravelias, 1999; Maravelias & Reid, 1997; Bailey *et al.*, 1998; Maravelias *et al.*, 2000; Daskalov, 1999; Welch *et al.*, 1995; Borchers *et al.*, 1997; Augustin *et al.*, 1998; Forney, 2000; Bartsch & Coombs, 2001), in addition to research modelling other types of wildlife (Fewster *et al.*, 2000; Forney, 2000).

Unfortunately GAM derived relationships were so weak or were not apparent that it was considered that the models would not produce adequate distribution maps. The extent of the errors were unacceptable, especially for the species with very narrow distributions within the study areas. A method was required which could be applied to all ichthyoplankton species found within the

sampling area, especially those with narrow distributions, as these may be of the most conservation importance. Nevertheless, these were the weakest GAM statistical models. An approach was necessary to accommodate all the species in the analysis, and one which could also could be easily replicated in other studies. Following similar suggested methods used elsewhere (van der Meer & Leopold, 1995; Maravellas *et al.*, 1996; Wanless *et al.*, 1997; Maynou *et al.*, 1998; Zhoug, 1998; Boyce & McDonald, 1999; Boone, 1999; Bez & Rivoirard, 2001), it was decided to test interpolation methods for their suitability and accuracy with the present ichthyoplankton spatial distribution and abundance data. These modelling methods allow inclusion of the ichthyoplankton elements (developmental stages) with the smallest distribution, therefore not biasing against rare ichthyoplankton. A test of the relevance of krigging and splining for interpolating environmental data is described in Chapter Three. These were also the chosen methods to model ichthyoplankton distribution (see Chapter Three for methodological details further to those given in section 4.2.1 below).

Section 4.2 contains a description of the test to identify an accurate interpolator for the ichthyoplankton abundance data from spline and krigging interpolation methods. The preparation of the interpolated abundance coverages for inclusion in the GIS database is explained in section 4.3. Section 4.4 is an account of the procedure for extracting ichthyoplankton abundance within selection units and section 4.5 is a summary of the chapter.

4.2 Interpolation of ichthyoplankton abundance and distribution

Two methods were used to build models for interpolation. These were tested for their accuracy using a subset of the samples that had been removed before the model-building process in a similar manner to the procedure described in Chapter Three.

4.2.1 Methods

Many of the ichthyoplankton species were absent from a large proportion of the sampling stations. This produced a dataset which contained a large proportions of zero readings. It was necessary to test the interpolation methods on samples containing a range of positive samples, to ensure the method is applicable to ichthyoplankton data with both a low number and a high number of non-zero abundance readings. It was decided to test the methods using 25 ichthyoplankton developmental stages (hereafter referred to as ichthyoplankton elements). The elements were stratified according to the number of stations at which they were present. One element from each group was chosen at random using the generate random number facility in MS Excel.

The data for each selected ichthyoplankton element were split into 6 model building groups and 6 corresponding model testing groups consisting of 83% and 17% of the data points respectively.

The arbitrary normal for model building and testing is 10% and 90%. The dataset consisted of 60 sample points however, and it was decided that at least 10 sample points were necessary for rigorous model testing. Points were allocated into these groups in MS Excel by using random number generation to assign a number from 1 to 10 to each point in the dataset. Random numbers were ranked and assigned 0 or 1 according to whether the rank was above or below 10, as it was necessary to allocate 10 of the numbers to 0 and to allocate 50 of the numbers to 1.

The division of the data was repeated 6 times for each of the selected 25 species. The 0 and 1 columns were then imported into the shapefile attribute table of abundance data points in ArcGIS. For each interpolation, the points used for the model building were selected using 'query builder'. The 'query builder' selects and highlights the sample points whose attributes (0 and 1 according to testing or model building groups) meet the criteria of the query equation entered. Only the selected points are then used in the model building.

Both interpolation methods were used 6 times on each of the 25 sets of species model-building data (300 coverages). Ordinary krigging and thin plate splines were used (Chapter Three). To analyse the accuracy of the interpolation methods, the corresponding model testing points for each species and for each repetition of the test was selected by 'query builder'. These were 'overlaid' on the coverage produced by interpolation. The values at the testing sites were extracted using the 'summarise zones' option in ArcView. These values were compared to expected values contained within the model testing abundance shapefile attribute table and the difference calculated. A Wilcoxon signed ranks test was used to determine if there was any significant difference between the errors (difference between the modelled and the measured abundance) obtained when using the two interpolation methods.

4.2.2 Results

The mean difference between the modelled and the measured abundance ranged from 24.5 to 18 (Table 4.1).

Method	Mean error	Maximum error	Minimum error
Spline interpolation	24.5	204.5	0.4
Krigging interpolation	18.0	183.6	0.2

Table 4.1 Accuracy of interpolation methods to predict abundance

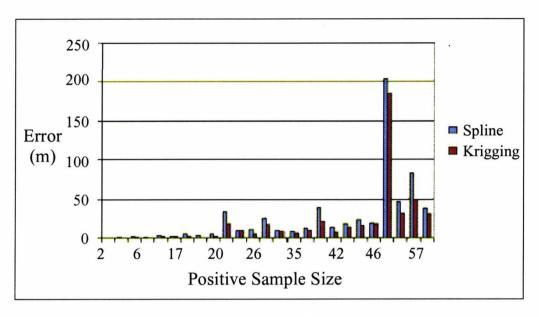


Figure 4.1 Errors produced by splining and krigging against sample size.

Krigging produced consistently lower errors across the range of positive sample sizes, and the difference was significant (Wilcoxon's signed rank test z=-4.345 p=0.000 n=150).

4.2.3 Discussion

Splining often generates a smoother interpolated surface, but consistently produced higher errors than krigging. The spline model values often lay outside the sample data range, and gave very exaggerated low and high values, particularly in small localised areas i.e. several large 'holes' in the surface. In addition to the ability to predict abundance more accurately, the krigging procedure also calculates a value of error. The error can be produced as a separate coverage, that can be displayed as contours, or with transparency so that the modelled surface and the error distribution can be viewed together. This could be a useful measure to include in selection algorithm procedures, as a measurement of the accuracy of the abundance values within each area under consideration.

Krigging is a time intensive method, but easier to replicate in practical situations than environmental modelling. It relies on the species source data only, rather than relationships between the taxa and other measured variables. Krigging also has the advantage of producing low errors when interpolating both well distributed positive samples and also samples with few positive measurements, unlike modelling based upon environmental variables.

Spatial autocorrelation is inherent in most ecological phenomena (Koenig, 1999), and can question the independence of samples (Augustin *et al.*, 1996). This can affect other modelling techniques. In contrast, krigging uses spatial autocorrelation to model the distributions. The abundance coverages were produced to enable calculation of the abundance and area of ichthyoplankton

elements within the selection units. The following section describes the methods used to enable this calculation from the coverages.

4.3 Preparing abundance coverages for inclusion in the GIS database

Interpolation modelling in ArcGIS produces a rectangular coverage extending to the outermost sampling stations. It therefore includes areas outside the study area. Hence, the coverages needed to be clipped to the spatial limits of the study site. The values contained within each pixel represent numbers of ichthyoplankton elements per 100 cubic metres. The selection of units for conservation planning is based on the individuals within the complete water column beneath the selection units. Values in the abundance coverages therefore require adjustment to represent the total abundance. This is achieved by multiplying by 200 (the pixel size) then overlaying the abundance coverages with the depth coverage and calculating the product.

Due to the nature of the interpolation technique, the abundance of each ichthyoplankton element often ranges from the highest abundance to zero, including areas of very low abundance. It was therefore decided that a cut-off level beneath which small quantities of ichthyoplankton could be assumed to be negligible should be established.

4.3.1 Methods

The standard deviation of the 'non-zero' abundances in each cell of the abundance maps was used to calculate the cut off level for each ichthyoplankton element. Abundances were reclassified to zero if less than one standard deviation below the mean. If the mean minus the standard deviation was less than one, abundances were cut off at one. It was assumed that less than one individual per 200m^2 could not be considered appropriate for including in a protection network. The number of these was minimal as one standard deviation below the mean suited the structure of the data. Standard deviation gives an idea of the data spread, so it can distinguish if the lower levels of abundance are a result of the interpolation and not characteristic of the remaining samples in the coverage. For example, if a coverage has mostly high values, its standard deviation would be small, so the cut off point would be higher. If the coverage contains a spread of data, however, then the lower values are valid, so the cut off point is lower.

To remove areas of the coverages that were not within the study site, a polygon of the area of interest was necessary. This was created by 'dissolving' the selection unit grid polygons into one polygon. This was achieved by dissolving based on a common feature in the attribute table using 'geoprocessing wizard' in ArcView. The 300 coverages were cut to the study area using 'extract grid theme using polygon' in 'grid analyst' extension of ArcView. To remove negative abundance areas, these regions were identified in each coverage using 'map query' in ArcView. A Boolean

coverage was produced which contained a value of one in the positive areas and zero in the negative and zero areas. Negative pixels within the abundance coverages were clipped by multiplying with the Boolean coverage of positive areas using 'map calculator' in 'spatial analyst' extension to ArcView, thereby causing the negative abundances to be reclassed as zero abundance. The values were multiplied by 200 using 'map calculator' to produce abundance per 200m³ pixel. The values in the bathymetry coverage were also clipped to the study site and then multiplied by –1 using 'map calculator' to produce a bathymetry coverage with positive values.

Abundance coverages now containing only positive values were then multiplied by the positive bathymetry value coverage using 'map calculator'. This produced coverages with abundance values considering the whole water column. The process of identifying positive or 'non-zero' abundance pixels was repeated on the resultant coverages and a second Boolean image per ichthyoplankton element was created as using the 'map query' option in spatial analyst. The mean and standard deviation for these 'non-zero' areas were then calculated using 'summarize zones' option in 'spatial analyst'.

To remove the areas one standard deviation or more below the mean from the abundance coverages, their pixel values were reclassified to zero. This was achieved by using the 'map query' command to identify and create a new Boolean coverage containing polygons that indicate all the areas where 're-classing' was necessary. The Boolean coverages contained a value of zero where the abundance values were less than one standard deviation (or less than one, whichever was greater) and a value of one where the abundances were above this cut off point. These coverages were then multiplied with the abundance coverage, using 'map calculator', to re-class the lower measurements to zero.

4.3.2 Results

The resulting coverages contained values taking into account the depth of the water. Lower unrealistic values of abundance had also been removed. An example is shown in Figure 4.2.

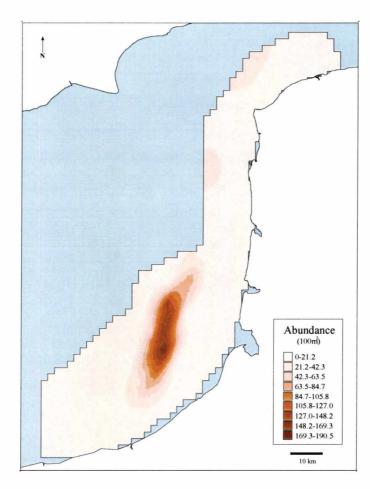


Figure 4.2 An example of an abundance coverage

4.3.3 Discussion

The preparation of the coverages was extremely time intensive (approximately four months intensive work), but the preparation of the database with good quality data is important for conservation planning. Krigging takes significant time and a constraint on the efficiency of both methods was the significant time taken to save each distribution coverage after each model building. This was due to the large number of pixels involved. It will be reduced with the rapidly increasing power of personal computers.

A major assumption of this method is that the number of individuals at each depth of water is constant throughout the water column. This is not always the case, although samples of ichthyoplankton were taken throughout the water column, from the bottom to the top. It may be a fair assumption, but also a possible cause of error.

The coverages contained spatial and numerical information concerning each ichthyoplankton element identified in the study. Very small, unrealistic values, a product of the modelling technique, were removed before inclusion in the selection database. This allows an analysis of MPA network selection methods considering the depth of the sea under each area of consideration.

4.4 Extracting abundance values within the selection unit grid from distribution coverages

Abundance coverages contain abundance values in each pixel. The pixels in the coverage are highly spatially auto-correlated, and also too small to consider for reserve selection. A selection unit grid was used to combine measurements over an area of 4km². This lowers the effects of spatial autocorrelation and allows analysis of areas large enough to consider as selection units.

4.4.1 Methods

The selection unit grid was overlaid on each abundance grid coverage and the 'summarise zones' option in spatial analyst was used to extract the total sum of the abundance within each 4 km² selection unit. The results are displayed in dbase tables. This was repeated for each ichthyoplankton element identified during the three sampling surveys. The abundance calculations for each ichthyoplankton were exported from the ArcView dbase table into MS Excel spreadsheets.

4.4.2 Results and Discussion

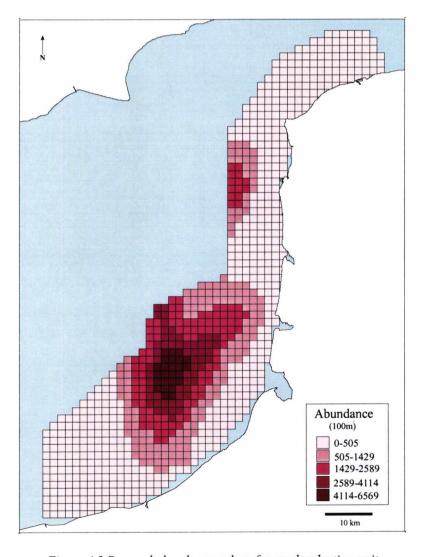


Figure 4.3 Summed abundance values for each selection unit

The summed abundance within selection unit coverages are at a lower resolution of 4Km² (Figure 4.3). The three spreadsheets each contained a matrix of abundance measurements, with ichthyoplankton element total abundance within each selection unit. The rows corresponded to the unit identification, and the columns corresponded to the ichthyoplankton elements. The spreadsheets were used for testing PA network selection methods in Chapters Five to Nine.

4.5 Summary

- Modelling methods were applied to map the abundance of ichthyoplankton elements. It
 was found that interpolation techniques were the most suitable for the data. Other methods
 did not produce suitable results or were not appropriate for use with the distribution of the
 data, especially the more range restricted species.
- Two methods of interpolation were tested, those of krigging and splining. It was found
 that krigging interpolation was the most accurate method for use with these data and was
 therefore used to produce coverages of abundance.
- The coverages were modified to enable the calculation of abundance within larger selection units by transforming them to include a measurement of depth, thereby considering all abundance within the water column. Spreadsheets containing abundance measurements within selection units were created for use in MPA selection exercises.

Chapter 5: Identifying MPA Networks Using the Hotspot Approach

5.1 Introduction

An early view was that "conservationists will seek and accept whatever reserves they can acquire" (Meffe & Carroll, 1994). It is now recognised it is essential to select PAs with clear, explicit procedures driven by quantitative reservation goals, provided by systematic techniques to provide adequate protection to allow the persistence of populations within them.

Protection of the ichthyoplankton by means of ensuring the safety of fish spawning and nursery grounds in the Dover Strait and surrounding waters requires both management and protection of the habitat (Hall, 1998). Spawning fish also require protection from fishing. Off site management is equally important, to minimise effects of changes in the seabed, hydrographic systems or water. Most ichthyoplankton have limited independent movement through the water. The ability to move through the water increases with age and developmental status. Later stages of development are capable of independent vertical migration through the water (Grioche *et al.*, 2000; Cotonnec *pers com.*). Ichthyoplankton have been shown to exert some control over their large scale movement, through vertical migration (Grioche *et al.*, 2000). This process is necessary for the larvae to be transported in currents from the spawning grounds to the nursery grounds. The location of marine ichthyoplankton, although dynamic, therefore appears to be predictable (Grioche, 1998). Methods of locating areas and seasons during which protection could be provided from harmful anthropogenic activities therefore seems possible.

The debate concerning PA selection algorithms has largely been developed and tested in the terrestrial environment (Chapter One). Methods for PA design in marine ecosystems have been based for the most part, on entirely different approaches and methods. Vulnerable and important species or habitats are often identified, and candidate sites then tested against appropriateness criteria for designation as a MPA by a panel of experts. There has been little investigation of alternative approaches to locating PAs within the marine environment, or the number and total area needed to reach explicit conservation objectives (Pressey & McNeill, 1996). The database of ichthyoplankton sampled in the Dover Strait provides such an opportunity.

The effectiveness of the hotspot method of selecting PA networks is under debate (Chapter One). Most analyses have been carried out at a scale at least an order of magnitude larger than most reserve sites. The effectiveness of the method may be scale dependant (Chapter One). Many analyses have been carried out in terrestrial environments and researchers were cautious about

translating their findings to the marine environment (CSRIO, 1996). Smith (2001) tested species richness (number of species) hotspots and species proportional richness (the sum of the proportions of biodiversity elements distribution within selection units) hotspots. Species richness hotspots were found to be a poor surrogate for species proportional richness hotspots as they did not did not coincide significantly. Although a mixture of habitat is expected in species richness hotspots, it was concluded that many would be expected to contain small, fragmented patches of these habitats with little conservation value. The ichthyoplankton dataset from the Dover Strait can be used to investigate the coincidence of hotspots using three types of data; presence / absence, proportional area and abundance.

Identification of presence richness hotspots (ichthyoplankton element richness) using presence / absence data is outlined in section 5.2. Section 5.3 is a description of the identification of hotspots using proportional area of ichthyoplankton within the selection units. Section 5.4 provides a description of the final identification of hotspots, using ichthyoplankton abundance. Section 5.5 is an illustration of the spatial coincidence of the three types of hotspots. Section 5.6 outlines an analysis of the protection provided to ichthyoplankton by these methods.

5.2 Identifying hotspots using presence / absence data

Many studies have utilised species lists to identify areas scoring highly on a species richness scale. Abundance coverages can be re-classed as presence / absence coverages. These were used to test the appropriateness of this method with presence / absence data to protect ichthyoplankton.

5.2.1 Methods

The MS Excel spreadsheet containing the ichthyoplankton abundance data within each selection unit (Chapter Four) was used to identify presence richness (similar to species richness but so called as the elements are ichthyoplankton developmental stages). A new presence / absence matrix was created from the abundance spreadsheet using the 'if' command in MS Excel to identify the ichthyoplankton elements with an abundance greater than zero within each selection unit. 'Presences' were then summed, thereby calculating the total number of ichthyoplankton elements per unit i.e. the presence richness score.

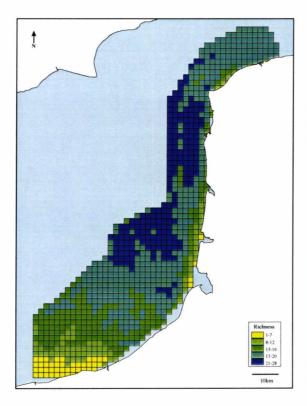
The richness data were exported in dbase format from MS Excel for importing into ArcView, where it was joined to the shapefile containing the selection unit polygons. ArcView was used to identify selection units ranked amongst the top 10% of the units according to presence richness score. Although 5% is often used as the hotspot criteria, 10% was chosen to allow comparisons with other 10% sets, chosen to follow recommendations of the IUCN (1992). This proportion allows the identification of selected unit patterns and to test differences between methods of hotspot calculation. Many units had the same richness score. Therefore slightly more than 10% of

the units were identified as hotspots so that units with identical scores to the unit with the lowest score of the top 10% would not be excluded.

5.2.2 Results

High presence richness values were concentrated in the mid off shore area in Survey One (Figure 5.1), with the lowest values being distributed in the south western coastal edge. Survey Two presence richness values (Figure 5.3) show a cluster of high values in the north western part of the survey area in deeper water. Presence richness in Survey Three (Figure 5.5) shows a concentration of high values in the mid eastern waters of the Dover Strait. Lower values occurred towards the coastal waters, the Atlantic origin waters and the estuarine waters of the Thames. A few units with high presence richness values were observed in the coastal waters in the Dover area.

It was not possible to identify the highest ranking 10% of areas as presence hotspots due to a number of identical values in the score of the lower units. The number of presence hotspots identified was therefore 145 (15.78%), 98 (10.66%) and 116 (11.45%) for Surveys One, Two and Three, respectively.





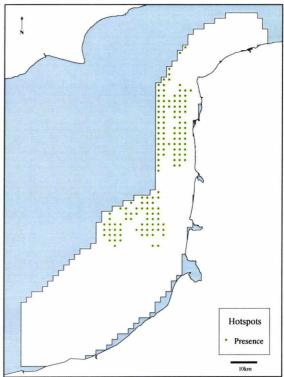
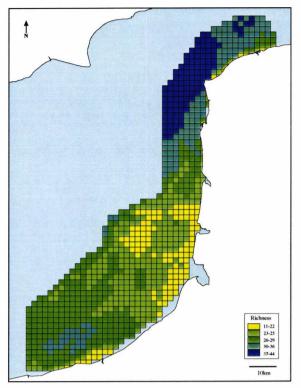


Figure 5.2 S1 Presence richness hotspots

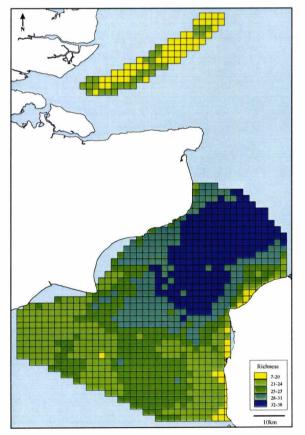


Hotspots

• Presence

Figure 5.3 S2 Presence richness

Figure 5.4 S2 Presence richness hotspots





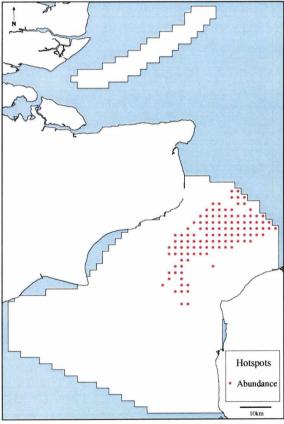


Figure 5.6 S3 Presence richness hotspots

The presence hotspots are distributed within the central area of Survey One, within two main clusters. Survey Two shows one clear cluster of presence hotspots in the north western part of the study area in mid water with few in coastal water (Figure 5.4). Survey Three also contains presence hotspots towards the mid waters of the Dover Strait, and several hotspots in the coastal waters of the UK, but not the French coastal waters or estuarine waters of the Thames (Figure 5.6).

The hotspots of presence richness are concentrated in a more westerly position in Survey One which took place in April, and have 'moved' towards the east to the most north westerly point in the study area in Survey Two which took place in May. Survey Three hotspots are also towards the eastern portion of the study area, which was undertaken in late April and early May.

5.2.3 Discussion

The areas of high presence richness identified as hotspots are concentrated, in all three surveys, in the central deeper waters. Concerns exist about the influence of depth in the identification of hotspots and priority areas due to higher abundances. Scores in this analysis are calculated only from presence without inclusion of depth and have been identified in deeper waters. Depth has a little influence in the calculation, as the cut-off point for consideration as a 'presence' rather than 'absence' was based on the abundance calculated using depth of water column. Therefore, the hotspots in the central waters can be indicative of waters supporting a higher number of ichthyoplankton elements rather than an undue influence of depth on the calculations. This influence is noted, however, as a possible influence on the results.

The apparent movement of the hotspots in a north easterly direction from Survey One to Two and confirmed in Survey Three (although different survey locations are used) could reflect the model proposed for the movement of the larvae by Grioche *et al* (1999). The Picarde Bay in the south western side of the study area appears to be a productive region enhanced by hydrological stability and nutrient enrichment from the Seine estuary (90 km to the south). Grioche *et al* (1999) explain that as the phytoplanktonic bloom initiates in April, maximum abundance of larvae is found in the bay. The best larval conditions (measured by various morphological and physiological indices) are also found in this region (Grioche, 1998). The production is later taken to the north by currents. Young ichthyoplankton elements were found offshore at spawning grounds in Survey One, and then drifted in the northbound currents. During Survey Two, better larval conditions are found in the Strait of Dover and in the North Sea (Grioche, 1998), where the hotspots were identified. During Survey Three, hotspots are also positioned towards the eastern side of the study site, also corresponding to the areas where phytoplankton production was shown to be high at this time of year (Grioche *et al.*, 1999).

5.3 Identifying hotspots using proportional richness

Distribution maps of the ichthyoplankton species were modelled at a resolution of 0.04 km² (Chapter Four), allowing proportional areas occupied within the 4 km² selection units to be calculated. Using this measurement, the units are selected on a more precise basis than presence or absence of ichthyoplankton elements. This will enable distinction between areas containing similar numbers of ichthyoplankton elements. Such measurements may also indicate quality of habitat. If many habitats occur within a small area the proportional richness may be low reflecting only small parts of each species range within the selection unit. Selection units located on larger patches of habitat should hold a larger proportion of the distribution of the elements occurring there. Fine scale distributional data are less available than presence / absence, but more available than abundance data.

5.3.1 Methods

Using the abundance coverages created by modelling methods (Chapter Four), data on the areas occupied by the ichthyoplankton elements within each selection unit were extracted. The coverage pixels were first reclassified according to whether each represented abundance greater or less than zero by using the 'map query' option in spatial analyst extension to ArcView. This created Boolean images of presence and absence. These coverages were used to identify areas within each selection unit occupied by each ichthyoplankton element, by using the 'tabulate areas' command in spatial analyst. This process was repeated for each element and the three sampling surveys. These values were then exported into an MS Excel spreadsheet. Rows represented the selection units and columns represented ichthyoplankton elements, with the cells depicting the areas of coverage. The proportions of each element range was calculated by dividing each area value by the total area occupied within the study site. These proportional areas were then summed and used to rank the selection units. The resulting selection unit scores were exported as dbase tables and imported into ArcView. The dbase tables were joined to the shapefile containing information on the polygons representing selection units. Each row in the shapefile then also contained information on the proportional richness score of each unit, which could be mapped. The top 10% ranks were then identified as hotspots using ArcView.

5.3.2 Results

An example of a presence / absence map used to calculate proportional area is shown in Figure 5.7.

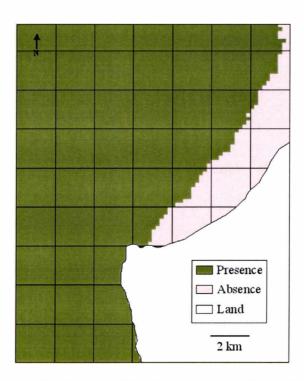
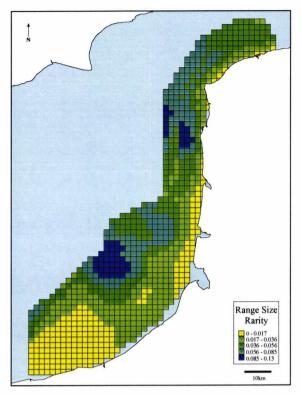


Figure 5.7 An example of an area of distribution coverage (zoomed in for display)

Proportional richness showed a similar distribution to presence richness, with high values positioned in the offshore waters in all three surveys. Two main clusters of higher values were observed in Survey One (Figure 5.8), one distinct cluster in Survey Two (Figure 5.10). High values are seen in the central offshore waters to the north east of the study area with a few in the western end of the Thames Estuary part of the study area in Survey Three (Figure 5.12).

Proportional richness allowed exactly 10% of the areas to be identified as hotspots in Surveys One and Two (Figure 5.9 and Figure 5.11). Two units with the same score at the lower end of the top 10% of units for Survey Three caused an additional hotspot to be identified (Figure 5.13).

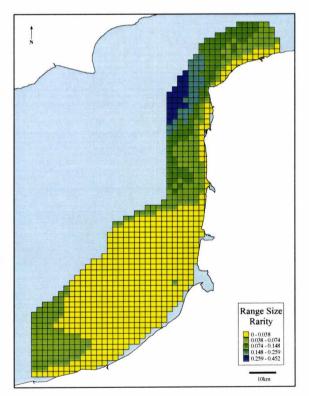
The proportional richness hotspots were spatially arranged in a similar way to the presence richness hotspots. Two main clusters are seen in Survey One, although several hotspots exist between the two clusters. The majority of hotspots are positioned in offshore waters, although a few are seen in the coastal waters within the most northern cluster(Figure 5.9). Survey Two showed one main cluster of hotspots in the north west portion of the study area. This contained the majority of the hotspots, with several positioned just to the south in offshore waters (Figure 5.11). The majority of Survey Three hotspots are positioned in the mid waters between France and England in the most north eastern part of the study area. There are also several hotspots positioned at the western end of the Thames Estuary portion of the study area (Figure 5.12).

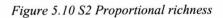


Hotspots • Proportional

Figure 5.8 S1 Proportional richness

Figure 5.9 S1 Proportional hotspots





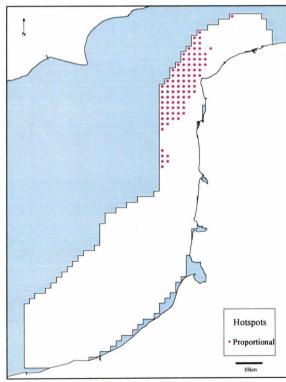


Figure 5.11 S2 Proportional hotspots

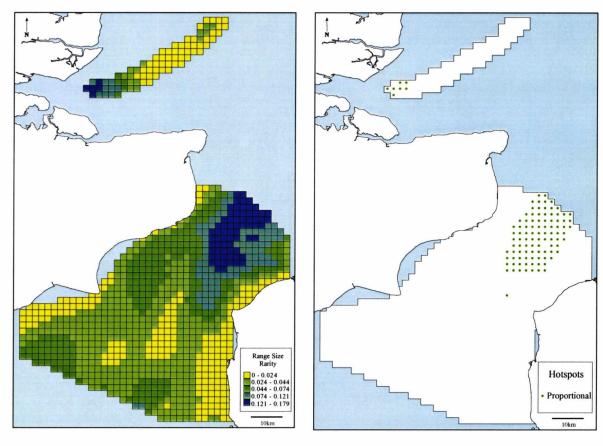


Figure 5.12 S3 Proportional richness

Figure 5.13 S3 Proportional hotspots

5.3.3 Discussion

The distribution of high proportional richness and proportional richness hotspots in the central deeper waters supports the conclusion that distributions are not unduly influenced by the depth of the water in the abundance calculations, but rather through the conditions to be found in these areas. It is also worth noting that clusters of hotspots are concentrated in a more westerly position in Survey One (April), and have apparently moved towards a north westerly point in Survey Two (May) in a very similar way to the presence hotspots in section 5.2. This concurs with the interpretation of ichthyoplankton movement from spawning grounds in the western part of the study area towards the north east. Survey Three was undertaken during late April and early May, so is also consistent with this interpretation, although they are slightly further north east than in Survey Two.

5.4 Identifying hotspots using abundance data

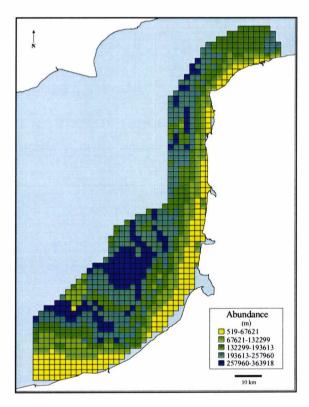
Methods using presence / absence and proportional data have been used to identify hotspots. Smith (2001) found that the hotspot approach identified very different areas using presence / absence from those identified using proportional data. The present research is able to utilise abundance data to further investigate the influence of data type.

5.4.1 Methods

Spreadsheets containing data on the abundance of ichthyoplankton elements within the selection units (Chapter Four) were used to calculate the total abundance of all ichthyoplankton in each selection unit by summing the cells in each row corresponding to the selection units. This column of values was then exported as a dbase file for import into ArcView where it was joined to the shapefile representing the selection unit grid. It was then used to identify the top 10% ranking units. The selection unit scores were then mapped.

5.4.2 Results

It was possible to identify the top 10% of units due to the high discrimination between the scores of the units.



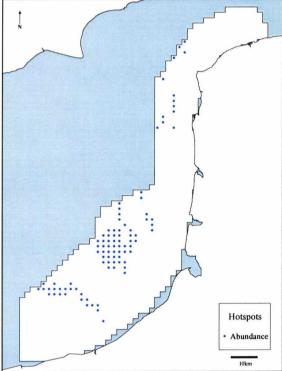
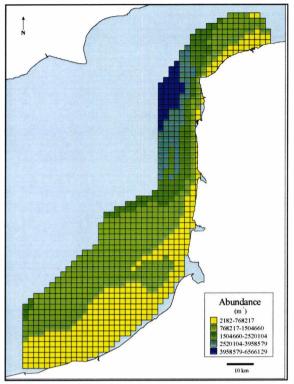


Figure 5.14 S1 Abundance

Figure 5.15 S1 Abundance hotspots



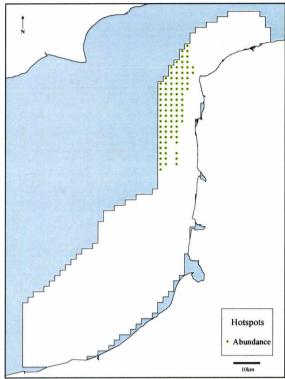


Figure 5.16 S2 Abundance

Figure 5.17 S2 Abundance hotspots

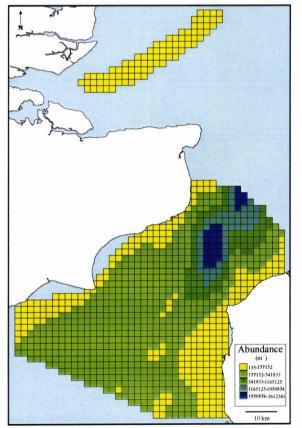


Figure 5.18 S3 Abundance

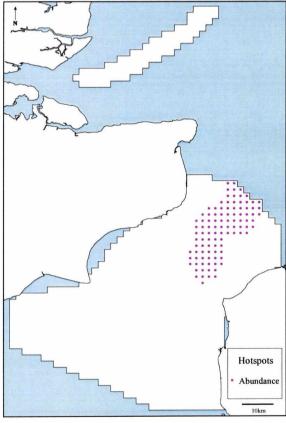


Figure 5.19 S3 Abundance hotspots

Areas of high abundance richness, identified as hotspots in Survey One, were less clustered than those identified by the other hotspot methods, although two indistinct groups are present (Figure 5.15). Many hotspots occurred in the central part of the study area and also tended to be offshore rather than in the coastal waters. Survey Two showed one large cluster of abundance hotspots in the mid north western offshore part of the study area (Figure 5.17). The hotspots identified in Survey Three were also clustered into one large group in the central offshore waters. There were not any selection units identified as hotspots in the Thames Estuary waters (Figure 5.19).

5.4.3 Discussion

Hotspots chosen using abundance appeared to 'move' across the study area in a similar way to those identified using the other methods although Survey One hotspots were a less distinct group. Actual comparison of the difference seen in location identified by the three hotspot methods illustrate any differences between the methods and indicate whether presence or proportional hotspot methods provide good surrogates for abundance methods. This is described in the following section.

5.5 Hotspot method comparisons

The spatial coincidence between hotspots identified by the three methods was calculated to identify how similar or different the sets of selection units identified as hotspots were, and whether the overlap was greater or less than would be expected by random.

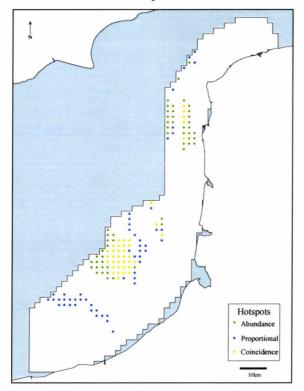
5.5.1 Methods

The spatial coincidence between the hotspots was identified using the 'query builder' option in ArcView on the shapefile containing the hotspot locations. The shapefile attribute table contained three columns that held data on the identity of the units that had been identified as hotspots, one column per method. A series of pair-wise queries was performed to select the overlapping units. These units were then mapped and a chi squared test used to find if the coincidences were significantly different from the number expected by random.

82

5.5.2 Results

In Survey One there were 39 selection units identified as both abundance and proportional hotspots (Figure 5.20), 46 units identified as both proportional and presence hotspots (Figure 5.21) and 27 units identified as both presence and abundance hotspots (Figure 5.22).



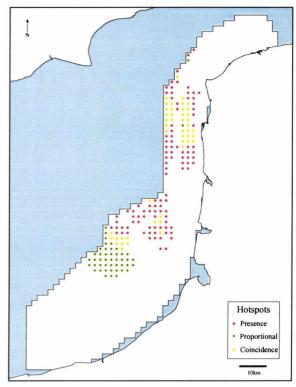


Figure 5.20 S1 Coincidence between abundance and proportional hotspots

Figure 5.21 S1 Coincidence between proportional and presence hotspots

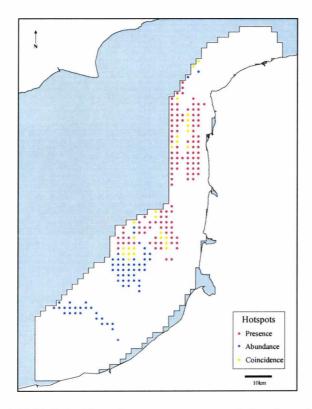
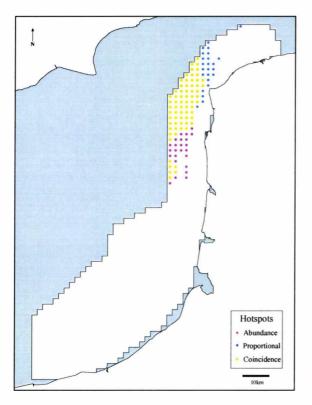


Figure 5.22 S1 Coincidence between presence and abundance hotspots

In Survey Two there were 68 selection units identified as both abundance and proportional hotspots (Figure 5.23), 83 units identified as both proportional and presence hotspots (Figure 5.24) and 64 units identified as both presence and abundance hotspots (Figure 5.25).



Hotspots

Presence

Proportional

Coincidence

Figure 5.23 S2 Coincidence between abundance and proportional hotspots

Figure 5.24 S2 Coincidence between proportional and presence hotspots

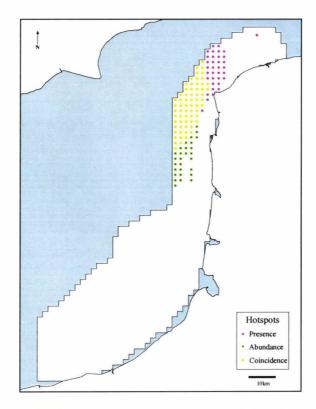
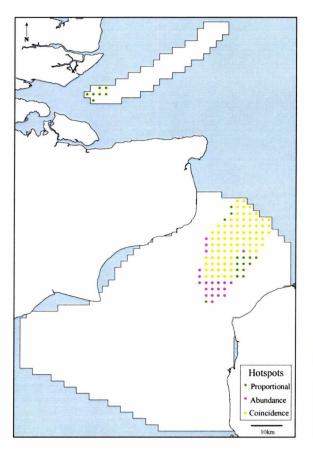


Figure 5.25 S2 Coincidence between presence and abundance hotspots

84



Hotspots
Proportional
Presence
Coincidence

Figure 5.26 S3 Coincidence between abundance and proportional hotspots

Figure 5.27 S3 Coincidence between proportional and presence hotspots

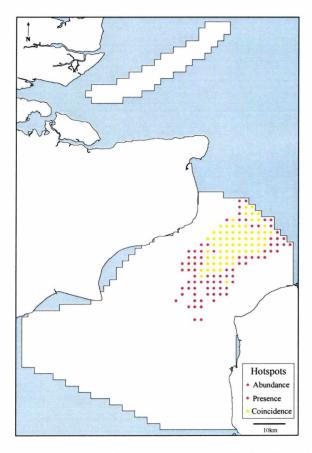


Figure 5.28 S3 Coincidence between presence and abundance hotspots

In Survey Three there were 80 selection units identified as both abundance and proportional hotspots (Figure 5.26), 102 units identified as both proportional and presence hotspots (Figure 5.27) and 67 units identified as both presence and abundance hotspots (Figure 5.28).

Survey	Comparison	No of hotspots	Coincidence between hotspots	Significance
One	Pres & prop	145 & 92	46	< 0.001
	Pres & abun	145 & 92	27	< 0.001
	Prop & abun	92 & 92	39	< 0.001
Two	Pres & prop	99 & 92	83	< 0.001
	Pres & abun	99 & 92	64	< 0.001
	Prop & abun	92 & 92	68	< 0.001
Three	Pres & prop	116 & 102	102	< 0.001
	Pres & abun	116 & 101	67	< 0.001
	Prop & abun	102 & 101	80	< 0.001

Table 5.1 Spatial coincidence between hotspot methods

All pair-wise comparisons of the three methods were significant. All of the proportional hotspots in Survey Three were also identified as presence hotspots. All of the methods shared more hotspots than would be expected from random samples (Table 5.1).

5.5.3 Discussion

This analysis investigated similarities and differences between the spatial location of units identified as hotspots using three methods for each survey. The three methods identified hotspots that were similarly arranged and located, therefore showing a high degree of spatial coincidence. The smallest degree of overlap was seen between presence and abundance hotspots. This might be expected due to the great difference in the form of the data. The coincidence between proportional and abundance hotspots was higher than between presence and abundance hotspots. The highest coincidences were between proportional and presence hotspots. The overlap, however, was significantly greater than would be expected by random in all three surveys for all three methods.

The coincidence between the hotspots in Survey One was the lowest of all three surveys. Underlying data showed a less distinct pattern in this survey as seen by the lower degree of clustering than in Surveys Two and Three. In contrast to the results found by Smith (2001) the significant overlap suggests that the presence hotspots could provide a surrogate for proportional hotspots and even, to a less extent, abundance hotspots. Perhaps one reason could be due to the underlying marine habitats that might be expected to be more homogeneous than the terrestrial habitat analysed by Smith (2001).

5.6 Protection provided by hotspot methods

The effectiveness of the hotspot methods was tested by analysing the proportion of the distributional area and the proportion of the abundance of ichthyoplankton protected within the hotspot sets.

5.6.1 Methods

The shapefile containing polygons representing the selection units contained a column in the attribute table which showed the identification of the units selected as hotspots. The spreadsheets containing information on the abundance and proportional area of ichthyoplankton elements were exported from MS Excel to a dbase table to allow import into ArcView. One dbase table at a time was then joined to the selection unit shapefile. A set of queries was performed on the attribute table of the shapefile to select the units included in each set of hotspots. The rows of the table highlighted by the query were exported to MS Excel, using the '1st tools' extension to ArcView. The abundance within the hotspot sets, and the proportion of the total abundance protected by that set could then be calculated. This procedure was repeated for each survey by adjoining the appropriate abundance and area tables. The number of ichthyoplankton elements protected to at least 0.1% of their abundance was also calculated using the spreadsheets. A one-way anova was used to test if there was a significant difference in the protection provided by the three hotspot methods.

5.6.2 Results

Presence hotspots represented 91.7 to 94.0% of the total number of ichthyoplankton elements to at least 0.1% of abundance. Many ichthyoplankton were represented in many units within the hotspot network i.e. were repeat representations.

Survey	Type of hotspot	No of units (%)	Total no of elements prot. (%)
One	presence	15.8	94.0
	proportional	10.0	94.0
	abundance	10.0	97.2
Two	presence	10.8	92.0
	proportional	10.0	94.0
	abundance	10.0	94.0
Three	presence	11.5	91.7
	proportional	10.0	89.6
	abundance	10.0	85.4

Table 5.2 Number of hotspots and ichthyo plankton protected by three hotspot methods

Proportional hotspots represented 89.6% to 94.0% of ichthyoplankton. Abundance hotspots represented 85.4% to 97.2% of ichthyoplankton (Table 5.2).

The mean area of distribution represented by the hotspot methods falls between 15.3% and 30.6%, with a range of 0.0% to 100.0% for all hotspot methods and all surveys. Presence hotspots represented a mean of 20.4% to 30.6% of the area of distribution of ichthyoplankton. Proportional hotspots represented a mean of 15.3% to 27.3% of the area of ichthyoplankton (Table 5.3).

Survey	N° of units	Type of hotspot	% of area represented		
	(%)		Mean	Min	Max
One	15.8	presence	22.9	0	71.8
	10.0	proportional	15.3	0	37.6
Two	10.8	presence	30.6	0	100.0
	10.0	proportional	28.0	0	96.0
Three	11.5	presence	20.4	0	71.0
	10.1	proportional	17.5	0	68.2

Table 5.3 Representation of area of distribution by hotspot methods

The mean abundance represented by hotspot methods varies from 16.39% to 39.74%. Presence hotspots covered a mean of 25.39% to 39.74% of abundance. Proportional hotspots covered a mean of 24.16% to 39.03% and abundance hotspots covered a mean of 16.39% to 36.86% of abundance (Table 5.4). The minimum and maximum levels of protection ranged from 0 to 100% for all hotspot methods and surveys.

Survey	Type of	% of units	% of abundance represented		sented
	hotspot		Mean	Min	Max
One	presence	15.8	26.7	0.0	71.4
	proportional	10.0	24.2	0.0	63.4
	abundance	10.0	16.4	0.1	43.8
Two	presence	10.8	39.7	0.0	100.0
	proportional	10.0	39.0	0.0	99.6
	abundance	10.0	36.9	0.0	92.5
Three	presence	11.5	25.8	0.0	79.2
	proportional	10.1	28.4	0.0	79.7
	abundance	10.0	25.3	0.0	83.0

Table 5.4 Representation of abundance by hotspot methods.

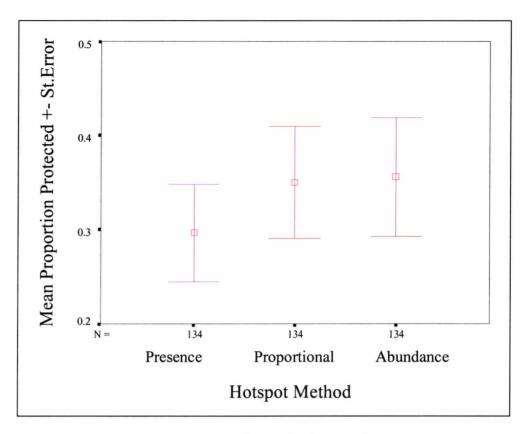


Figure 5.29 Mean protection provided to abundance by three hotspot methods

The three hotspot methods did not provide protection to a significantly different proportion of abundance (f=1.233, df=2, P=0.292).

5.6.3 Discussion

The methods provided a small range of mean representation within each survey but also showed variation between the surveys (Table 5.3 and Table 5.4). The mean value of protection coincidentally provided to ichthyoplankton proportional area and abundance provided by the hotspot methods was high, above 10% in each case. Individual levels of protection varied widely amongst the elements within each method and each survey. Many elements were under protected and others were represented to a high level. This could imply their protection was being provided at the expense of others. These issues are addressed with methods that utilise the concept of complimentarity. This has increasingly led to a move away from the hotspot methods of PA selection. Complimentarity selection algorithms aim to select units that provide protection to all the biodiversity elements to a certain minimum target, or maximise biodiversity representation within a set area, considering the complimentarity between units. The following section describes the use of a selection algorithm to identify protected area networks, using presence / absence and proportional area data at the same 4km² scale.

5.7 Summary

- Presence / absence, proportional area and abundance data were used to identify 10% ichthyoplankton presence richness, proportional richness and abundance hotspots at a scale of 4km². The methods identified hotspots that overlapped significantly more than would be expected by random.
- Presence richness hotspots protected a mean of 20% to 31% of the distribution and 25% to 40% of the abundance of ichthyoplankton. Proportional hotspots protected a mean of 15% to 28% of the distribution and 24% to 40% of the abundance of the ichthyoplankton. Abundance hotspots protected 16% to 37% of ichthyoplankton abundance.
- The protection provided by all three hotspots methods within the ichthyoplankton elements varied widely. From 3% to 14% gained no protection at all. This wide variation in the protection is due to overrepresentation of some elements at the cost of others. These results emphasise the increasingly widely held belief that hotspot methods of priority area selection should be replaced by methods based on the concept of complimentarity.

Chapter 6: Selecting MPA Networks Using Presence / Absence and Proportional Area Data

6.1 Introduction

The previous chapter has confirmed that the hotspot approach to designing PAs is not a reliable method for protecting quantitative conservation goals for ichthyoplankton in the Dover Strait. The belief that PA selection should be carried out using a form of complimentarity is becoming more widely held and will be analysed with the ichthyoplankton database in this and the following chapters.

Two forms of data derived from the distributions of the ichthyoplankton were used in the complimentarity analysis in this chapter. The first data type is the presence or absence of an ichthyoplankton element within a selection unit. This is similar to most species data used in conservation planning. It usually forms a list of the number of species present in each of the selection units. The second data type is proportional area of ichthyoplankton elements within each selection unit. This type of data is more readily available than abundance data and more informative than presence / absence data. The sum of the proportional distribution for all biodiversity elements in a selection unit produces a bias towards species with small ranges, but the resulting areas have more conservation relevance as they would protect a larger proportion of the habitat of their associated elements. Selection algorithms were applied to both these measurements of biodiversity to select MPA networks (sets of selected units) and test their relevance in conservation planning.

The most efficient and exact minimum sets can be identified using linear programming techniques. These are less useful in practical conservation planning scenarios than heuristic algorithms, for reasons outlined in Chapter One, although linear programming techniques now generate rapid solutions to most PA selection problems. One of the main advantages of heuristic algorithms is the transparency with which each selection is made and indication of flexible units. Contribution of flexible units is a valuable advantage in practical PA selection procedures where conservation planners often choose between a large number of equally representative networks, with varying advantages in other (non biological) factors. For this reason it was decided to use heuristic algorithms to analyse the ichthyoplankton dataset.

The selection of units by a complimentarity selection algorithm could be used to solve two types of PA selection problem. The first is to minimise the number of selection units (or area when using selection units of differing areas) necessary to represent each biodiversity element a target number

of times or to a proportional target. The second is to maximise the biodiversity elements within a given number of selection units (or area) available for protection (Chapter One). The first analysis of this chapter aims to identify the minimum number of units required to protect the presence of ichthyoplankton to two target representations. The second analysis uses proportional data to identify the units that would maximise the area of each element within a proportion of the selection units. The third analysis uses proportional area to identify networks of selection units that would protect proportional area targets of each element. The use of this type of data is more relevant to many practical applications where areas (very often vegetation or habitat types) are conservation targets (Pressey *et al.*, 1999).

Information on distribution of ichthyoplankton elements in locations outside the survey areas was not available. This information should be incorporated into measurements based on range size, as the proportion of the total range within the study site would presumably be different for each element. This has consequences for the conservation targets relevant to each element. It could be argued, however, that the portions of the distributions that occur outside the study area cannot be relied upon for their persistence as management decisions may differ in other areas.

The identification of MPA networks in the Dover Strait using presence / absence data is described in Section 6.2 and the protection they would provide to ichthyoplankton abundance is analysed in Section 6.3. A recently developed 'summed rarity' complimentarity algorithm is described in Section 6.4. This is used to identify the network of selection units representing the largest distribution of the most biodiversity elements within 10% of the units available, described in Section 6.5. Section 6.6 contains a description of the use of the summed rarity algorithm to identify the near-minimum sets of areas representing proportional distribution conservation targets. Section 6.7 presents an analysis of the abundance protection provided by the networks chosen using proportional data. The chapter is summarised in Section 6.8.

6.2 Identifying minimum sets using presence / absence data

The presence / absence dataset (Chapter Five) was used to identify (near) minimum sets of units that would, if protected, represent ichthyoplankton elements to two conservation targets. The conservation targets were 1 and 6 representations of each ichthyoplankton element found within the study area. One representation is the presence of an ichthyoplankton element within one selection unit.

Worldmap software was used to identify the minimum sets. The algorithm used was a 'progressive rarity' algorithm based on Margules *et al.*, (1988), and is discussed in Williams, (1998b; 2000). As described in Williams, (2000) the steps in the algorithm are as follows:

1 select all units with species that have single records;

2 the following rules are applied repeatedly until all species are represented:

A) select units with the greatest complementary richness in just the rarest species (ignoring less rare species),

if there are ties between the units, then:

- B) select units among ties with the greatest complementary richness in the next-rarest species and so on, if there are persistent ties, then:
- C) select units among ties with the greatest complementary richness in the next-next-rarest species and so on, if there are persistent ties, then:
- D) select units among ties with the greatest complementary richness in the next-next-rarest species and so on, if there are persistent ties, or no next- or next-next-next-next-rarest species, then:
- E) select units among persistent ties with the lowest grid-cell number or at random (lowest grid-cell number may be used rather than random choice among ties in order to ensure repeatability in tests)

(repeat steps A-E until all biodiversity elements are represented)

3 identify and reject any units that in hindsight are unnecessary to represent all biodiversity elements; and

4 re-order areas by complementary richness

If, before all areas are re-ordered, the complementary richness reaches all biodiversity elements, or the maximum complementary richness increment declines to 0, it will continue to re-sequence units re-setting the cumulative richness to 0, ignoring previously re-ordered units and starting again with scoring complementary richness from the current position on the unit list, repeating this re-setting as often as is necessary to re-order all units.

The algorithm has been shown to be similar to, but perform better, than the rarity weighting method used in Williams *et al.* (1996; an algorithm based on iteration as for 'greedy set' but using range-size rarity) (Williams, 2001) and has been demonstrated using Worldmap in Csuti *et al.* (1997).

The method identifies irreplaceable and flexible sites. This allows the identification of alternatives for negotiation by conservation planners. The algorithm is also transparent in allowing access to information regarding the biodiversity elements which cause the choice of each particular unit. This also assists planners with flexibility and information to allow informed decisions regarding replaceable units. It can provide justification when negotiating areas for conservation. Many studies have identified networks of areas necessary for a single representation of each species

(Williams *et al.*, 1996), but it has been suggested that a single representation strategy is not sufficient for ensuring the maintenance of species in the long term (Margules *et al.*, 1994; Virolainen *et al.*, 1999; Rodrigues *et al.*, 2000a; 2000b). Minimum sets required for a conservation target of both one and six ichthyoplankton representations were therefore identified (Williams *et al.*, 1996).

6.2.1 Methods

The Worldmap software was used with presence / absence data matrix spreadsheets (Chapter Five) to identify minimum sets for 1 and 6 representations of each ichthyoplankton element within each survey. The tie-breaking rule selected the cell with the lowest id, to allow repeatability. The minimum set scores for the sets chosen were exported to ArcView, via a report format. The report required formatting using MS Word and Excel to facilitate import into ArcView. It was then possible to map the minimum sets and identify the coincidence between Surveys One and Two (Survey Three is spatially distinct).

6.2.2 Results

The efficiency of the algorithm was similar across surveys, with approximately 0.3% of selection units being necessary for one representation, and approximately 2% of units necessary for six representations (Table 6.1).

Survey	Target	% of selection units chosen
One	1 representation	0.33
	6 representations	2.39
Two	1 representation	0.32
	6 representations	1.96
Three	1 representation	0.40
	6 representations	2.67

Table 6.1 Efficiency of presence / absence complimentarity networks.

Three selection units were required in Survey One to represent each ichthyoplankton element once (Figure 6.1) and 21 units for six representations (Figure 6.2). Three selection units were required in Survey Two to represent each ichthyoplankton once (Figure 6.1) and 15 units for six representations (Figure 6.2). There were two units that were identified as required for both minimum sets of six representations of ichthyoplankton in Surveys One and Two (Figure 6.2). Four selection units were required for one representation of each ichthyoplankton element in Survey Three (Figure 6.3) and 28 units for six representations (Figure 6.4).

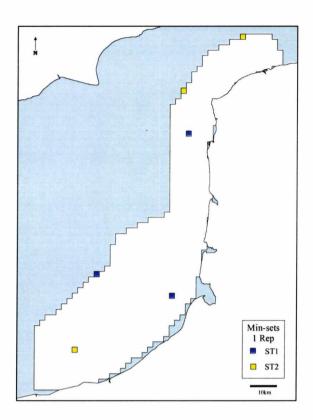


Figure 6.1 S1 and S2 minimum sets for 1 representation.

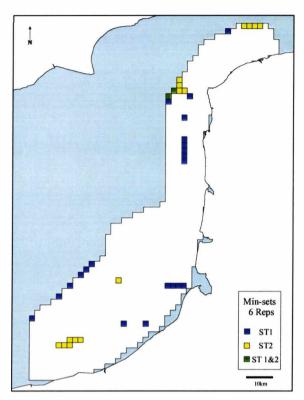


Figure 6.2 S1 and S2 minimum sets for 6 representations

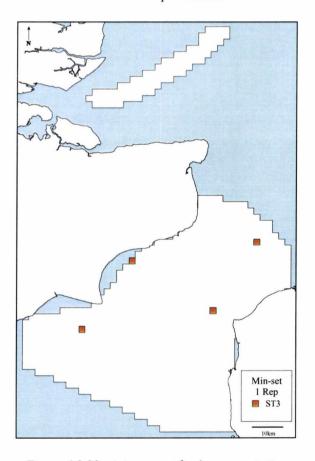


Figure 6.3 S3 minimum set for 1 representation

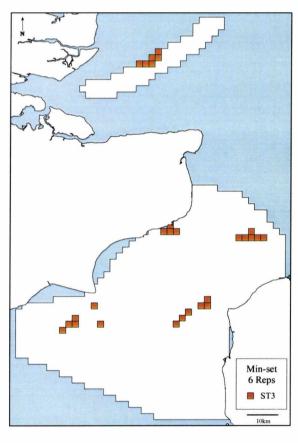


Figure 6.4 S3 minimum set for 6 representations

6.2.3 Discussion

The complimentary selection algorithm identified a very small proportion of the units to include one and six representations for each ichthyoplankton element. This method obviously offers an efficient identification of units to protect one and six representations of each biodiversity element, ensuring that all elements have an equal representation, rather than the hotspot method which simply identifies the areas scoring highest. This has the possibility of excluding a number of elements whilst providing multiple representations of others. For this reason the hotspot methods have largely been superseded in use (Prendergast *et al.*, 1993; Hacker *et al.*, 1998; Harcourt, 2000).

6.3 Coverage of ichthyoplankton abundance by presence / absence minimum sets

The presence of an ichthyoplankton element within a selection unit can represent a wide range of distributional area within the unit, ranging from 0.04 km² to 4 km². The protection provided by one and six representation minimum sets to the ichthyoplankton distribution and abundance is therefore analysed.

6.3.1 Methods

The shapefiles containing the polygons representing selection units and the identification of the units selected in minimum sets for section 6.2 were used to calculate the protection provided by coverage to ichthyoplankton abundance. The rows in the attribute tables, corresponding to the units, contained information concerning whether the unit was part of a near-minimum set, and if so, to which set it belonged.

The dbase table containing information on the abundance of the ichthyoplankton elements within the selection units of the Survey One was joined to Survey One shapefile attribute table. A set of queries was then performed on the attribute table to select the units included in each minimum set, one minimum set selected per query. The selected rows were exported to MS Excel, where the abundance of each ichthyoplankton element within each minimum set and the proportion of the total abundance protected by that set were calculated. This procedure was repeated for each of the minimum sets, and for each of the surveys, by adjoining relevant abundance tables for each survey.

6.3.2 Results

The proportion of elements represented within each minimum set varies within each survey from approximately 0.01% to 3.5% for one representation and 3.0% to 20.0% for six representations (Table 6.2). The lowest coverage was 0.01% for 1 representation and 0.2% for 6 representations.

The mean coverage for 6 representations was approximately 6 times the coverage for 1 representation.

Survey	1 representation			6 representations		
	Mean%	Min%	Max%	Mean%	Min%	Max%
One	0.5	0.01	1.7	3.5	0.4	14.9
Two	0.9	0.2	3.4	5.8	0.5	19.7
Three	0.6	0.01	2.6	3.1	0.2	7.8

Table 6.2 Representations of abundance by presence / absence complimentarity networks

6.3.3 Discussion

The minimum sets identified for the conservation targets of both one and six representations protected lower mean proportions of their abundance than that protected by hotspot methods (Table 6.2), although a wide range of protection is provided using hotspot methods (Chapter Five).

The proportional relationship between coverage for 1 representation and 6 representations is surprising as the data do not include abundance. There is a large difference between the two extremes of abundance which would constitute a presence within a selection unit. The proportions of ichthyoplankton abundance covered was very low, but the conservation target was also an extremely low level of one or six representations. Abundance in the water column below the selection units classified as containing a particular element could vary wildly because the criteria for a representation could simply be a presence in a unit as small as 0.04 km². Abundance can also vary to a larger extent than the area of distribution within selection units, as the range of depth within the study area is wide. This variability can be decreased with use of a fine scale measurement within the selection units, enabling finer discrimination between units based on their conservation importance and relevance. Data concerning the distribution within the selection units were available and their use to select minimum sets is described in the following section.

6.4 'Summed rarity' complimentarity selection algorithm

Many reserve selection algorithms have utilised presence / absence data (Pressey & Tully, 1994). Questions of minimum viable population size and probability of extinctions for biodiversity managers mean that such approaches have limited appeal. A partial solution is to develop methods based on quantitative data that will represent proportional conservation targets (Nicholls, 1998). In answer to this need, a summed rarity algorithm was developed and tested by Smith (2001), initially to analyse terrestrial biodiversity of Maputaland, South Africa. It was developed to select priority sites based on the following three criteria:

- 1) Units containing a large number of biodiversity elements would have higher scores than units containing a small number of biodiversity elements.
- 2) Units containing elements under-represented in a PA network would have higher scores than units containing over-represented elements.
- 3) Units containing a large proportion of an element's range would have a higher score than units containing a small proportion.

The conservation value of a unit for a biodiversity element is calculated using the following equation:

Area or abundance of element in grid square

* Area or abundance of element unprotected in study area

Area or abundance of element in study area

Area or abundance of element in study area

A score is calculated for each selection unit. The score is calculated by summing all the values for each associated biodiversity element (ichthyoplankton abundance, area of distribution or surrogate). The algorithm then identifies the highest ranking selection unit and gives it PA status. The chosen selection unit is then removed from further analysis, and the amount of each associated biodiversity element, which is unprotected, changes. The iterative process then recalculates the conservation scores and identifies the next highest ranking unit and repeats this process until the required number of selection units has been identified.

Java programming language was used to create software to process the selection algorithm (Fischer, 2001), and ArcView used to map the resulting PA networks. The software uses two input tables: the 'grid table' and the 'element details table'. The 'grid table' contained details about the amount of the biodiversity elements in each selection unit. Rows represent selection units, and columns represent biodiversity elements, either ichthyoplankton or surrogate. The cells contain proportional data for the corresponding element in the corresponding selection unit (this represents the first half of the equation). The 'elements table' contains information on the total quantity of elements and the quantity of elements already protected. As there are no existing PAs in the study area, the total abundance (or area) and the unprotected abundance (or area) were initially identical.

The program utilises an iterative approach by using the following steps:

- 1) The unprotected proportional area (or abundance) of each element is calculated by using data in the 'Element details table' to divide the unprotected area by the total area;
- 2) The proportional data in each cell is multiplied by its corresponding unprotected proportional abundance;
- 3) The resultant data for each unit that does not have PA status is summed;

- 4) Units are ranked according to their proportional data score and the unit with the highest rank is identified:
- 5) The highest ranking unit is reclassed as having PA status;
- 6) The proportional data for each element found in the highest ranking unit is multiplied by the total area data to calculate the area of each element found in the selected unit;
- 7) The area of each element in the selected unit is subtracted from the unprotected abundance data stored in the 'Element details table';
- 8) The process begins again at step 1.

The previous section described the use of a selection algorithm based on complimentarity to identify minimum sets using presence / absence information in the Worldmap software. The protection provided to both the area and the abundance of ichthyoplankton elements, by sets of one and six representations, was extremely low especially when compared to the 10% levels recommended by the IUCN (1992). The variance in distribution and abundance within the selection units when only 'presence' is recorded may account these low levels of protection. The summed rarity algorithm utilises the qualitative nature of proportional data in the following analyses.

6.5 Complimentarity networks using proportional area

Data on area of distribution are more frequently available than abundance data, and more informative than presence / absence data. The effectiveness of using area data in terms of protecting ichthyoplankton abundance when used to identify MPA networks is analysed in the following sections. The top 10% of areas were identified using the summed rarity algorithm and proportional area data.

6.5.1 Methods

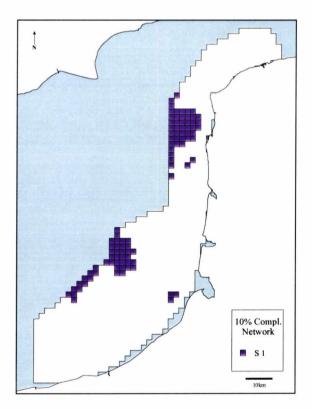
The MS Excel spreadsheet containing proportional areas of ichthyoplankton elements (described in Chapter Five) was used to create the 'element details table' required by the summed rarity selection software. The 'grid table' was created using data on the total area of each element in the study site. The initial unprotected area of each element equalled the total area, as no MPAs exist in the study area.

The summed rarity algorithm software was used to identify the highest ranking 10% of selection units (92 units for Surveys One and Two, and 101 units for Survey Three) by complimentarity. The scores of each selection unit was generated in a report. It was necessary to convert the format of the report so that the selected set of units could be mapped. The report was imported into MS Word and manipulated into a format for import into MS Excel. The information included the list of

the selection units selected in each set, the rank and conservation score of each unit. Using MS Excel, this information could be converted into a dbase format suitable for import into ArcView. The dbase table was joined to the attributes table of the shapefile containing the polygons representing the selection units. When the two tables join, the information from the dbase file only joins to the relevant rows in the table i.e. the rows which correspond to the selection units identified for each analysis in question. Units selected in each network can then be identified in the selection unit shapefile. The top ranking 10% of the units was identified and mapped.

6.5.2 Results

Survey One contains two main clusters of selection units, with a third smaller less distinct linear cluster to the west of the study area (Figure 6.5). Survey Two contains one large cluster of selected units and a much smaller cluster to the eastern part of the study area, with one further single unit to the south west (Figure 6.6). Survey Three has selected units positioned in the central waters in the Dover Strait with very few in the coastal regions and none to the south west or in the Thames estuary (Figure 6.7).



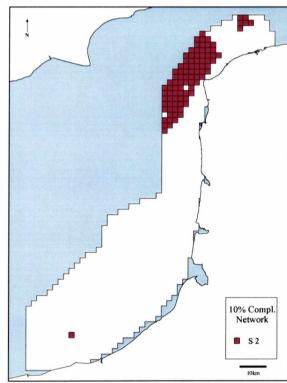


Figure 6.5 S1 10% highest complimentarity networks

Figure 6.6 S2 10% highest complimentarity

networks

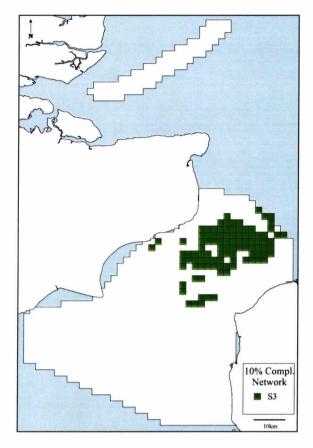


Figure 6.7 S3 10% highest complimentarity networks

6.5.3 Discussion

The top 10% complimentarity units show similar distributions to the presence, proportional and abundance hotspots identified in the previous chapter. In Survey One, there are two clusters of units in both sets of analyses. The top ranking 10% complimentary units in Survey Two are even more similar in distribution to those units identified as presence hotspots (Chapter Five).

The similar distribution of complimentary units and hotspot units is surprising. Complimentarity methods choose areas that compliment each other by adding new taxa not represented (or adequately represented) in areas already selected. The hotspot methods rank the areas according to their richness either in numbers of species, proportional richness or abundance, irrespective of repeating representations of the actual taxa involved. Methods to quantify the elements contained within each selection unit are also very different. The presence hotspots were based on presence / absence only, and the present analysis utilised area of distribution within the selection units. The efficiency is difficult to compare as the number of hotspots were predetermined as 10% of the selection units. It is recognised, however, that complimentarity methods are more efficient when quantitative representation targets are used.

6.6 Complimentarity networks using proportional conservation targets

The IUCN has recommended that at least 10% of each nation or in each ecosystem should be protected to ensure the persistence of the biodiversity within them (IUCN, 1992). As discussed in Chapter One, the actual figure appropriate for practical conservation is debated. High figures such as 50% may be unrealistic, but to identify patterns and the number of selection units that would be required, the program was modified (Fischer, 2001) and used to identify the selection units required for conservation targets of 10%, 20% and 50% cover of the biodiversity elements.

6.6.1 Methods

The two tables prepared for previous analysis were used. These tables contained details of the proportional richness. The selection software was used to run the summed rarity algorithm with proportional targets of 10%, 20% and 50% of the area of each ichthyoplankton element. This was repeated for the three surveys. The output reports were exported to MS Word, MS Excel and then ArcView, in a similar way to the previous analysis, to allow the networks of selected units to be mapped.

6.6.2 Results

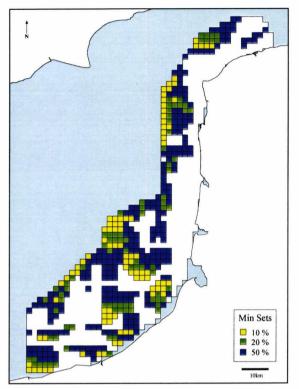
The number of units identified as required for the three proportional conservation targets ranged from 9.7% to 9.9% for the 10% target, 19.48% to 19.7% for the 20% target and 48.86% to 50.7% for the 50% target (Figures 6.8 to 6.10 and Table 6.3). There was a near linear relationship between the proportion of selection units required and the conservation target. The protection provided by the 10% target to individual elements ranged from 10% to 34.5% of the area of ichthyoplankton elements (Table 6.4).

Survey	Number of selection units required (% of total units) for three targets			
	10%	20%	50%	
One	9.8	19.5	50.7	
Two	9.9	19.7	49.1	
Three	9.7	19.7	49.0	

Table 6.3 Number of units necessary for three proportional conservation targets

Survey	Mean Protection %	Minimum Protection %	Maximum Protection %
One	12.7	10.0	21.0
Two	14.5	10.1	34.5
Three	12.7	10.0	22.1

Table 6.4 Protection given to ichthyoplankton elements based on 10% area conservation target.



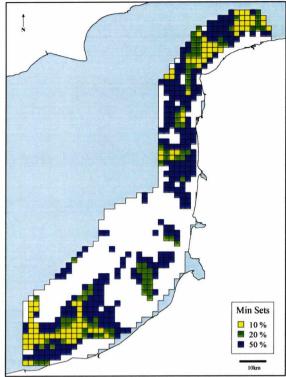


Figure 6.8 S1 Minimum sets for 10%, 20% and 50% of area conservation targets

Figure 6.9 S2 Minimum sets for 10%, 20% and 50% of area conservation targets

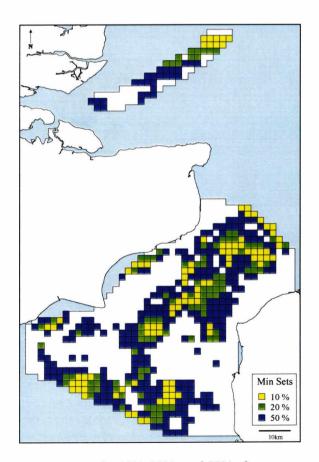


Figure 6.10 S3 Minimum sets for 10%, 20% and 50% of area conservation targets

6.6.3 Discussion

The 'summed rarity' algorithm has allowed the use of proportional conservational targets in addition to ranking by complimentarity (section 6.5). Units ranked within the top 10% by complimentarity in the previous analysis were similar to those identified using richness and rarity hotspots. The areas identified to protect 10% of the distribution of each element in this analysis, however, are very different in their distribution, although the numbers of units required are similar. The selected units are more scattered, which may be regarded as less desirable, due to both edge effects and more difficult enforcement of use restrictions.

There was a near linear relationship between the proportion of selection units needed and the conservation target. Conversely, Bedward *et al.* (1992) found that a relatively small increase in the area of a network was required to fulfil much higher representation targets for area of biodiversity elements, although their analysis used areas rather than proportional areas. Representing the domains in their analysis to 20% required only 3% more of the study area than was required in an analysis that initially required 5%. This may be due to the over-representation of the elements in the 5% analysis. This appears to have occurred to a much smaller extent in the present analysis.

Problems associated with aiming to protect a proportion of the biodiversity element's range include a lower total area being assigned to the more restricted species. If the elements are taxa, they may be restricted due to several reasons including habitat transformation. In the study area the extent of transformed habitat is unknown. From distribution data, it is unknown whether the restricted taxa are at lower abundances (and requiring smaller ranges), prefer to live at higher abundances in smaller areas or are restricted due to restricted habitat.

It is not known to what extent the distributions of these taxa or the networks identified using their distributions could represent other taxa and so provide protection for them. The selection algorithm has also only recently been developed, although it has been successfully tested (Smith, 2001; Smith *pers comm.*). Results need to be interpreted in this context and used as indicative of possible methods. Advances and improvements are being made to the algorithm, some of which will be tested in the following chapters. These include the use of abundance data and the provision for preferentially selecting adjacent sites.

6.7 Coverage provided to ichthyoplankton abundance by MPAs selected using proportional area

The protection provided by the proportional area networks (identified in the previous section) to abundance was calculated to identify the effectiveness of proportional data to identify PA networks.

6.7.1 Methods

The spreadsheet containing ichthyoplankton element abundances was converted into a dbase file in MS Excel, and imported into ArcView. The quantity of ichthyoplankton elements protected by the proportional data minimum sets could then be calculated. The imported table was joined to the shapefile containing the polygons representing the selection units and the ranks of each unit in the minimum set analysis. The rows of the shapefile contained information on the location of each selection unit, whether it was included in each minimum set, its rank if it was included, and the abundance of each ichthyoplankton element contained within that unit. This process was repeated for each proportional conservation target.

For each minimum set, the rows corresponding to the cells within the minimum sets were identified using the 'query builder' in ArcView. These rows were exported into MS Excel, where the abundances of each element were summed. The proportion of the abundance protected by each minimum set was calculated by dividing the total abundance of each element in the minimum set by the total found in the study area. The percentage of all the species that were protected to the relevant conservation target was calculated. The proportions of each species protected by the minimum set in question were listed and the 'IF' command in MS Excel used to assign a one or zero in a new column according to whether the target had been reached or not. These values were then summed. The proportion of all the elements protected by area to the conservation target in use was then calculated. The mean, minimum and maximum protection given to the ichthyoplankton elements was also calculated. The process was repeated for each conservation target.

6.7.2 Results

Survey	Cons	Cells	Species abun	Mean	Minimum	Max
	target	needed (%)	protected to	protection	protection	protection
			conservation	(%)	(%)	(%)
			target(%)			
One	10%	9.8	69.4	12.1	0.002	24.6
	20%	19.5	69.4	23.5	7.1	39.3
	50%	48.5	80.6	60.0	27.3	78.5
Two	10%	9.9	40.0	13.9	3.4	35.9
	20%	19.7	45.6	26.0	12.4	52.3
	50%	49.1	50.0	66.2	44.6	93.5
Three	10%	9.7	25.0	10.4	0.3	39.7
	20%	19.8	27.1	21.0	0.6	71.5
	50%	49.2	43.8	50.5	26.6	77.1

Table 6.5 Coverage of abundance levels provided by proportional area data

The protection provided by proportional area to ichthyoplankton abundance ranged from 0.002% to 39.71% for the 10% target with a mean protection of 10.38% to 13.91%. The more relevant result regarding the ability of proportional area to adequately protect the biodiversity is the proportion of those elements that are protected to the conservation target in use. For a conservation target of 10%, between 25% and 69.44% of all ichthyoplankton elements were protected to 10% of their abundance (Table 6.5, Figure 6.11, Figure 6.12 and Figure 6.13) depending on the survey.

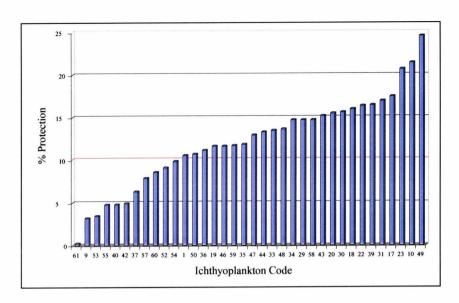


Figure 6.11 SI Protection given to all ichthyoplankton by 10% area *

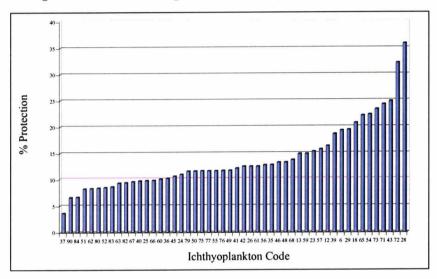


Figure 6.12 S2 Protection given to all ichthyoplankton by 10% area *

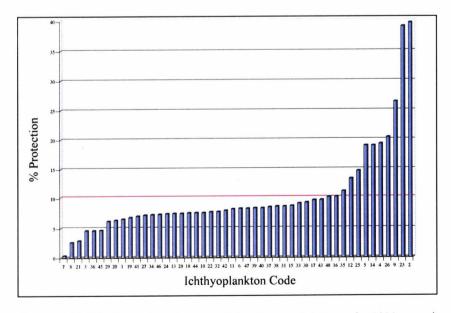


Figure 6.13 S 3 Protection given to all developmental stages by 10% area *

^{*}Red line indicates 10% protection level

6.7.3 Discussion

Proportional area provided protection to the 10% conservation target for between 25.0% and 80.6% of the elements in the three surveys. Mean values of protection, however, were quite wide ranging. There is also great variability between the surveys. During Survey One, proportional area was a fairly adequate surrogate with 69.5% to 80.6% of species protected to the conservation target. Survey Two protected fewer of the ichthyoplankton elements to the conservation target, although the range of mean protection level was similar to that in Survey One. Survey Three performed the worst using this measure, but the range of mean protection levels was similar to the other surveys. Mean protection figures are very encouraging for use with each of the conservation targets. The minimum protection, however, is indicative of the range of protection. Efficiency was very similar across surveys.

The wide range of protection provided by proportional area suggests that this measure would not provide adequate protection of all elements to abundance conservation targets. It is, however, a very much more effective measure than using presence / absence data with multiple representations, although only low levels of repeat representations were tested. The following chapter will analyse the networks identified using the abundance dataset.

6.8 Summary

- Presence / absence data was used with a 'progressive rarity' complimentarity algorithm in the Worldmap software to identify MPA networks to protect one and six representations of ichthyoplankton elements. These were found to require low numbers of selection units but provided poor coverage of ichthyoplankton proportional area and abundance.
- A recently developed 'summed rarity' selection algorithm was used to identify networks of selection units that represent the largest distribution of the most ichthyoplankton elements within 10% of the selection units available. The distribution of the resultant networks of selection units shared a similar distribution to those identified using the hotspot approaches.
- The 'summed rarity' algorithm was adapted to identify networks of selection units that represent proportional distribution conservation targets. A near linear relationship was found to exist between the conservation target and number of units required to achieve the target. Representation for the 10% target ranged from 10.0% to 34.5% of ichthyoplankton element area, with mean protection levels ranging from 12.5% to 12.7%. The 10% conservation target networks were widely dispersed for all three surveys, but became progressively clustered with increasing proportional targets.

Chapter 7: Selecting MPA Networks Using Abundance Data

7.1 Introduction

PAs are chosen with the aim to represent and protect biodiversity elements, maximising the protection efficiently. It has been suggested (Rodrigues *et al.*, 2000b) that efficient reserve networks in terms of cost (or area) might not protect the original set of biodiversity elements of features for an extended period of time. This may be due to local extinctions or colonisation of sites regardless of their protected status. Rodrigues *et al.* (2000a) suggest from studies on British birds, that fewer species are lost if sites are selected according to population density or local abundance. Such methods might favour smaller sites containing elements at higher density rather than larger sites with large populations and lower densities. Other suggestions for improving robustness of the selection procedure using abundance data, include the use of only those sites where biodiversity elements occur above a certain abundance value (Kershaw *et al.*, 1995). Another suggestion is the establishment of a minimum population size as a required representation target for each element (Nicholls, 1998). The comprehensive Dover Strait ichthyoplankton dataset allows analysis of selection methods using abundance data.

The following section is a description of the use of the 'summed rarity' complimentarity selection algorithm with abundance data to identify the top 10% ranking selection units to protect the highest proportion of ichthyoplankton elements. Section 7.3 is an outline of the identification of minimum sets of units necessary to satisfy proportional abundance conservation targets. Section 7.4 describes the coincidence between minimum sets identified in the two comparable surveys. The chapter is summarised in Section 7.5.

7.2 Complimentarity networks using abundance data

The conservation target was identified as the top ranking 10% selection units in each sampling survey. This is an arbitrary number chosen to identify groups of high ranking areas. It is the figure recommended by the IUCN (1992) and follows the targets used in previously described hotspot and complimentarity analyses (Chapters Five and Six). It may be a large enough figure to allow flexibility in the selection unit choice should some become unavailable or unsuitable for protection.

7.2.1 Methods

The summed rarity algorithm was used in the PA selection software (described previously) to rank selection units according to their proportional score using abundance data. The top ranking 10% of

selection units were identified. A total of 92 units were selected in Surveys One and Two and 101 in Survey Three. A Chi squared test was used to test whether the coincidence between units selected in Surveys One and Two were more than would be expected by a random selection.

7.2.2 Results

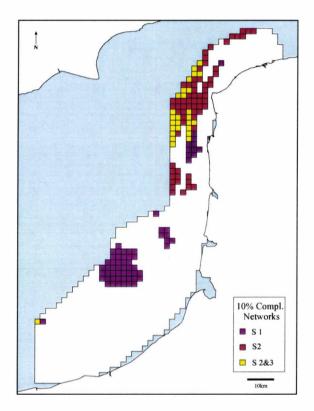


Figure 7.1 S1 & S2 Highest ranking 10% complimentarity units using abundance data

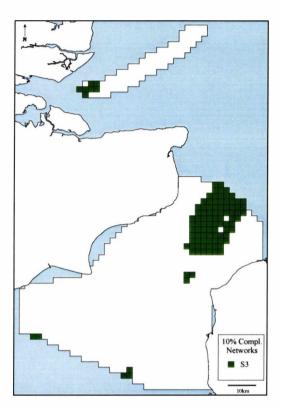


Figure 7.2 S3 Highest ranking 10% complimentarity units using abundance data

The selected units are clustered and mainly located in the central off-shore water for all three surveys (Figure 7.1 and Figure 7.2). The selected units are mostly clustered towards the western part of the study area in Survey One and towards the eastern side during Survey Two. The selected units are in the eastern part of the mid off shore water in the middle of the Dover Strait and at the western end of the Thames Estuary portion of the study area in Survey Three. The 10% complimentary networks in Surveys One and Two overlapped more than would be expected from a random selection (p<0.000).

7.2.3 Discussion

The apparent movement of the main clusters of identified units across the study area from west to east during spring of 1995 is interesting and reflects the distributions of the hotspots. It also supports interpretation of ichthyoplankton movement from western spawning sites to more easterly

nursery grounds. This is despite units being chosen to reflect areas for all the species and stages (which have different ecological niches and needs) considering differences between units unlike hotspots that are chosen to reflect high values using various scores.

7.3 Identifying MPA networks for three conservation targets using abundance data

Conservation targets for PA selection can be based on maximising the elements within a restricted area of land or sea as described in the previous analysis. They can also be based on proportions of biodiversity elements, areas or abundances. As identified in Chapter Six, proportional targets represent a lower area of the restricted range taxa or elements. This could be undesirable as these taxa could be most at risk. In light of uncertain climatic change, however, it may be argued that protecting every taxon to the same proportion of its range should be encouraged. A 10% target is recommended by the IUCN (1992), but has been questioned for its ability to protect effectively all the biodiversity elements (Soulé & Sanjayan, 1998). Larger targets may be unrealistic, but worth investigation. Targets of 10%, 20% and 50% were chosen for the analysis using proportional area data and so are also used for abundance data analysis here.

7.3.1 Methods

The summed rarity algorithm selection software was used to select units to satisfy proportional abundance conservation targets. Once an element is protected to the required level, it is not included in further iterations of the algorithm. Conservation targets were similar to previous analyses, 10%, 20% and 50%. The output reports were manipulated in the way described for previous analyses, using MS Word and MS Excel, to allow import into ArcView as dbase tables. The tables were joined to the selection unit shapefile and the MPA networks mapped.

7.3.2 Results

The proportion of selection units needed to protect 10% of the abundance of each ichthyoplankton element ranged between 7.0% and 7.9% for the three surveys. The number of selection units required is near linearly related to the conservation target. The number required to protect 20% of the abundance is approximately double the number required for 10%, but the 50% target requires a little more than five times the number of units necessary for the 10% target (Table 7.1).

The spatial distribution of the minimum set networks are quite different across the surveys. The 10% target sets were scattered in all three surveys and the sets were progressively more clustered with increasing protection, as might be expected. The largest patches within the 50% set occurred in the west in Survey One and are towards the north east in Survey Two (Figure 7.3 and

Figure 7.5). In the third survey the large clusters within the 50% minimum set are situated in the mid waters between France and England, but with a gap in the central area (Figure 7.5). All three conservation target sets for Survey Three included clusters of units extending north east from the mouth of the Thames estuary.

Survey	% of Selection Units Needed for Three Conservation Targets			
	10%	20%	50%	
One	7.6	15.1	40.0	
Two	7.9	15.9	40.9	
Three	7.0	14.4	38.3	

Table 7.1 Numbers of selection units required to satisfy different conservation targets

Protection provided to individual ichthyoplankton elements by the selected network of units varied a little, the highest protection was 28.1% in Survey One, 30.5% in Survey Two and 24.7% in Survey Three. The range of protection given to individual elements can be seen from the graphs (Figure 7.6, Figure 7.7, and Figure 7.8).

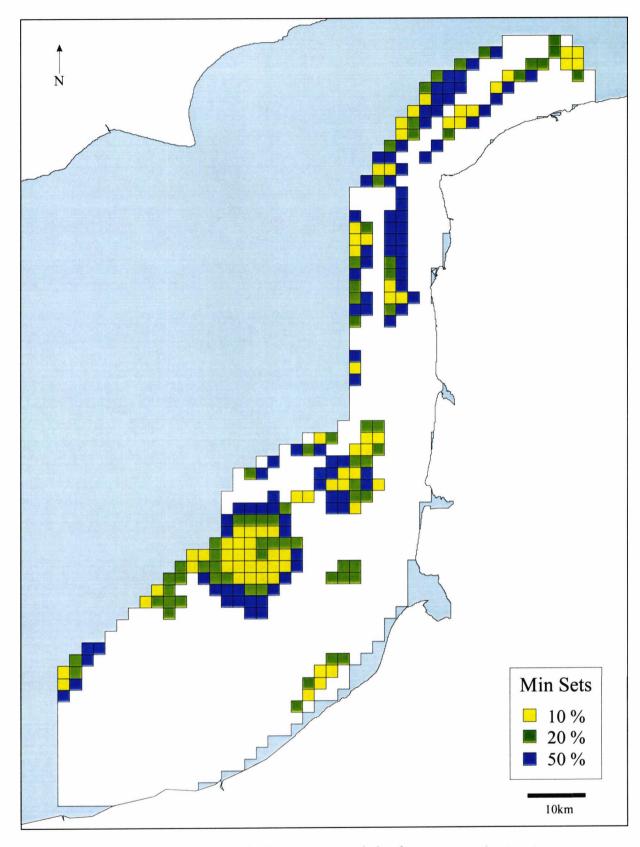


Figure 7.3 S1 Minimum sets for three proportional abundance conservation targets.

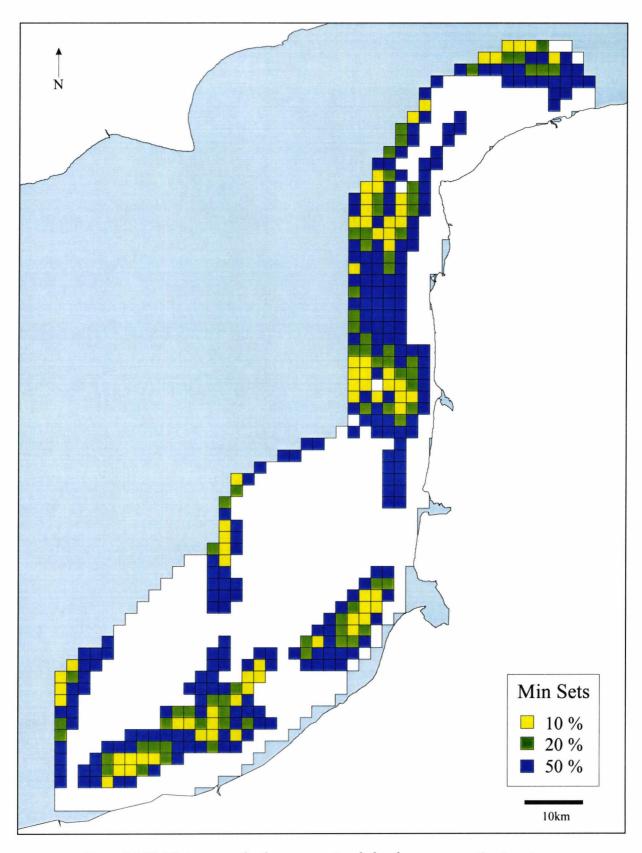


Figure 7.4 S2 Minimum sets for three proportional abundance conservation targets.

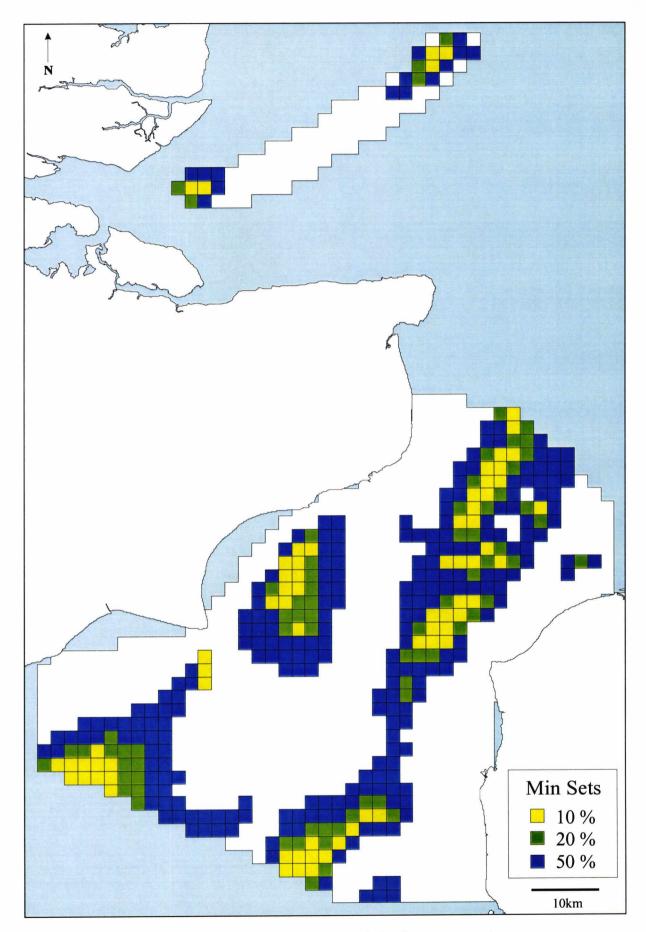
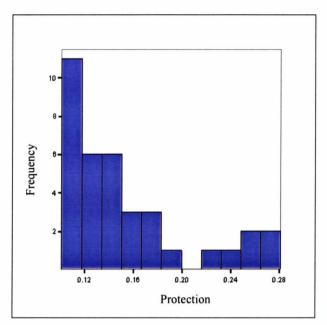


Figure 7.5 S3 Minimum sets for three proportional abundance conservation targets.



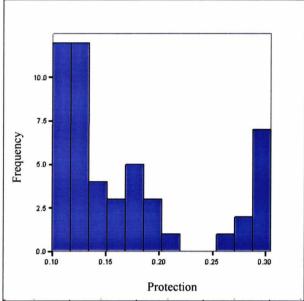


Figure 7.6 S1 Frequency of protection levels for all ichthyoplankton based on 10% abundance target.

Figure 7.7 S2 Frequency of protection levels for all ichthyoplankton based on 10% abundance target

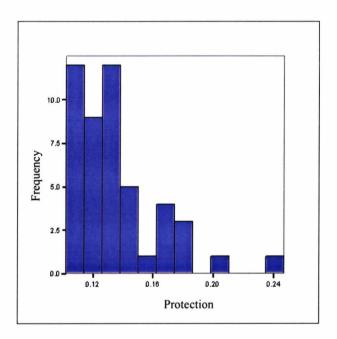


Figure 7.8 S3 Frequency of protection levels for all ichthyoplankton based on 10% abundance target.

7.3.3 Discussion

The efficiency (number of units necessary for a conservation target) of the algorithm was similar across surveys. The relationship between conservation targets and the required number of selection units found by Smith (2001) using the same algorithm was found to be linear. The 50% target in the current study required slightly more than five times the number of units required for 10%. The proportion of the selection units identified as necessary to protect each conservation target is lower

than the proportional target, i.e. less than 10% of the total number of units was needed to protect 10% of the abundance of ichthyoplankton.

Bedward *et al.* (1992) found that more than the target proportion of units were selected for area proportional targets. As discussed, the reason may be over-representation of some biodiversity elements at the expense of others. Another reason could be the lower proportional target used. It can be seen from the graphs (Figure 7.6, Figure 7.7 and Figure 7.8) that some overprotection occurs in this study, but only to a small extent. Bedward *et al* (1992) also found a small increase in the target did not produce a large increase in the number of units identified, unlike this study. Possibly a further consequence of the overprotection of some elements within the small conservation target networks.

The selected networks were less clustered when using a proportional conservation target than networks of the top ranking 10% complimentarity units and hotspot methods (section 7.2 and Chapter Five). Clustering of units selected in the networks increased as the conservation target increased when proportional targets were used. This would be expected as the ratio of 'units chosen' to 'units available' increases. This may be a reflection of the concept of complimentarity which chooses units different from each other in terms of the biodiversity elements they contain. This may be reflected by the conditions present in the units chosen, therefore heterogeneous units are chosen, these may be expected to be further apart. The position of the networks was also very different to those selected by the previously used methods.

The majority of units in the minimum sets were positioned further towards the east in Survey Two than in Survey One, but less clearly defined than for the 10% ranked sites. Generally there were more sites in the south westerly portion of the study area in Survey One and north eastern portion in Survey Two. The movement of ichthyoplankton elements from the usual spawning grounds of many fish species in the south western part of the study area towards the Strait of Dover and coastal nursery grounds (Grioche *et al.*, 1997b), following phytoplankton production, is therefore reflected, although to a lesser degree. The movement illustrates the value of reassessing areas necessary for protection at different times of the year, when the ichthyoplankton groups are at different stages of development.

It is unknown whether abundance data can select units with an increased probability of population persistence, or whether choosing a smaller number of units (more efficient in terms of area or cost) would be a good general strategy for reserve design. Networks smaller in area could be focused on good quality but possibly small areas, where local extinction risk could be higher (Cabeza & Moilanen, 2001). These uncertainties have fewer implications for marine environments where populations are less likely to be isolated and more able to migrate. It is hoped that methods using

abundance data can provide a better guide than presence / absence data, although provisions to increase clustering of the units in the network may improve the practicalities of the PA networks.

7.4 Overlap of minimum sets for abundance data at two sampling times

The coincidence between Surveys One and Two was calculated, as they are comparable due to their identical spatial extent. Survey Three, although overlapping, does not share the same spatial extent, so was not included in the comparison.

7.4.1 Methods

ArcView shapefiles containing the minimum sets for Surveys One and Two 10% abundance target (identified in Section 7.3) were used with the 'select by theme' command in ArcView to select all the areas that are common to both 10% target minimum sets. A Chi-squared test was used to calculate whether the coincidence was more than would be expected by random selections.

7.4.2 Results

The coincidence between 10% abundance conservation target networks for Surveys One and Two was 27 selection units, which is significantly more than would be expected by a random selection (p<0.000).

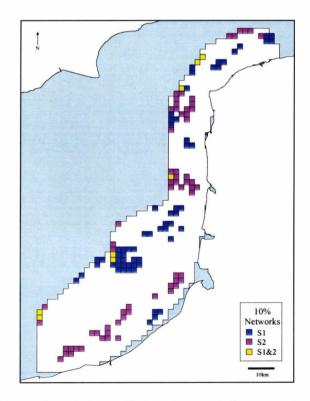


Figure 7.9 Coincidence between 10% minimum sets for Surveys One and Two.

7.4.3 Discussion

Coincidence is higher than would be expected by chance, but lower than those between hotspot sets in the same surveys. This might be expected, if interpretation of the north easterly movement of many of the ichthyoplankton from spawning grounds towards nursery grounds in the month between the surveys is valid.

7.5 Summary

- A 'summed rarity' complimentarity selection algorithm was used with abundance data to
 identify the top ranking 10% of areas that would protect the highest proportion of
 ichthyoplankton. Networks of selection units were clustered and showed a similar
 distribution to the networks of hotspots identified previously.
- Minimum sets of selection units were identified to satisfy conservation targets of 10%, 20% and 50% of abundance. The proportion of units necessary to satisfy the 10% conservation target ranged from 7.0% to 7.9% between surveys. The 20% target required 14.4% to 15.9% of the selection units and 38.3% to 40.9% of the units were required for the 50% target.

Chapter 8: Identifying MPA Networks in the Dover Strait Using Ichthyoplankton Surrogates

8.1 Introduction

PA networks represent biodiversity, but the methods by which biodiversity can be measured in both a meaningful and a practical way are highly debated and difficult to achieve. Ecological processes that support biodiversity need to be represented in reserves, but are also poorly known and understood (Conroy & Noon, 1996). Biodiversity is organised hierarchically from the molecular, genetic and character level within populations, to the functioning ecosystem level. Genes and taxa represent the products of evolution over the past 3.5 billion years, therefore containing different combinations of shared and novel genetic systems (Humphries *et al.*, 1995). The complexity of biodiversity, the fact that inventories for only about 1.4 to 1.8 million of the estimated 5 to 15 million extant species have been produced (see Humphries *et al.*, 1995) and the urgent need for action to better manage and protect it, means that surrogates for character diversity must be used to measure biodiversity (e.g. Faith & Walker, 1996), especially when differences between areas need to be evaluated for processes such as conservation planning. The most frequently used surrogates include sub-sets of species, assemblages and habitats.

Biodiversity databases that exist, on which analysis and selection of representative reserve networks must be based, are often inadequate or patchy due to the time-consuming and costly nature of collecting such information (Balmford & Gaston, 1999; Margules & Pressey, 2000; Polasky *et al.*, 2000). It has been estimated that ocean research costs approximately \$10,000-\$25,000 per typical research day (Wright, 2000). The ichthyoplankton database used in this study is unusual for its completeness of spatial and quantitative information. The samples in the ichthyoplankton database were collected, identified and counted by trained personnel. This constitutes an extremely time consuming and costly task. If good surrogates could be identified, they may not replace these sampling techniques, but could be a complimentary measure to facilitate assessment and hence protect biodiversity. Furthermore, problems associated with different taxonomic, methodological and sampling criteria employed by different authorities and the resulting problems of database capabilities, could also be lessened.

Many surrogates have been suggested, including higher taxa (Gaston & Blackburn 1995; Andersen, 1995; Balmford *et al.*, 1996a; 1996b; Williams *et al.*, 1997; Balmford *et al.*, 2000), different or indicator taxa (Beccaloni & Gaston, 1995; Gaston & Blackburn, 1995; Caro & O'Doharty 1999;

Flather *et al.*, 1997), various forms of environmental variables (Belbin, 1993; Franklin, 1993; Kirkpatrick & Brown, 1994; Gaston & Blackburn, 1995; Faith & Walker, 1996; Wessels *et al.*, 1999; Fairbanks & Benn, 2000; Fairbanks *et al.*, 2001), habitats (Ward *et al.*, 1999) and taxa assemblages (Ward *et al.*, 1999; Fairbanks *et al.*, 2001).

Due to the hierarchical nature of biodiversity, it is believed that any approach concentrating solely on one level is less able to represent biodiversity (Fairbanks *et al*, 2000). The most tested surrogate, however, is that of indicator taxa i.e. a different taxa or group of taxa that are more easily (or previously) sampled. Many tests of taxa surrogates adopted a spatial approach by comparing taxonomic groups for their degree of spatial coincidence in several types of hotspots. Many found minor correspondence, suggesting that locations selected for one taxonomic group will not capture features in other taxonomic groups (Prendergast *et al.*, 1993; Saetersdal *et al.*, 1993; Flather *et al.*, 1997; Dobson *et al.*, 1997; Reid, 1998). When PA networks selected using complimentarity were tested by spatial coincidence, limited coincidence was also found (van Jaarsveld *et al.*, 1998). Other analyses have tested the number of biodiversity elements in other taxonomic groups incidentally covered by hotspots (Prendergast *et al.*, 1993) and reserve networks selected by complimentarity (Ryti, 1992; Csuti *et al.*, 1997; Howard *et al.*, 1998; Pharo *et al.*, 2000; Reyers *et al.*, 2000). This method of comparison offers a more realistic reflection of the ability of surrogate taxa to represent other taxa, rather than spatial coincidence.

Studies in Uganda showed that those reserves selected just for butterflies or birds included the same percentage of all species as those selected to protect all species (Howard *et al.*, 1998). Studies that measure the incidental coverages of networks suggest that some surrogate taxa may prove useful when selecting reserve networks and that initial analysis by coincidence may have been over pessimistic (Reyers *et al.*, 2000; Rodrigues *et al.*, 1999). It has been suggested, however, that in Uganda surrogate groups may have performed well due to the heterogeneous environment in which each taxon exhibits similar biogeographical patterns across the country (Howard *et al.*, 1998; Balmford, 1998). Marine surrogate taxa tested in Australia showed that although there was only 54% spatial coincidence of locations selected for each macroalgae and mollusc indicator groups, 95% of all the rocky shore species sampled were included within the selected sets (Gladstone, 2002).

Higher taxa were found to be a good predictor of species richness across the Americas (Gaston & Blackburn, 1995). The higher taxa approach has therefore also been suggested as a surrogate for biodiversity when selecting reserve networks (Williams *et al.*, 1997; Gaston & Blackburn 1995; Balmford, 2000). It could be a more effective level at which to prioritise biodiversity conservation than species, as more taxonomically distinct groups are protected (Vane-Wright *et al.*, 1991; 1996a;

1996b; Rodrigues & Gaston, 2002b). Important limitations concern the way tests on the effectiveness of higher taxonomic classification, when selecting PA networks, have been conducted (Andersen, 1995; Balmford *et al.*, 1996b). Analyses have concentrated on large and / or widely-spread sampling units, unlike candidate areas for practical PA networks. Nearly all studies have examined the extent of correspondence in the richness of areas measured at different taxonomic levels, whereas PA networks consist of complimentary sites very different from each other. Methods for testing the effectiveness of the higher taxon approach should, in a similar way to methods to assess indicator taxa, include calculations of how well networks selected using genera or families capture lower taxa, rather than the spatial coincidence (Reyers *et al.*, 2000; Balmford, 1996a).

Few studies have tested potential marine surrogates, reflecting the limited application of systematic reserve selection procedures in this environment (Pressey & McNeill, 1996). Ward *et al.* (1999) analysed the selection of MPAs using habitats and species assemblages as surrogates for marine biological diversity. They found that PA networks chosen using fish or invertebrate assemblages for lower levels of protection (10% or 20%) were good at coincidentally protecting all available taxa. Habitats were also good surrogates when selecting networks to represent higher proportions of biodiversity (> 40%). As with terrestrial habitats, different results on the effectiveness of surrogates may be attributable to differences in methodological details, scales, and biogeographical histories of the regions tested.

Despite the fact that surrogates lose biological detail and complexity, they have to be accepted for the foreseeable future. Methods should be adopted for optimising the use of available and emerging knowledge from new surveys (Margules & Pressey, 2000). The choice of surrogate will depend on several factors. These include type of data available and the resources available for modelling and new data collection. In many situations the only spatially consistent information available is on higher-order surrogates such as vegetation types and environmental classes (Margules & Pressey, 2000).

In the present study, methodologies are tested for PA selection based on ichthyoplankton data. This has been well sampled in a relatively small area over three sampling surveys. Such quality of data is not often available, so this research tested methods that could be applied in other, less data rich areas. The methodologies are advocated for PA selection in both terrestrial and marine environments. The surrogates tested with these data are not suggested as surrogates for marine biodiversity, only for ichthyoplankton, as the extent to which ichthyoplankton can be an effective surrogate for marine biodiversity as a whole is unknown. It is suggested that the methodologies,

however, can be applied to situations where the surrogates used as the units for selection are representative of a wider range of biodiversity.

The following sections describe the surrogates identified and their preparation for inclusion in the GIS database for PA selection analysis. Section 8.2 is an explanation of the assemblages identified within the study area that were tested as surrogates. Section 8.3 is a description of the formulation of seascapes as surrogates for ichthyoplankton and section 8.4 is a description of the classification of the ichthyoplankton to species level without discriminating between levels of development. Section 8.5 is a description of the analysis using commercial fish species ichthyoplankton as a surrogate for all ichthyoplankton in the study area. Section 8.6 is an outline of the analysis to quantify the effectiveness and efficiency of the ichthyoplankton surrogates to identify MPA networks. The chapter is summarised in section 8.7.

8.2 Ichthyoplankton assemblages

Species assemblages have been considered good surrogates for biodiversity, because it was often thought that those species that occur together in time and space in a particular habitat, are more representative of biodiversity than the number of species present (Vanderklift *et al.*, 1998). Ordination techniques enabling simultaneous examination of species distribution and their relationship to environmental parameters have been used to identify assemblages and assess the indicator properties of a wide array of organisms (Kremen, 1992). Higher levels in the biological hierarchy, such as species assemblages may have advantages as surrogates as they could integrate more of the ecological processes that contribute to the maintenance of ecosystem function. This issue is still debated (Margules & Pressey, 2000). Ichthyoplankton assemblages identified for the current dataset were used to test their appropriateness as a surrogate for ichthyoplankton abundance.

8.2.1 Methods

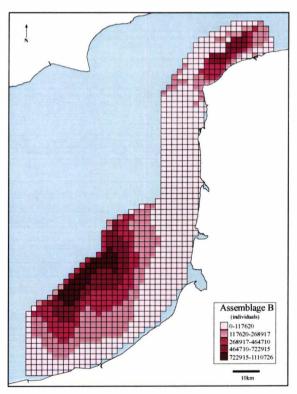
Ichthyoplankton assemblages were identified by Grioche *et al.* (see Grioche *et al.*, 1999b for full methodological details). In survey one, three main groups of assemblages were noted. The first group, assemblage A, was present in most of the offshore area in the eastern English Channel. The second group, assemblage B, was found offshore to the south of the Canche estuary. The third group, assemblage C, was the most coastal assemblage, close to the estuaries. All three assemblages, however, exhibited abundances offshore from Picarde Bay. In survey two, two main assemblage groups were identified, which were further split into five assemblages. Assemblage D contained older larvae. Assemblage E comprised younger ichthyoplankton except for two elements (stages of development). Assemblage D1 was localised in the coastal and offshore area off Dieppe

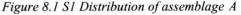
and the Opale coast. Assemblage D2 were transition larvae which were mainly coastal. Assemblage E were mostly located offshore in the south of Picarde Bay and near the Strait of Dover. E3 assemblage was found off the Somme Estuary and E2, the most extensive, was present over much of the eastern Channel, both coastal and offshore (Figures 8.1 to 8.8).

The MS Excel spreadsheet containing abundances per selection unit were used to calculate the abundance of all the ichthyoplankton within each assemblage. The values of abundance for each individual ichthyoplankton element were summed according to their assemblage groups. These values were imported into MS Excel spreadsheets for inclusion in the selection analysis.

8.2.2 Results

Three assemblage groups were collated and mapped in survey one, and five in survey two (Grioche *et al.*, 1999b). Their distributions are shown in Figure 8.1 to Figure 8.8.





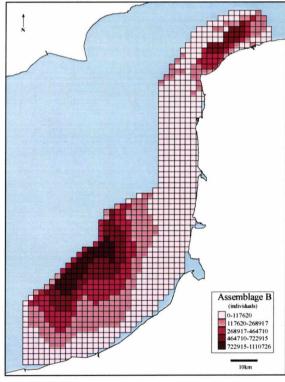


Figure 8.2 S1 Distribution of assemblage B

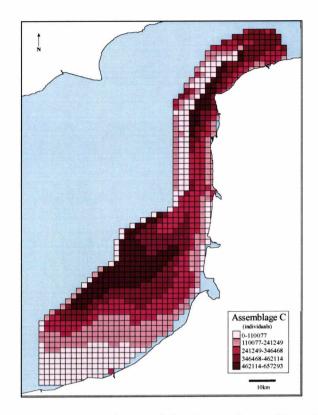


Figure 8.3 S1 Distribution of abundance of assemblage C

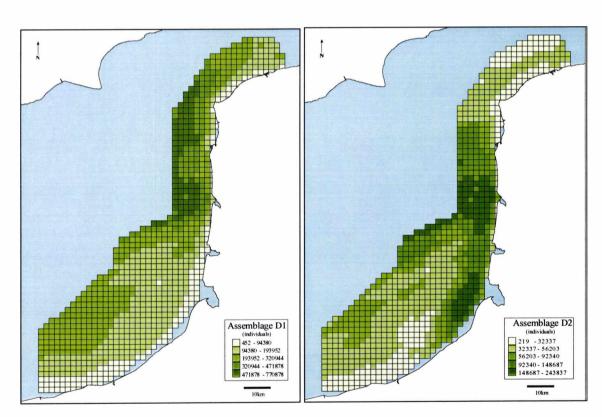


Figure 8.4 S2 Distribution of abundance of assemblage D1

Figure 8.5 S2 Distribution of abundance of assemblage D2

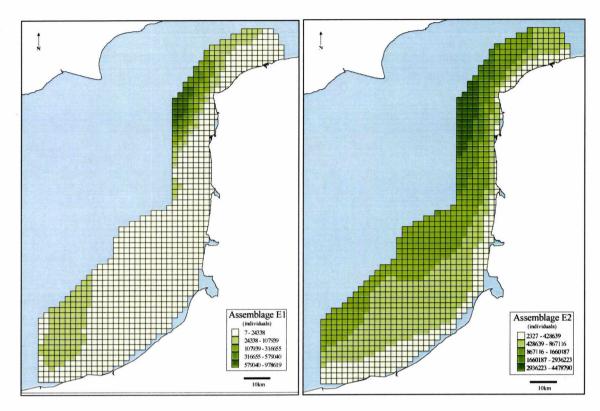


Figure 8.6 S2 Distribution of abundance of assemblage E1

Figure 8.7 S2 Distribution of abundance of assemblage E2

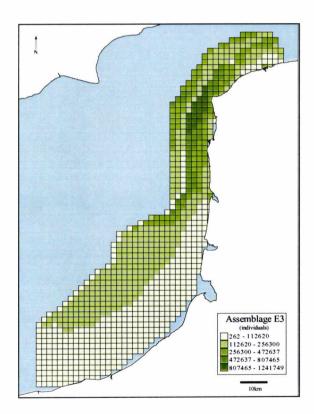


Figure 8.8 S2 Distribution of abundance of assemblage E3

8.2.3 Discussion

The distributions of assemblages in each of the three surveys was used to select MPA networks. The coincidental coverage of all ichthyoplankton identified in each survey is described in section 8.6.3.

8.3 Seascapes

Recognition that environmental and physical attributes drive biological systems implies that such attributes, together with available biological data, could be useful surrogates (Wessels, 1999; Laut et al., 1975 see Brunckhorst & Bridgewater, 1994; Faith & Walker, 1996; Pressey et al., 2000; Seymour et al., 2001). Ray & McCormick-Ray (1994) suggest that environmental attributes offer the most practical biodiversity surrogate for both scientific and management purposes, as comprehensive inventories of species, genetics, or populations are difficult if not impossible to secure. Environmental variables are relatively easy to assess and much less costly to measure than information on species distributions. Franklin (1993) suggests that approaches at land and seascape level are the only way to conserve the overwhelming mass of existing biodiversity. PA selection based on environmental variables aims to represent the variation in biodiversity found in an area on the basis of their correlation (Ward et al, 1999; Belbin, 1993; Nicholls & Margules, 1993; Faith & Walker, 1996).

It has been emphasised that the relationship between the environmental variables to be used and the biodiversity elements to be protected should be demonstrated (Bedward *et al.* 1992; Pressey, 1994). Environmental variables are suggested due to the efficiency of climatic variables to model the distribution of a range of species in terrestrial ecosystems (Belbin, 1993). Environmental data are known to model the distribution of marine fish species (Swartzman *et al.*, 1992; Maravelias *et al.*, 2000; Welch *et al.*, 1995; Maravelias and Reid, 1997; Swartzman *et al.*, 1994; Swartzman, 1997; Maravelias, 1999; Horne & Campana, 1989), so have the possibility to perform equally well as a surrogate for ichthyoplankton diversity in the marine environment.

Problems especially associated with the use of environmental data include the assumption that the underlying data are accurate. Many climatic variables are created by interpolating from very few data points, or by deriving one set of information from another. Other problems include those considered for using any data in a system such as GIS. These include that of the age of the data and the scale at which is was collected (Estes & Mooneyhan, 1994). Any errors are compounded when data are combined (Lunetta *et al.*, 1991).

Many types of environmental surrogates have been used; landscapes (Fairbanks & Benn, 2000), climatic variables (Belbin, 1993), land systems (recurring patterns of landform, soil and vegetation) (Pressey & Tully, 1994), environments (Margules *et al.*, 1994), landform-vegetation classes (Awimbo *et al.*, 1996) and environmental domains (Bedward *et al.*, 1992). Land facets used to select PAs were found to be effective at representing bird and dung beetle species but only over a small area using fine scale abiotic data (Wessels *et al.*, 1999). Other studies, however, have found less encouraging results (Kirkpatrick & Brown, 1994; Wright *et al.*, 1998). Environmental surrogates therefore need testing for their effectiveness when used to select PAs.

To enhance persistence of populations in a PA network, the retention of underlying biodiversity patterns and processes is important (Fairbanks *et al.*, 2000). These are extremely difficult to measure and to ensure their protection. Environmental surrogates may allow the representation of processes that drive biological diversity in the marine ecosystem. They may therefore also offer increased probability of long-term persistence. They are often more easily reassessed than biological surveys, which may be important due to climate change. Environmental variables were used to construct seascapes and tested for their effectiveness at selecting PA networks that would coincidentally protect ichthyoplankton abundance.

8.3.1 Methods

Methods described in Fairbanks *et al.* (2000) were utilised to create seascapes based on environmental variables collected during the field surveys. Several parameters were monitored and their data collected during the surveys. Only those collected on all three surveys were utilised to create seascapes in combination with bathymetry.

Environmental variable coverages created from the interpolated field survey measurements (described in Chapter Three) were clipped to the study area using 'grid analyst' extension to ArcView. Null value pixels were converted to zero using 'grid machine' extension in ArcView, to allow stretching when imported into Idrisi. Following such import, the coverages were stretched to values ranging from 0 to 255. This enabled the variation of each variable to be on the same scale, allowing comparison across the environmental variables.

The portions of the coverages outside the study area were assigned values during the stretching process. These were removed (the pixels were reclassed as zero) using the 'overlay' command in Idrisi. The variable coverages were then converted to byte binary format and entered into a PCA analysis. This method produces a coverage of the main component explaining most of the variation in the constituent variables. The coverages were then exported from Idrisi into ArcView using the

'export to ArcRaster' conversion format. Categories of the seascapes were calculated using Jenks optimisation method (the 'natural breaks' method used in ArcView). Jenks optimisation minimizes the sum of the variance within each of the classes while maintaining the heterogeneity among the classes, and finds groupings and patterns inherent in the data (Dent, 1990 and Slocum, 1999 in Harries, 1999).

A new coverage was created for each survey containing pixel values reclassed into the seascape categories. The selection unit vector grid was overlaid on the seascape coverages and the areas of each category within the units calculated using the 'tabulate areas' option in ArcView. The calculations were exported in a dbase table and imported into MS Excel spreadsheets for inclusion in the PA selection analysis.

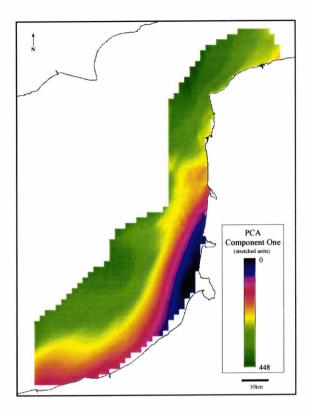
8.3.2 Results

The following table indicates the variation explained by the first component for each of the PCAs carried out for each of the three surveys.

Survey	Proportion of the variation explained in component 1
One	86.7%
Two	87.1%
Three	92.6%

Table 8.1 Environmental variation explained by PCA analysis

The first component of Survey One PCA analysis is shown in Figure 8.9, the first component of Survey Two PCA analysis is shown in Figure 8.10 and the first component of Survey Three PCA analysis is shown in Figure 8.11. Seascape categories calculated for Survey One are shown in Figure 8.12, those calculated for Survey Two are shown in Figure 8.13 and those calculated for Survey Three are shown in Figure 8.14.



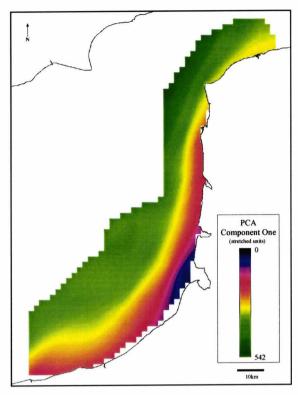


Figure 8.9 S1 Component 1

Figure 8.10 S2 Component 1

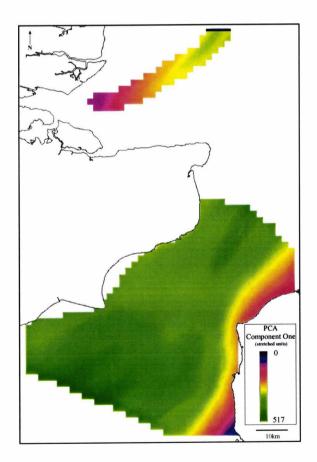
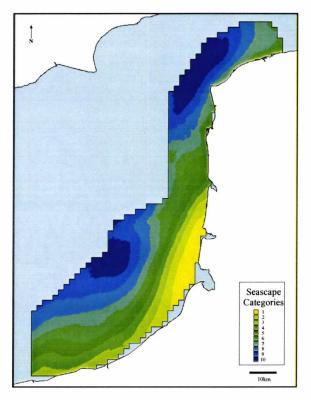


Figure 8.11 S3 Component 1



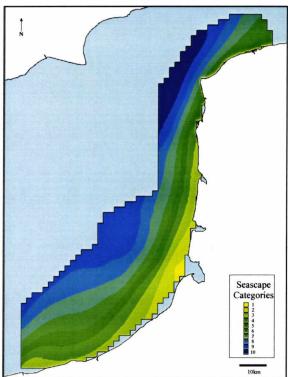


Figure 8.12 S1 Natural breaks seascape categories.

Figure 8.13 S2 Natural breaks seascape categories.

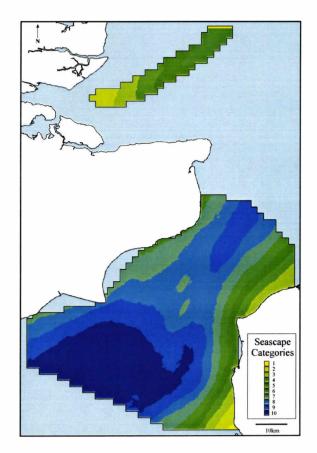


Figure 8.14 S3 Natural breaks seascape categories.

Many of the seascape categories lie in groups parallel to the coast. This possibly reflects the high environmental gradients between the coastal waters and the offshore waters. These show slightly different positions in the three surveys (Figure 8.12, Figure 8.13 and Figure 8.14).

8.3.3 Discussion

The seascape categories represent different waters occurring in the three surveys. These reflect changes in all the environmental variables, and indicate water of different origin. The coverages were used to identify MPA networks representing conservation targets of each seascape category. These were tested for coincidental representation of ichthyoplankton abundance to identify the appropriateness of seascapes, derived from environmental data, to represent ichthyoplankton (section 8.6.2).

8.4 Higher taxa

The use of higher taxa categories as surrogates for species has been suggested when mapping the worlds biological diversity (Williams *et al.*, 1997). This would have obvious benefits, in the context of limited financial and human resources, for survey efficiency. It is believed that it is not currently possible to comprehensively inventory all areas at a species level (Vanderklift *et al.*, 1998). Costs may be reduced if the ichthyoplankton were identified to a higher taxonomic level than species developmental stage (Fox *et al.*, 1999; Balmford *et al.*, 1996a). As discussed, higher taxa have also been suggested as a surrogate for biodiversity when selecting reserve networks (Gaston & Blackburn 1995; Balmford *et al.*, 2000). Higher taxon classification was used to select MPA networks for the three proportional conservation targets in three surveys, and the level of protection coincidentally provided to the ichthyoplankton elements assessed.

8.4.1 Methods

The methods to create the spreadsheets containing the ichthyoplankton element (developmental stage) abundances were described previously (Chapter Four). Abundances for each species per selection unit were calculated by summing all elements within one species in the spreadsheet.

8.4.2 Results

Many species were recorded at more than one developmental stage. Manipulating the data set in this way therefore reduced the numbers of elements (Table 8.2).

Survey	Resulting number of species
One	15
Two	20
Three	22

Table 8.2 Reduction in the dataset to lower taxonomic resolution.

The revised abundances were stored in an MS Excel spreadsheet.

8.4.3 Discussion

The abundances of each species were used to identify MPA networks using proportional conservation targets. Its appropriateness as a surrogate for developmental stages is analysed in Section 8.6.

8.5 Commercial species

It is possible that information on commercial species is more readily available. It is also possible that greater political interest in conservation is generated with the use of information concerning only species commercially fished.

8.5.1 Methods

The commercial status of each species found within the sampling areas was determined using various sources and advice (Doody *et al.*, 1993; European Commission, 2000; Grotte, Walkey and Koubbi pers comm.). Abundances of ichthyoplankton that are not target species for commercial fisheries were removed from the data set and the revised abundances exported to a new MS Excel spreadsheet.

8.5.2 Results

Survey	Commercial Species	% of original
One	25 of 36	69.4
Two	31 of 50	62.0
Three	29 of 48	60.4

Table 8.3 Reduction in the dataset by removing non-commercial species

The subset of data that are commercial species is 69.4% of the original number of ichthyoplankton in survey one, 62.0% in survey two and 60.4% in survey three.

8.5.3 Discussion

The datasets contain approximately 60% commercially exploited fish species, therefore the dataset was not reduced greatly in any of the three sampling surveys. The effect of the reduction is analysed (Section 8.6.4) by using the revised commercial species abundance to select MPA networks. The networks were tested for their incidental spatial coverage of all ichthyoplankton abundance.

8.6 Effectiveness and efficiency of surrogates to identify MPA networks at proportional conservation targets

To test effectiveness of the surrogates, the location and number of cells within minimum sets for the three conservation targets was identified using the summed rarity algorithm. The quantity of the ichthyoplankton abundance incidentally covered by each of the surrogate MPA networks was calculated to determine how well these networks might protect ichthyoplankton.

8.6.1 Methods

Each biodiversity surrogate was used to identify MPA network minimum sets using the summed rarity algorithm in the java selection software. The two input tables were created for each surrogate, detailing the quantity of each surrogate element within the selection units. The program was then used to identify the minimum sets of units necessary to satisfy three proportional conservation targets of 10%, 20% and 50%.

The selected MPA networks were mapped in ArcView using the methods described for previous analyses. This involved converting the report produced by the selection software into a format suitable for import into ArcView, using MS Word and MS Excel. The resulting dbase table was joined to the attributes table of the shapefile containing the polygons representing the selection units. The units selected for MPA networks could then be identified.

The spreadsheet containing ichthyoplankton element abundance was imported into ArcView, to allow calculation of the protection provided by each surrogate using the method described for previous analyses. This process was repeated for each proportional conservation target, and for each surrogate.

For each selected network, conservation target and surrogate, rows in the shapefile corresponding to selection units within a selected network minimum set were selected. This was achieved by performing a query with the 'query builder' in ArcView. Using 'first table tools' extension in ArcView, these rows were exported into MS Excel, where the abundances of the ichthyoplankton elements were summed. The proportion of abundance protected by each selected network was calculated by dividing the total abundance of each element in the minimum set by the total found in the study site. The percentage of all elements protected to the relevant conservation target was calculated by listing the proportions of each element protected by the minimum set in question. The 'IF' command in MS Excel was used to list a one or zero according to whether the target had been reached or not. These were then summed. The mean, minimum and maximum protection given to the ichthyoplankton elements were also calculated. The process was repeated for each conservation target, for each survey and for each biodiversity surrogate (45 in total).

The data did not meet the assumptions of a parametric distribution so a Kruskall-Wallis test was used to determine whether the surrogates protected significantly different proportions of the ichthyoplankton elements to the conservation target.

A one-way anova was used to determine whether using different surrogates gave significantly different efficiencies with the summed rarity algorithm. Arcsine and square root transformations were applied to the proportions of the selection units required for each conservation target, so that they met the assumptions of normality that this test requires.

The following section is divided into several subsections. Each deals with a separate biodiversity surrogate.

8.6.2 Seascape surrogate

4.6.2.1 Results

Survey	Cons	Cells	Abundance	Mean	Minimum	Max
	Target	needed (%)	protected to	protection	protection	protection
			conservation	(%)	(%)	(%)
			target (%)			
One	10%	10.4	44.4	11.3	0.0	24.4
	20%	20.1	47.2	21.2	0.3	38.4
	50%	49.4	41.7	47.0	28.2	67.4
Two	10%	10.6	60.0	11.7	1.0	42.1
	20%	20.6	42.0	19.0	2.9	43.4
	50%	50.4	32.0	45.7	12.1	70.8
Three	10%	10.3	66.7	15.4	0.0	49.9
	20%	20.2	70.8	26.6	0.2	54.7
	50%	49.5	77.1	53.4	11.5	75.7

Table 8.4 Coverage of abundance levels provided by seascape surrogate

Seascape surrogate provided cover for 44.4% to 77.1% of ichthyoplankton elements to the appropriate abundance proportional target. Using a 10% seascape surrogate target, a mean protection of 11.3% to 15.4% was provided to the ichthyoplankton elements.

Selection units identified as MPA networks for conservation targets of 10%, 20% and 50% are illustrated in Figures 8.15 to 8.17.

Percentage of each ichthyoplankton element protected by 10% seascape surrogate is illustrated in Figures 8.18 to 8.20. Figures 8.21 to 8.23 illustrate the frequency of protection provided to the ichthyoplankton elements by 10% seascape elements and are included for clarity of surrogate effectiveness (the red line indicates the 10% conservation target).

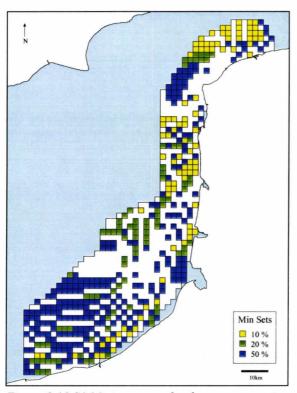


Figure 8.15 S1 Minimum sets for three conservation targets of seascape biodiversity surrogate.

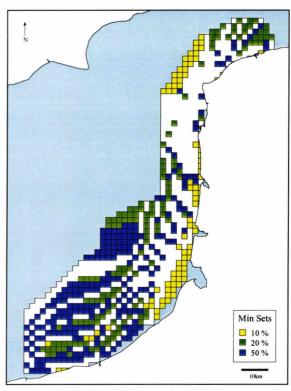


Figure 8.16 S2 Minimum sets for three conservation targets of seascape biodiversity surrogate.

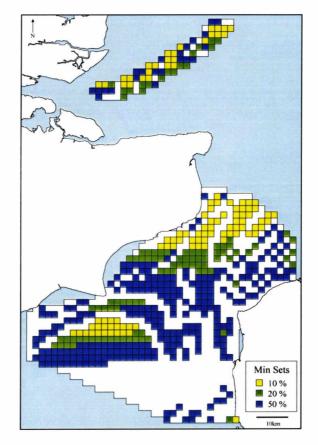


Figure 8.17 S3 Minimum sets for three conservation targets of seascape biodiversity surrogate

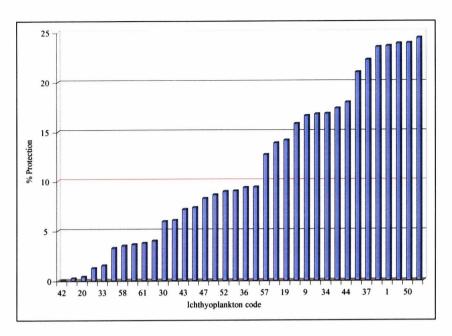


Figure 8.18 S1 Percentage of each ichthyoplankton protected based on 10% target of seascapes

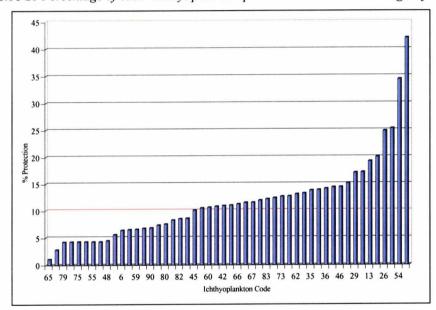


Figure 8.19 S2 Percentage of each ichthyoplankton protected based on 10% target of seascapes

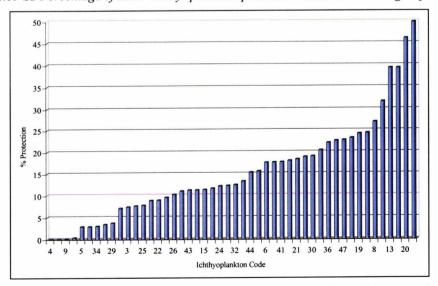
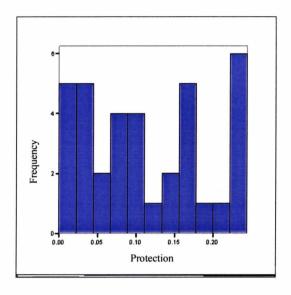


Figure 8.20 S3 Percentage of each ichthyoplankton protected based on 10% target of seascapes



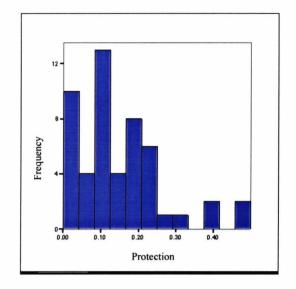


Figure 8.21 S1 Frequency of protection provided to abundance by seascapes

Figure 8.22 S2 Frequency of protection provided to abundance by seascapes

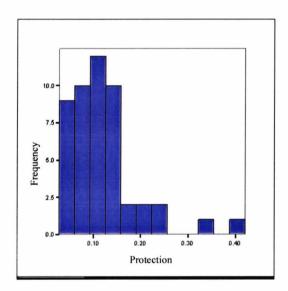


Figure 8.23 S3 Frequency of protection provided to abundance by seascapes

4.6.2.2 Discussion

The proportion of ichthyoplankton elements adequately protected to the conservation target ranged between surveys from a minimum of 32.0% to a maximum of 77.8%. The mean protection was higher than that provided by proportional area during survey three, but was not so high in surveys one and two. The 50% conservation target produces an unusual pattern, forming curved lines of units (Figure 8.15, Figure 8.16 and Figure 8.17). This is not apparent with lower levels of protection. A possible source of this pattern is the underlying pattern of the seascape categories corresponding to the different layers of water, especially in survey three.

8.6.3 Ichthyoplankton assemblages surrogate

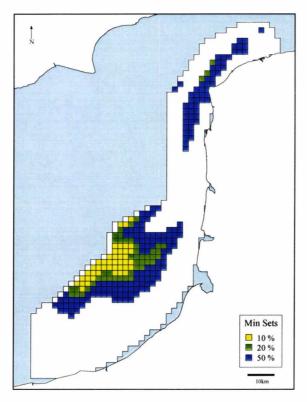
4.6.3.1 Results

Survey	Cons	Cells needed (%)	Abundance protected to conservation	Mean protection (%)	Minimum protection (%)	Max protection (%)
			target (%)			
One	10%	4.7	41.7	10.8	0.0	43.6
	20%	9.8	41.7	19.1	0.0	62.8
	50%	28.6	44.2	44.2	0.0	89.1
Two	10%	4.8	62.0	15.2	0.0	36.2
	20%	10.0	62.0	28.7	0.0	62.0
	50%	29.5	64.0	57.0	0.0	99.8

Table 8.5 Coverage of abundance levels provided by assemblage surrogate

Assemblage surrogate provided cover for 44.2% to 64.0% of ichthyoplankton elements to the appropriate abundance proportional conservation target. Using a 10% assemblage conservation target, a mean protection of 10.8% to 15.2% was provided to the ichthyoplankton elements. Minimum sets of selection units identified for MPA networks for conservation targets of 10%, 20% and 50% are illustrated in Figures 8.24 to 8.26.

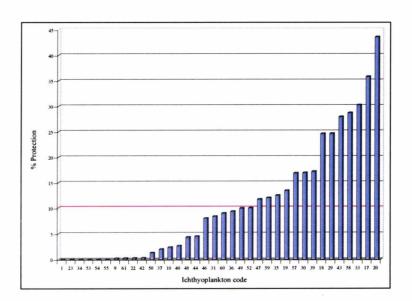
Percentage of each ichthyoplankton element protected by 10% assemblage surrogate is illustrated in Figures 8.26 to 8.27. Figures 8.28 to 8.29 illustrate the frequency of protection provided to the ichthyoplankton elements by 10% assemblage conservation target and are included for clarity of surrogate effectiveness.



Min Sets
10 %
20 %
50 %

Figure 8.24 S1 Minimum sets for three conservation targets using assemblage surrogate.

Figure 8.25 S2 Minimum sets for three conservation targets using assemblage surrogate.



Figure~8.26~S1~Percentage~of~each~ich thy op lankton~protected,~based~on~10%~assemblages~target

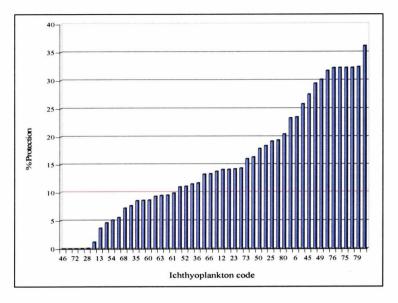


Figure 8.27 S2 Percentage of each ichthyoplankton protected, based on 10% assemblage target

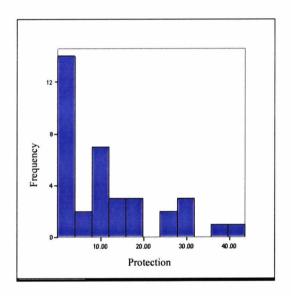


Figure 8.28 S1 Frequency of protection levels for all ichthyoplankton based on 10% assemblage target

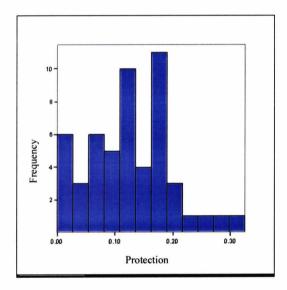


Figure 8.29 S2 Frequency of protection levels for all ichthyoplankton based on 10% assemblage target

4.6.3.2 Discussion

Assemblages were the most efficient surrogates. This may be because only 3 assemblages were identified. For all data, however, the minimum protection was 0.0% i.e. some elements had no protection at all, and general protection was low. The proportion protected to the required target was also lower than all other surrogates.

8.6.4 Commercial Species Surrogate

4.6.4.1 Results

Survey	Cons	Cells	Abundance	Mean	Minimum	Max
	target	needed (%)	protected to	protection	protection	protection
			conservation	(%)	(%)	(%)
			target (%)			
One	10%	7.2	83.3	14.0	3.2	28.0
	20%	14.5	83.3	26.7	11.7	53.3
	50%	37.9	83.3	57.4	32.0	86.5
Two	10%	7.6	86.0	16.3	0.2	42.0
	20%	15.5	88.0	30.7	0.0	75.8
	50%	36.5	86.0	62.5	14.4	95.4
Three	10%	6.6	85.4	13.1	4.0	27.8
	20%	13.4	81.3	25.1	9.2	51.7
	50%	35.9	83.3	55.3	34.0	84.5

Table 8.6 Coverage of abundance levels provided by commercial species surrogate

Commercial species surrogate provided cover for 81.3% to 88.0% of ichthyoplankton elements to the appropriate abundance proportional conservation target. Using a 10% commercial species target, a mean protection of 13.1% to 16.3% was provided to the ichthyoplankton elements. Minimum sets of selection units identified for MPA networks for conservation targets of 10%, 20% and 50% are illustrated in Figures 8.30 to 8.32.

Percentages of each ichthyoplankton element protected by 10% commercial species surrogate is illustrated in Figures 8.33 to 8.35. Figures 8.36 to 8.38 illustrate the frequency of protection provided to the ichthyoplankton elements by 10% commercial species target and are included for clarity of surrogate effectiveness.

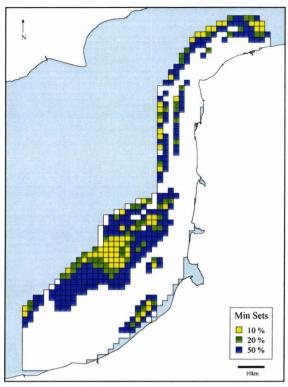


Figure 8.30 S1 Minimum sets for three conservation targets based on commercial fish surrogate.

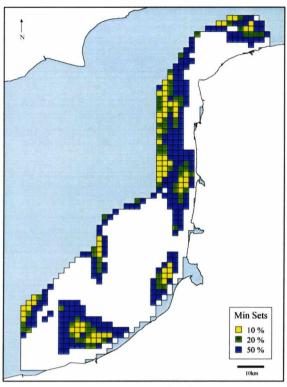


Figure 8.31 S2 Minimum sets for three conservation targets based on commercial fish surrogate.

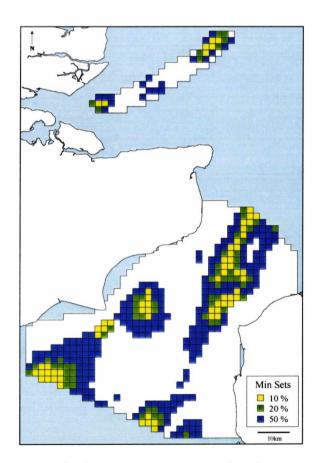


Figure 8.32 S3 Minimum sets for three conservation targets based on commercial fish surrogate.

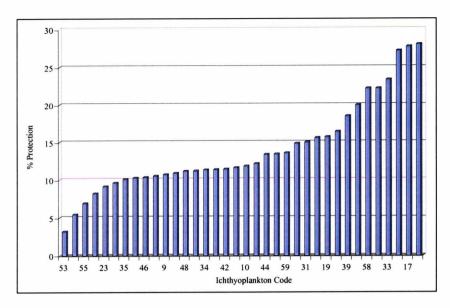


Figure 8.33 S1 Percentage of each ichthyoplankton protected, based on 10% target of commercial species

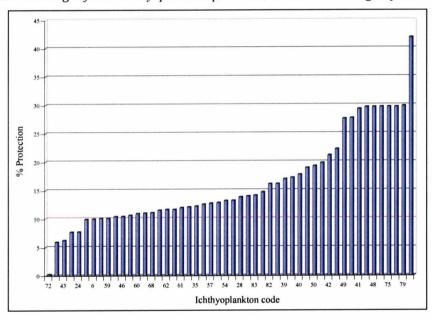


Figure 8.34 S2 Percentage of each ichthyoplankton protected, based on 10% target of commercial species

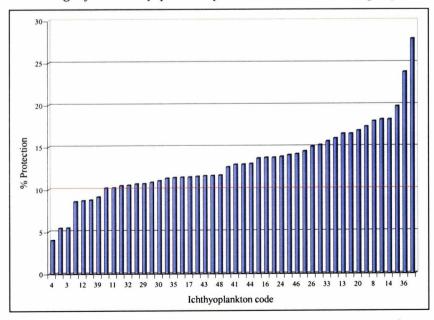


Figure 8.35 S3 Percentage of each ichthyoplankton protected, based on 10% target of commercial species

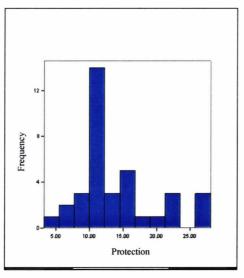


Figure 8.36 S1 Frequency of protection levels provided to abundance by commercial species.

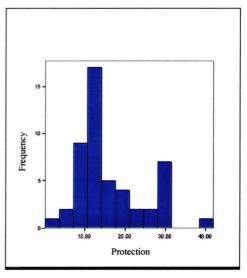


Figure 8.37 S2 Frequency of protection levels provided to abundance by commercial species

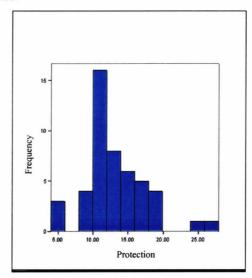


Figure 8.38 S3 Frequency of protection levels provided to abundance by commercial species.

4.6.4.2 Discussion

The identified network of selection units were very similarly situated to those identified for all the species. Commercial species surrogate provided good coverage to all species ichthyoplankton, possibly due to the fact that it is a substantial subset of the original database. Nonetheless, coverage was good. Therefore if data were only to be available on commercial species, the coverage of non-target ichthyoplankton species could be adequate for MPA network selection.

8.6.5 Higher taxa surrogate

4.6.5.1 Results

Survey	Target	Cells needed (%)	Abundance protected to conservation target (%)	Mean protection (%)	Minimum protection (%)	Max protection (%)
One	10%	6.0	72.2	14.2	0.0	35.5
	20%	12.4	75.0	25.7	0.0	53.3
	50%	34.7	77.9	56.8	0.0	89.3
Two	10%	5.6	64.0	22.5	0.0	65.6
	20%	11.6	36.0	11.2	0.0	65.6
	50%	35.0	72.0	62.9	5.83	100.0
Three	10%	6.0	75.0	13.6	0	34.3
	20%	12.4	77.1	25.5	2.3	57.5
	50%	31.2	72.9	54.7	14.7	86.1

Table 8.7 Coverage of abundance levels provided by higher taxa(species level)

Higher taxa (species level) surrogate provided cover for 36.0% to 77.9% of ichthyoplankton elements to the appropriate abundance proportional conservation target. Using 10% higher taxa conservation target, a mean protection of 13.6% to 22.5% was provided to the ichthyoplankton elements, and 64.0% to 75.0% of the elements were protected to 10% abundance target. Minimum sets of selection units identified for MPA networks for conservation targets of 10%, 20% and 50% are illustrated in Figures 8.39 to 8.41.

Percentages of each ichthyoplankton element protected by 10% species taxonomic resolution surrogate is illustrated in Figures 8.42 to 8.44. Figures 8.45 to 8.47 illustrate the frequency of protection provided to the ichthyoplankton elements by 10% species taxonomic resolution target and are included for clarity of surrogate effectiveness.

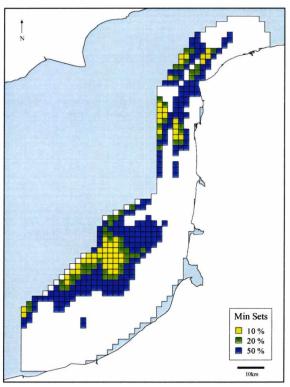


Figure 8.39 S1 Minimum sets for three conservation targets based on higher taxa surrogate.

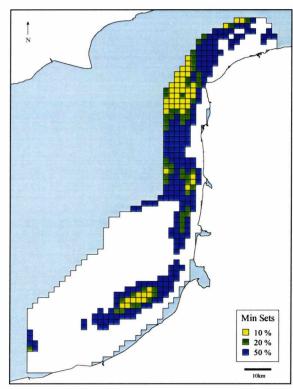


Figure 8.40 S2 Minimum sets for three conservation targets based on higher taxa surrogate.

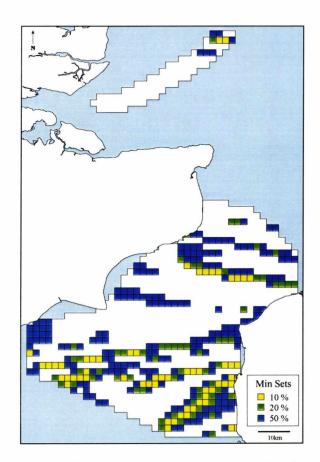


Figure 8.41 S3 Minimum sets for three conservation targets based on higher taxa surrogate.

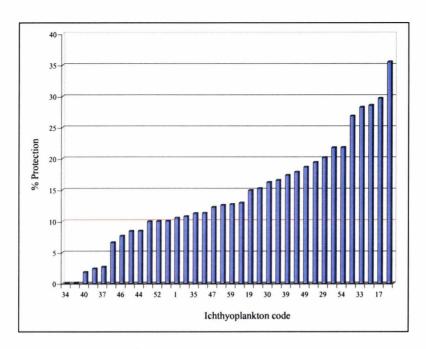


Figure 8.42 S1 Percentage of each ichthyoplankton protected, based on 10% higher taxa target

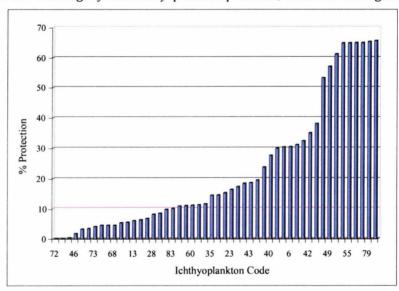


Figure 8.43 S2 Percentage of each ichthyoplankton protected, based on 10% higher taxa target

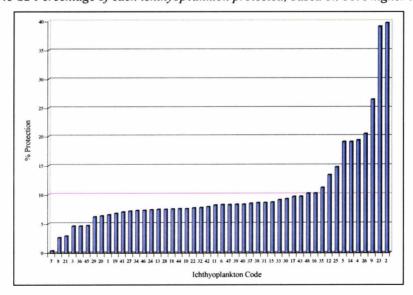


Figure 8.44 S3 Percentage of each ichthyoplankton protected, based on 10% higher taxa target

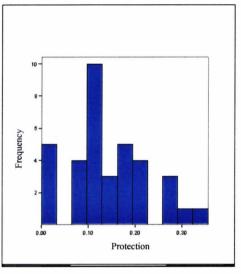


Figure 8.45 S1 Frequency of protection provided by higher taxa surrogate to ichthyoplankton abundance

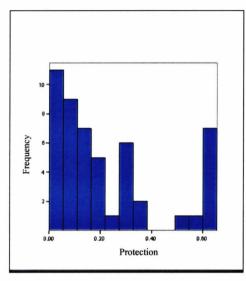


Figure 8.46 S2 Frequency of protection provided by higher taxa surrogate to ichthyoplankton abundance

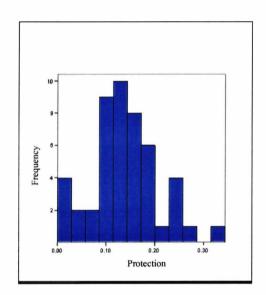


Figure 8.47 S3 Frequency of protection provided by higher taxa surrogate to ichthyoplankton abundance 4.6.5.2 Discussion

Reducing the dataset to species level taxonomic resolution performed well for the number of ichthyoplankton elements it protected to the required proportion. The minimum protection, however, was low, implying that elements not protected to the required level have very low levels of protection. The proportion of ichthyoplankton elements protected to the conservation target was substantial however, ranging from 64.0% to 77.0% for the 10% target. The minimum sets in survey three for 50% target was an unusual pattern of units making up rows of units across the water in an east west direction (Figure 8.41).

8.6.6 Overall surrogate results and discussion

The proportion of ichthyoplankton elements protected by each surrogate to the conservation target is the most appropriate measure of the success of the surrogate. The surrogates protected a significantly different proportion of the biodiversity elements ($X^2=25.028$, df=4, p<0.000). Assemblages protected 41.2% to 64.0% of the ichthyoplankton abundance to the target, seascapes protected 32.0% to 77.1% of the targets, higher taxa (species) protected 36.0% to 77.9% (although 64% to 75% for the 10% target) and commercial fish protected 81.3% to 88.0%.

Commercial species surrogate protected the highest proportion of ichthyoplankton elements to the required target. This might be anticipated since the dataset was a fairly large subset of the original data. The surrogates showed similar ranges of the proportions protected to the conservation target. The range was quite wide, showing a low level of consistency within the surrogates.

The surrogates tested were significantly different in their efficiency (surrogate df=4, f= 73.863 p<0.000 and target df= 1, f=2413.807, p<0.000, adjusted R Squared = 0.985, Figure 8.48 and Figure 8.49). Seascape was the least efficient surrogate. The most efficient surrogate was assemblages. These, however, provided the second worst protection.

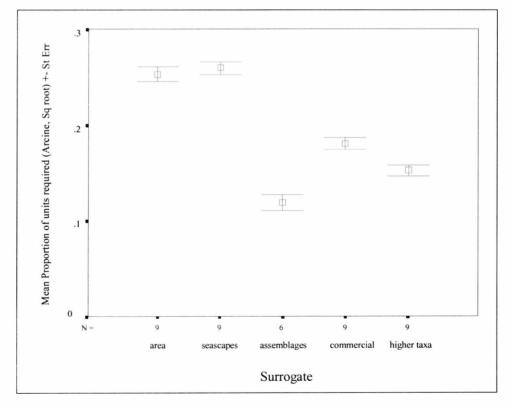


Figure 8.48 Mean number of units required for minimum sets using surrogates (adjusted for target).

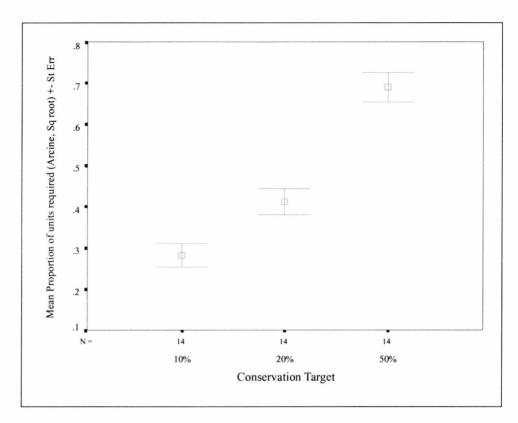


Figure 8.49 Mean number of units required for minimum sets for three conservation targets (adjusted for surrogate).

Previously the best groups of species for protecting other taxa have been found to be the more speciose groups such as plants. Ryti (1992) found they were the least efficient and had 10 or 20 times more species than some of the other taxa tested. In this study, commercial fish species may have provided good protection in a similar way because this surrogate was a large subset of all the species. Ryti suggests from the terrestrial results, that rather than an application of plants as PA selection surrogates, a better approach would be to collect preliminary distribution data for a number of taxa in the potential reserve network and use these preliminary data to define the focal taxon.

8.7 Summary

- Several surrogates for ichthyoplankton diversity were identified in an attempt to find solutions to the problems resulting from the paucity of biodiversity datasets to identify PA networks.
- Surrogates identified for ichthyoplankton diversity were; seascapes, higher taxa, ichthyoplankton assemblages and a subset containing only commercial species. They were mapped using GIS.
- The surrogates were used to identify minimum sets of MPA networks and their effectiveness analysed by calculating the proportion of ichthyoplankton abundance coincidently included by spatial coincidence.
- Using seascapes as a surrogate, the proportions of ichthyoplankton elements protected to the required proportional conservation targets ranged from 32.0% to 77.1%. Ichthyoplankton assemblage surrogate protected 41.7% to 64.0%, higher taxa protected 36.0% to 77.8% and commercial species protected 81.3% to 88.0% of the ichthyoplankton elements to the required conservation target. The proportions were significantly different from each other (X²=25.028, df=4, p<0.000).
- Surrogates showed significantly different efficiencies when used to select MPA networks using a 'summed rarity' algorithm (df=4, f= 73.863 p<0.000). Ichthyoplankton assemblage surrogate required 4.7% to 4.8% of the selection units for the 10% conservation target. Higher taxa required 5.6% to 6.0% of the units, commercial species required 6.6% to 7.6% of the units and seascape surrogate required 10.3% to 10.6% of the units for the 10% conservation target.

Chapter 9: Selecting MPA Networks with a Preference for Adjacent Units

9.1 Introduction

The need to consider persistence of biodiversity in PA network design has often been highlighted (Bedward *et al.*, 1992; Margules *et al.*, 1994; Pressey, 1996; Kiester *et al.*, 1996; Nicholls, 1998; Myers, 1998; Williams, 1998b; Margules & Pressey, 2000; Rodrigues *et al.*, 2000a; Cabeza & Moilanen, 2001). Local persistence has been addressed in several ways. It has been suggested that persistence may be more likely if algorithms are used to choose PA networks using abundance data, either prioritising selection units with the largest populations or high population density (Rodrigues *et al.*, 2000a; Nicholls, 1998). Kiester *et al.*, (1996) recommend selecting units larger than a particular area when there is a known size limit for the presence of a species. One suggestion requiring an unrealistic amount of high quality data (Cabeza & Moilanen, 2001) is to analyse population viability for each species (Bedward *et al.*, 1992).

To encourage persistence on a regional level, Williams & Araujo (2000) proposed combining the probability of local persistence (among local selection units) until the required level of persistence probability is reached for each species. It may, however, be difficult to obtain the probabilities of persistence (Cabeza & Moilanen, 2001). The protection of ecosystem pattern and processes has often been the aim of PA selection in order to increase the persistence of populations. It has proven extremely difficult to measure or map these ecosystem driving forces and thus ensure their inclusion in a system of PAs. Environmental factors in the form of seascapes were used as surrogates to select PA networks in the hope that they reflect elements of process and pattern (Chapter Eight).

The theory of island biogeography implies that to promote the persistence of populations, connected or close reserves are better than unconnected ones and that larger reserves are better than smaller ones (MacArthur & Wilson, 1963). Many PA selection procedures have neglected the inclusion of measures to consider spatial location or connectivity of selection units in their design (Possingham *et al*, 2000b; McDonnell *et al*, *in press*; Briers, 2002). As discussed in Chapter One, many impacts of PA boundaries and connectedness in the terrestrial realm has less significance in the marine environment due to its higher level of connectivity and traversable boundaries. Edge effects do operate, however, and need consideration. Most species rely on some degree of dispersal. Colonisation of new sites benefits from connectivity between sites. This is especially important when the distances between sites are large in comparison with the organisms. It is also significant when substrates are moved or destroyed between PA units. There is also increasing

evidence that species with pelagic larval stages may not disperse as widely as originally believed (Roberts *et al.*, 2002). Compact reserves could also have economic benefits due to the cost of management scaling more closely with the boundary length than with the reserve area (Possingham *et al.*, 2000a).

The few selection algorithms that have been designed to choose areas that are close together choose a selection unit nearest to previously selected units if a tie between units is encountered (Nicholls & Margules, 1993; Lombard *et al.*, 1997). Other methods aim to minimize a linear combination of reserve network area and boundary length with an option to select sites separated by a minimum distance, using simulated annealing to identify a number of solutions (Possingham *et al.*, 2000a).

The size of selection units in the present study was partly chosen with the principle that a single reserve would best be made up of at least several selection units (Chapter Three). Large selection units that require little or no amalgamation to produce viable reserves, inevitably over represent some features and result in lower efficiencies to achieve the same conservation target than smaller units (Bedward *et al.*, 1992). The networks of units selected using the 'summed rarity' algorithm with proportional targets were shown to be more scattered than those selected using all of three hotspot methods. This is especially apparent at the 10% conservation targets. The summed rarity algorithm was therefore adapted to include a procedure for increasing the selection of units clustered into larger areas. This is described in section 9.2 below. The algorithm uses a coefficient to alter the degree of clustering, allowing the effect to be adjusted according to the dataset.

9.2 Incorporating adjacency into the selection of units for a protected area network.

The summed rarity algorithm, used to select complimentarity PA networks described previously, was modified to preferentially select sites adjacent to those already selected (Fischer, 2001).

The method used to calculate an adjacency value is as follows:

$$w = (A * g/N)*v + v$$

N - number of neighbours under consideration (0,2,4,8)

g - number of neighbours that have already been selected

A - Adjacency coefficient

w - final weight of cell

v - initial value of cell (with no adjacency)

Thus if A is zero, adjacency has no effect. If A equals 1, the result is simply g/N. There are no positive or negative bounds for the value of A, so adjacency can be discouraged by using a negative coefficient. The coefficient can be modified until the level of adjacency between sites reaches a compromise between one large reserve and many small fragmented sites in the network. This process can form part of the interactive selection process undertaken by the panel of expert conservation planners. The effect of the coefficient on the units selected and the efficiency of the PA networks in terms of the area necessary for a 10% conservation target are described in the following section.

9.2.1 Methods

The algorithm was tested using several levels of the co-efficient to protect 10% of ichthyoplankton abundance. The reports detailing the results of each selection procedure were converted and imported into ArcView in the same way to the methods described previously. The coefficient was increased from one to one hundred and the resulting minimum set networks of selection units mapped.

9.2.2 Results

As the adjacency co-efficient was increased, clustering of the minimum sets increased as expected (Figure 9.1, Figure 9.2 and Figure 9.3). The coefficient was increased to a level which increased clustering to a point where the networks are elongated and the efficiency was greatly reduced. This was especially apparent in Survey Three (Table 9.1).

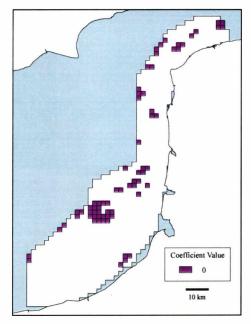


Figure 9.1 S1 10% Conservation target with the use of different levels of adjacency co-efficient (continued on following page)

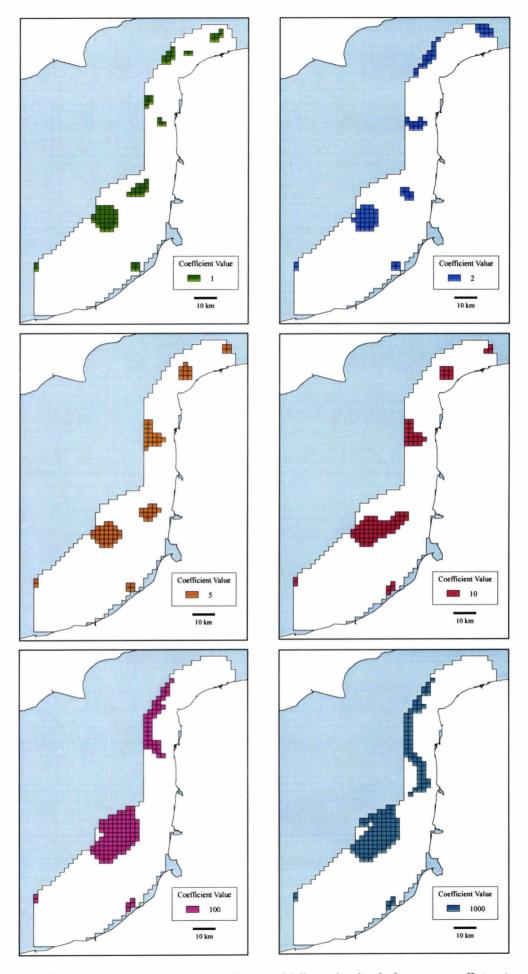


Figure 9.1 S1 10% Conservation target with the use of different levels of adjacency co-efficient(cont.)

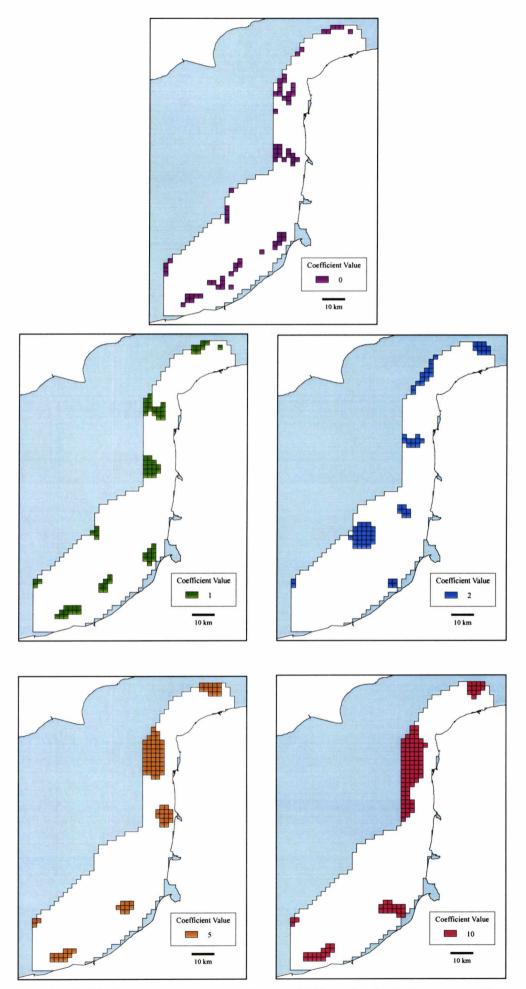


Figure 9.2 S2 10% Conservation target with the use of different levels of adjacency co-efficient

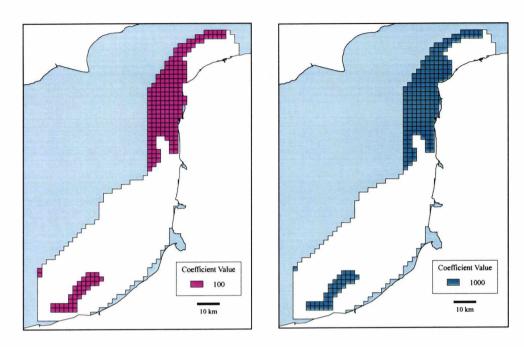


Figure 9.2 S2 10% Conservation target with the use of different levels of adjacency co-efficient (cont.)

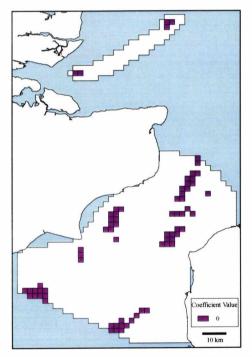


Figure 9.3 S3 10% Conservation target with the use of different levels of adjacency coefficient (continued on following page)

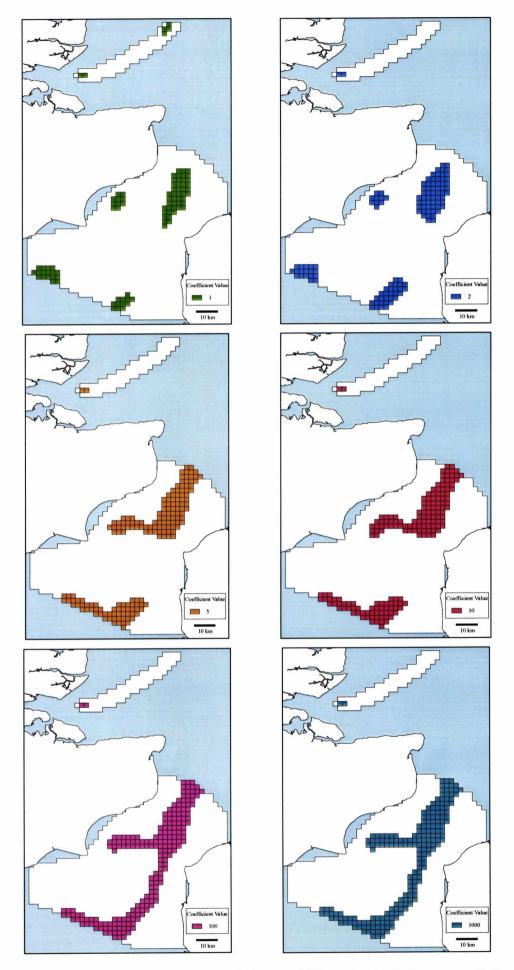


Figure 9.3 S3 10% Conservation target with the use of different levels of adjacency coefficient

The response of the data to the coefficient levels differs between the surveys. Survey Three requires an increase in the proportion of the units necessary to attain the conservation target at a lower level of coefficient. It then exhibits a more constant level for the higher levels of coefficient value. Survey Two requires a higher proportion of the units for the same conservation target and coefficient. The proportion of units necessary to attain the target in Survey One increases steadily, but to a lower level than Survey Two and slightly lower than Survey Three (Table 9.1). It can be seen that a considerable decrease in the fragmentation of the network can be produced with a relatively small decrease in efficiency (Figure 9.1, Figure 9.2, Figure 9.3 and Table 9.1). For example in survey one, a decrease in efficiency from requiring 7.62% of the units using no adjacency coefficient to requiring 8.16% of the units using of a coefficient of 2 (Table 9.1 and Figure 9.1). Survey Two clustering greatly benefits from the use of a coefficient of five, although the efficiency falls from requiring 7.95% of the units without consideration of adjacency to requiring 10.88%. A decrease in fragmentation, however, is observed with the use of a coefficient as low as one or two, with a decrease in efficiency from requiring 7.95% to 8.38% or 8.92% of the units respectively. Considerable decrease in fragmentation is seen in Survey Three with the use of a coefficient of one and two, reducing the efficiency from requiring 7.01% of the units without adjacency consideration, to 8.88% and 11.85% of the units with a coefficient of one and two, respectively (Table 9.1).

Survey	Coefficient Level									
	0	0 1 2 5 10 100 1000								
One	7.6	7.7	8.2	8.9	10.1	14.9	18.7			
Two	7.9	8.4	8.9	10.9	13.6	23.8	25.0			
Three	7.0	8.9	11.9	16.4	16.7	20.0	20.0			

Table 9.1 Efficiency of algorithm using different adjacency coefficients

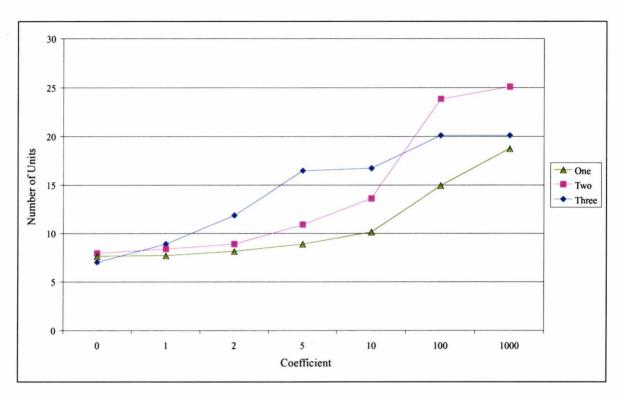


Figure 9.4 Effect of adjacency coefficient on efficiency

Efficiency decreased with increased adjacency coefficient as expected. The number of units selected increases at higher coefficient values than ten, although tested values were not increased linearly.

9.2.3 Discussion

Efficiency of the summed rarity selection algorithm is reduced by including the adjacency criteria (Nicholls & Margules, 1993; Possingham *et al.*, 2000a). There is a small difference in the response of data to the adjusted algorithm in different surveys. This highlights the need to test different scenarios with the data available for the situation being considered. The level of coefficient desirable for particular situations will need testing at the time of planning and integrated with other factors in the process. A large difference is seen in the effect of clustering at lower levels of the coefficient. This lessens with higher levels, due to the need for a much higher value necessary to force the selection of less suitable units. This was reflected in testing, by a non linear increase of coefficient test values. Interpretation of Figure 9.4 should be made accordingly. Subsequent versions of the algorithm will include the ability to incorporate a preference for adjacent sites at a reasonable level and then identify alternatives for single isolated units. This will reduce the need to force the selection of many compromised units.

There is loss of transparency due to the nature of the coefficient. This is disadvantageous for conservation planners especially when decisions need to be explicitly defended. Subjectivity is also introduced by decisions regarding the best level of the coefficient. Different conservation planning

situations, however, require different levels of prioritisation for connectivity. Conservation planners are able to explore a range of planning scenarios whilst still ensuring a minimum protection target for all biodiversity elements. Subsequent versions of the software will also calculate scores without addition of the original score in the final part of the procedure. This will not allow such a large range of effects, but will permit a linear relationship between the coefficient and the observed effects. It will also allow the ideal coefficient value to be identified more easily, as fine scale changes will be reduced.

Many factors are involved in planning decisions, some are independent of the biological database. Political, economic, other non-mathematical and non-biological factors may determine which of a range of solutions is the best to use (McDonnell *et al.*, *in press*). Briers (2002) comments that by also incorporating biological considerations, such as the importance of dispersal for persistence of populations, the practical utility of reserve selection algorithms may be improved. The costs in terms of efficiency would therefore be justified if the reserve network is more likely to support viable populations in the long term.

9.3 Summary

- The 'summed rarity' selection algorithm was modified to incorporate a preference to select
 units adjacent to those already selected when identifying PA networks. An adjacency
 coefficient was used to create the desired level of selection unit clustering.
- The level of clustering can be adjusted according to the planning situation and available data. Clustering effect can be incorporated in addition to the many non-biological factors involved in the decision process.

Chapter 10: Selecting MPA Networks Using Irreplaceability

10.1 Introduction

The concept of irreplaceability was formulated in response to needs to quantify the contribution of selection units both included and excluded from the selected PA network (Pressey, 1999b). The contribution of units can indicate optional replacements for selected units should they become unavailable and guide priority within the selected network. Irreplaceability is defined both as the potential contribution of any unit to a reservation goal and the extent to which the options for a representative reserve are lost if that unit is lost (Pressey, 1994). Information on the spatial pattern of optional conservation areas in a region, and the number of possible replacements for any particular unit, has obvious value in dealing with constraints on the location of new PA networks. A map of irreplaceability is a map of the options for achieving a desired outcome in planning new PAs or managing existing ones (Pressey, 1999b). The calculation of exact irreplaceability is currently intractable for most realistic datasets (the number of selection units and biodiversity elements that may be expected in a practical PA planning database) and conservation targets. The applications therefore rely on prediction of values (Ferrier *et al.*, 2000).

Areas of high irreplaceability can become nodes around which other units are preferentially chosen (Pressey *et al.*, 1994; Rebelo, 1994). This could encourage selected unit clustering. In some situations there may be many irreplaceable units that contain a varying number of unique elements. In response to this problem, an index known as 'summed irreplaceability' was designed. This is the sum of the irreplaceability of each element calculated separately (see Ferrier *et al.*, 2000). Irreplaceability methods facilitate an interactive planning process where planners can explore many scenarios according to differing economic and social pressures. It allows flexibility for negotiation among stakeholders and the organisation of inevitable compromises. It can also set priorities by indicating how easily conservation action or management zoning could be relocated if a particular unit were to become unavailable or have its natural values destroyed. Irreplaceability measures for area targets depend less on the frequency of a feature in a region than on whether an unit contains a small or large occurrence of an element relative to its target and relative to other occurrences in the region (Pressey, 1999b).

An interactive planning system (C-Plan, 2001) integrates irreplaceability selection algorithms with ArcView GIS. C-Plan was created at New South Wales National Parks and Wildlife Service, Australia (Pressey *et al.*, 1995). C-Plan has been developed through practical conservation applications. These include examples in New South Wales (Pressey, 1999b), Guyana (Richardson

& Funk 1999), South Africa, South America, the USA and Canada (Pressey 1999b) and is used here with kind permission.

C-Plan was used to calculate and map two measures of irreplaceability with the present dataset. They were derived from different ways of combining element irreplaceability values and provide complimentary information about selection units. The measures are calculated only from the elements in a unit that are still contributing to the conservation target (Cplan, 2001). The two measurements are 'site irreplaceability' and 'summed irreplaceability'. The C-Plan manual defines site irreplaceability as combining biodiversity elements irreplaceability values multiplicatively to produce an index for each unit, ranging from 0 to 1. A high value indicates that one or more features occurring in the unit will be reduced close to target, or below target, if the unit becomes unavailable for conservation. Low values indicate that the unit has many possible replacements for achieving conservation targets for the features it contains. The second measure, summed irreplaceability, is calculated by summing the element irreplaceability of all elements in that unit. Values can range from zero to a large number, perhaps 15, 20 or more, depending on the number of elements in the site. High values indicate that the site is important for achieving conservation targets for many features. Values much smaller than 1 indicate that the site is not important for any elements.

10.2 Site irreplaceability and summed irreplaceability scores

C-Plan was utilised to map selection unit irreplaceability and summed irreplaceability.

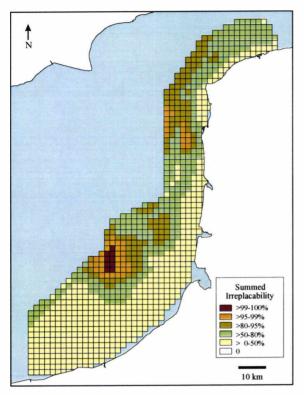
10.2.1 Methods

C-Plan (version 3.06) table editor was used to build a C-Plan database for the three surveys. The databases were created to hold information similar to those in the tables used for the 'summed rarity' algorithm described previously. Each is built from separate dbase tables and has the provision for including information on many aspects of the selection units. This includes cost, (for example loss to other activities such as timber or acquisition), area, tenure, conservation targets and any other information that may be necessary to include in order to allow as informed a decision process as possible. Many classifications of data were not available for the study site or not applicable to this research.

Site irreplaceability and summed irreplaceability were used to rank the selection units. C-Plan is linked to ArcView GIS, so allowed the display of the results directly.

10.2.2 Results

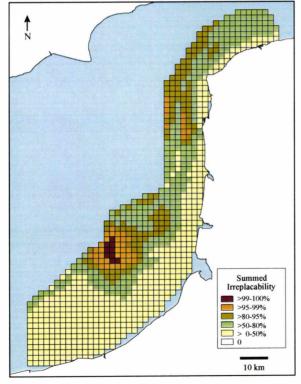
Site and summed irreplaceability scores gave similar overall patterns for proportional conservation targets (Figures 10.1 to 10.17) with finer discrimination between units using summed irreplaceability scores.

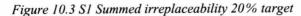


Site Irreplacability
| Itrreplacable | >0.8.<| >0.4.0.6 | >0.4.0.6 | >0.2.0.4 | >0.0.0.2 | 0 | 0 | | 0 | to km

Figure 10.1 S1 Summed irreplaceability 10% target

Figure 10.2 S1 Site irreplaceability 10% target





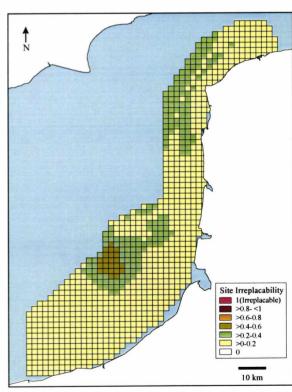


Figure 10.4 S1 Site irreplaceability 20% target

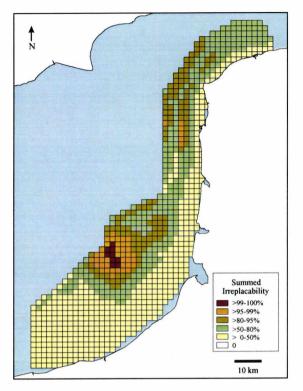
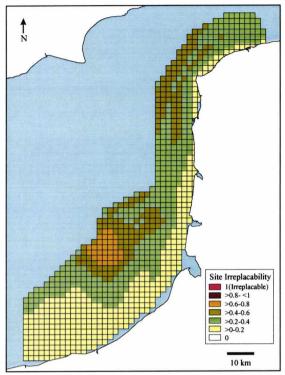


Figure 10.5 S1 Summed irreplaceability 50% target



Figure~10.6~S1~Site~irreplace ability~50%~target

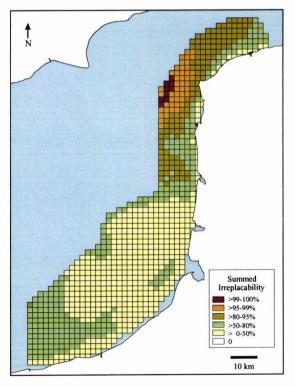
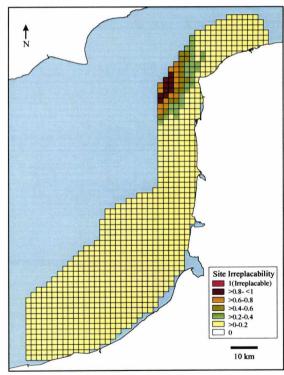


Figure 10.7 S2 Summed irreplaceability 10% target



Figure~10.8~S2~Site~irreplace ability~10%~target

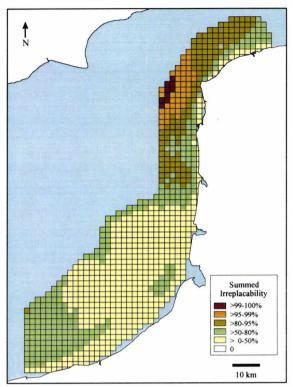


Figure 10.9 S2 Summed irreplaceability 20% target

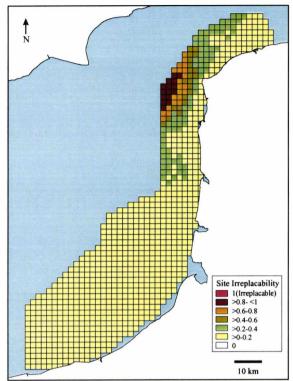


Figure 10.10 S2 Site irreplaceability 20% target

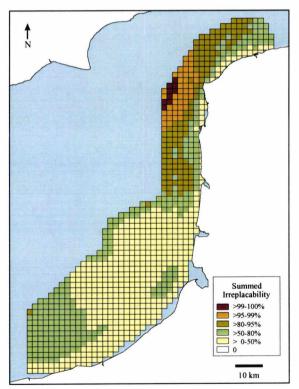


Figure 10.11 S2 Summed irreplaceability 50% target

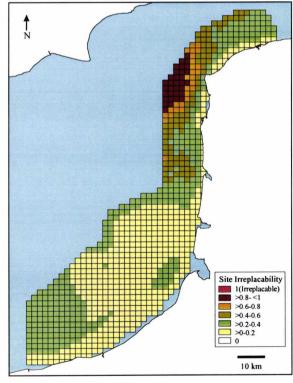


Figure 10.12 S2 Site irreplaceability 50% target

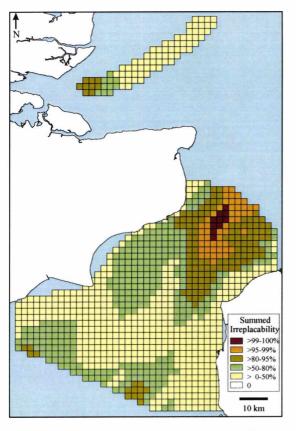


Figure 10.13 S3 Summed irreplaceability 10% target

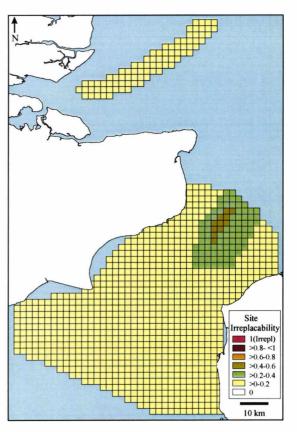


Figure 10.14 S3 Site irreplaceability 10% target

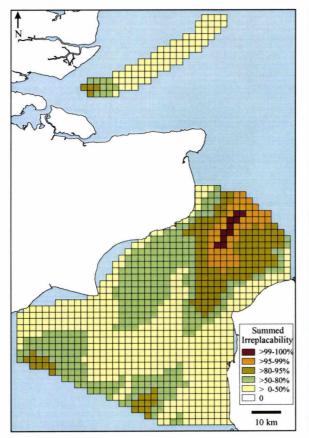


Figure 10.15 S3 Summed irreplaceability 20% target

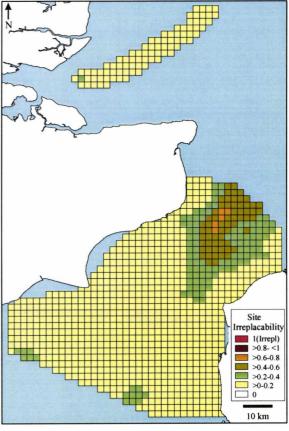


Figure 10.16 S3 Site irreplaceability 20% target

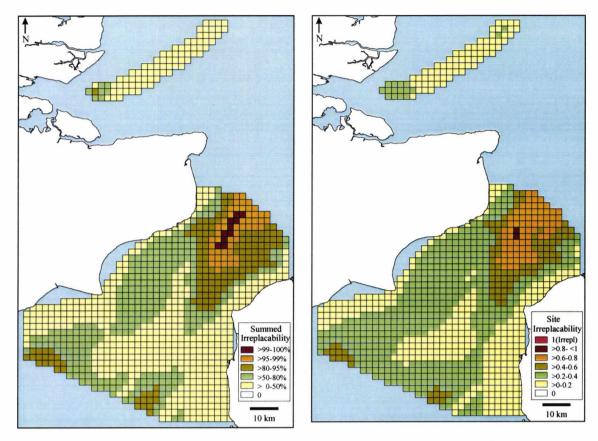


Figure 10.17 S3 Summed irreplaceability 50% target

Figure 10.18 S3 Site irreplaceability 50% target

10.2.3 Discussion

There were very few irreplaceable sites, so a very large number of combinations of units could be used. Summed irreplaceability scores provided more discrimination between the sites with similar site irreplaceability scores, as expected. This effect is more apparent at lower proportional conservation targets. Patterns of high irreplaceability show some similarities to the highest ranking areas from summed rarity analysis. More surprising is the similarity in positioning of the high irreplaceability scores and the hotspots. There are differences between the highly irreplaceable unit placement and the placement of the summed rarity units for the same proportional targets. The following analysis investigates the patterns of distribution of the networks of units selected for similar proportional conservation targets.

10.3 Minimum sets required for proportional conservation targets using site and summed irreplaceability

10.3.1 Methods

Two algorithms were defined and applied using C-Plan to select MPA networks of minimum sets required for proportional conservation targets in a similar way to summed rarity methods described previously. The two algorithms were based on site irreplaceability and summed irreplaceability as follows;

Site Irreplaceability (Algorithm One)

- Rule 1. Select the site with the highest site irreplaceability value (if there is a tie (>1 site) then go to Rule 2).
- **Rule 2.** Select a site with the highest summed irreplaceability value (if there is a tie then go to Rule 3).
- Rule 3. Select the first site in the list.

Start at rule one again and continue until the proportional conservation target has been met.

Summed Irreplaceability (Algorithm Two)

- **Rule 1.** Select a site with the highest summed irreplaceability value (if there is a tie then go to Rule 2).
- Rule 2. Select the first site in the list.

Start at rule one again and continue until the proportional conservation target has been met.

Minimum sets of selection units were identified for conservation targets of 10%, 20% and 50% of each ichthyoplankton element using both algorithms.

10.3.2 Results

Survey	Summed irreplaceability			Site irreplaceability then summed		
	10%	20%	50%	10%	20%	50%
One	7.4	15.7	48.3	7.4	15.6	39.4
Two	7.6	16.5	38.0	7.7	16.5	37.5
Three	7.0	14.4	38.1	7.0	14.7	38.0

Table 10.1 Efficiency of irreplaceability algorithms (% of units required)

The number of units required to protect 20% of ichthyoplankton elements is approximately double the number required for a 10% target. Most surveys required five times this number to satisfy a 50% target, but summed irreplaceability for Survey One required more units than expected (Table 10.1). Surveys one and three identified approximately double the number of units necessary for the 20% target than were identified for the 10% target. There were slightly more than double the units identified in Survey Two for the 20% target than for the 10% target.

The minimum sets identified as necessary for the 10% conservation target in Survey One are shown in Figure 10.19. The minimum sets required for the 10% conservation target in Survey Two are shown in Figure 10.20, and those required for the same target in Survey Three are shown in Figure 10.21.

The minimum sets required for the 20% conservation target in Survey One are illustrated in Figure 10.22, those required for Survey Two are shown in Figure 10.23 and those required for Survey Three are shown in Figure 10.24. The minimum sets required for the 50% target for Survey One are shown in Figure 10.25, those required for Survey Two are shown in Figure 10.26 and those required for Survey Three are shown in Figure 10.27.

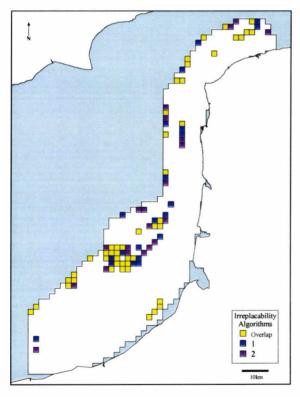


Figure 10.19 S1 Minimum sets identified using algorithms 1 &2, 10% target

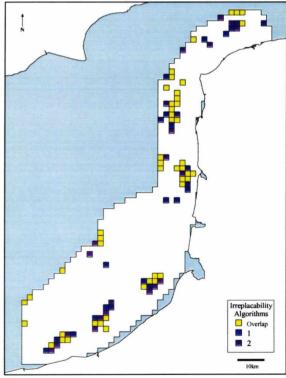


Figure 10.20 S2 Minimum sets identified using algorithms 1&2, 10% target

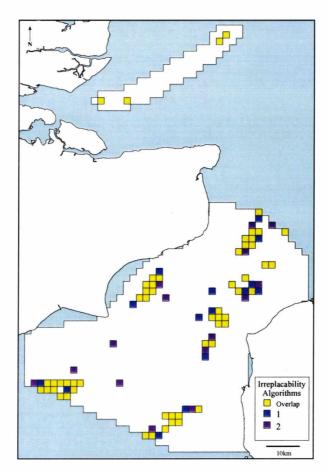


Figure 10.21 S3 Minimum sets identified using algorithms 1 &2, 10% target

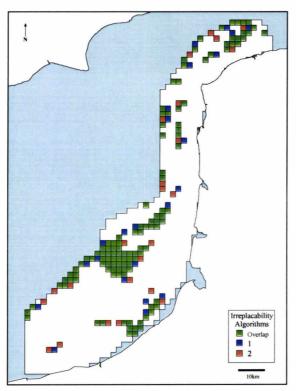


Figure 10.22 S1 Minimum sets identified using algorithms 1 &2, 20% target

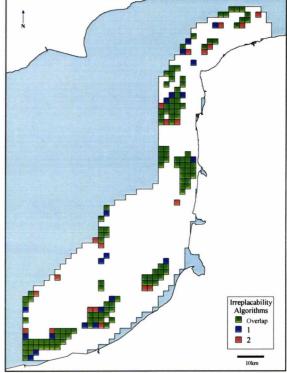


Figure 10.23 S2 Minimum sets identified using algorithms 1&2, 20% target

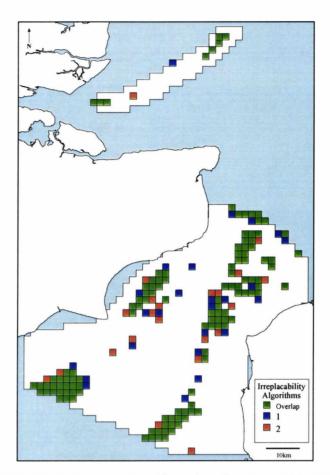


Figure 10.24 S3 Minimum sets identified using algorithms 1&2, 20% target

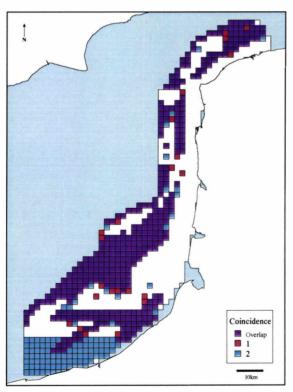


Figure 10.25 S1 Minimum sets identified using algorithms 1 &2, 50% target

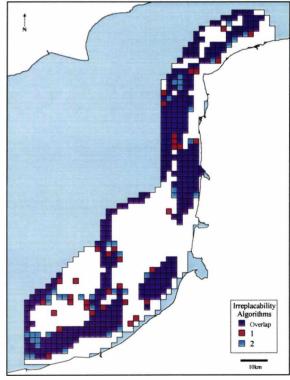


Figure 10.26 S2 Minimum sets identified using algorithms 1&2, 50% target

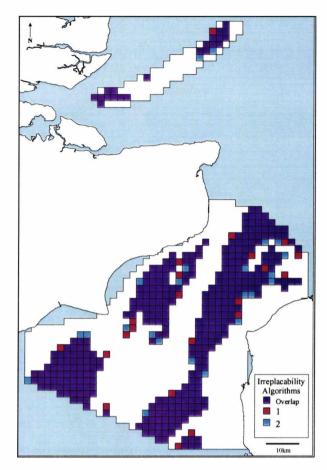


Figure 10.27 S3 Minimum sets identified using algorithms 1 &2, 50% target

10.3.3 Discussion

An unusually high number of units were identified using the summed irreplaceability algorithm in Survey One for the 50% conservation target. The same data and conservation target did not require a large number of units when using the site irreplaceability or summed rarity algorithms. Patterns in the underlying data do not indicate possible causes.

The selected networks were widely dispersed, although were more connected at the higher conservation targets as a result of the increased ratio of selected units to available units. This is similar to networks identified using the summed rarity algorithm and unlike networks identified using the hotspot approach.

10.4 Comparing MPA networks identified using three algorithms

10.4.1 Methods

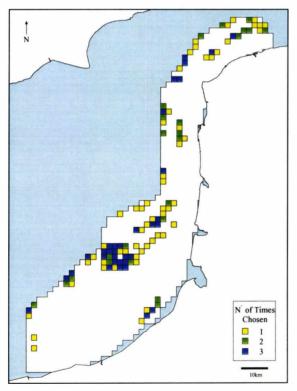
Networks identified by the two irreplaceability algorithms and the summed rarity algorithm were compared by mapping together using ArcView. Networks identified for the 10% target were chosen as this target is more realistic for immediate applications and allows a clearer view of the network overlap. This is due to the smaller ratio of selected units to available units. A set of

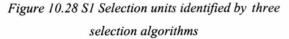
queries were performed on the shapefiles containing identified networks required for the 10% target for each survey using the 'query builder' in ArcView. The queries highlighted the rows corresponding to each network. These networks were exported to separate shapefiles. The shapefiles for all three algorithms for each survey were then 'unioned' using the 'geoprocessing wizard' in ArcView and a new column created in the attribute table to illustrate the identity of selection units identified by each algorithm.

The efficiencies of the three algorithms were compared using a univariate general linear model. Arcsine and square root transformations were applied to the proportions of the selection units required for each conservation target, so that they met the assumptions of the test.

10.4.2 Results

The number of times each unit, within the networks, was selected using the three algorithms is illustrated in Figure 10.28, Figure 10.29 and Figure 10.30. The three algorithms are site irreplaceability with summed irreplaceability tie breaker (algorithm one), summed irreplaceability (algorithm two) and summed rarity algorithm (algorithm three).





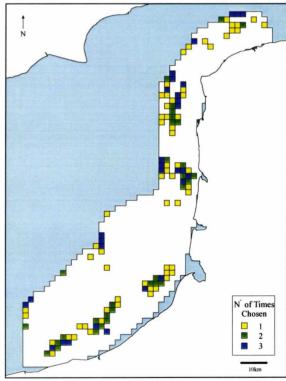


Figure 10.29 S2 Selection units identified by three selection algorithms

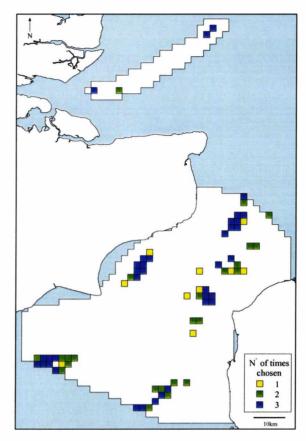


Figure 10.30 S3 Selection units identified by three selection algorithms

The selection units identified by the three algorithms are similarly distributed (Figure 10.28, Figure 10.29 and Figure 10.30). There is a slight concentration of selected units in the south western portion of the study area in Survey One and the units are more scattered in surveys two and three. Survey Two has slightly more units selected in the eastern part of the study area than Survey One. The units selected by all three algorithms in Survey Three are in the mid offshore waters and the far eastern and western ends of the Thames Estuary region of the study area.

The efficiencies of the three algorithms were not significantly different from each other (adjusted $R^2=0.98$, p>0.5).

10.4.3 Discussion

All three algorithms identified units in similar locations and showing similar patterns of clustering. The time taken for irreplaceability minimum set calculations is longer than that for the summed rarity algorithm, although both are acceptable for interactive scenario testing.

Similarities between both the efficiency and network patterns, identified using all three algorithms, indicates that the methods produce comparable results. The emphasis when using selection algorithms should perhaps therefore be placed not on finding the absolute minimum or exact minimum set, but on methods that provide transparency, efficiency, facilitate flexible interactive conservation planning, allow repeatability and the integration of non-biological factors.

10.5 Summary

- 'Site irreplaceability' and 'summed irreplaceability' for three conservation targets were mapped across the study area. Summed irreplaceability was found to provide finer discrimination between sites with similar site irreplaceability scores. This effect was more apparent at the lower proportional conservation target of 10%.
- Two irreplaceability algorithms were used to identify the minimum sets of selection units
 required for three proportional conservation targets. The algorithms used site
 irreplaceability, with a summed irreplaceability tie breaker, and summed irreplaceability.
 They produced similar efficiencies and similarly distributed MPA networks, in three
 surveys.
- The irreplaceability algorithms and 'summed rarity' algorithm results were compared and found to be similarly efficient to identify similar patterns of slightly different units. Three conservation targets were used in three surveys.
- It was concluded that the three algorithms gave comparable results. Qualities of transparency and flexibility should be considered rather than identifying absolute minimum sets when choosing methods to facilitate conservation planning. They should be explicit, repeatable, integrate non-biological factors, provide accountability and allow interactive scenario testing.

Chapter 11: Concluding Discussion

11.1 Introduction

This research has utilised a unique marine dataset to explore conservation planning methods. Distributions and abundance of the biodiversity elements were interpolated and mapped directly without the need for modelling based on supplementary data. It was found that the 'hotspot' approach to identify MPA networks protected too wide a proportion of both distributional area and abundance, and was consequently considered to be inefficient and unreliable. Complimentarity methods were found to be more efficient and reliable in providing protection for the complete range of ichthyoplankton elements. Proportional conservation targets (i.e. based on proportional area and proportions of abundance) were better at selecting networks of areas to protect abundance than multiple representations of presence / absence data. Using a 'summed rarity' complimentarity algorithm it was found that: 9.7% to 9.9% of the 4 km² selection units were required to protect 10% of the distribution of each ichthyoplankton element; and 7.0% to 7.9% of the selection units were required to protect 10% of the ichthyoplankton element abundance. Two algorithms using irreplaceability were found to identify similar networks of units for proportional abundance targets with similar efficiencies. The algorithm using site irreplaceability with a summed irreplaceability tie breaker identified 7.0% to 7.7% of the selection units required to satisfy the 10% conservation target and summed irreplaceability identified 7.0% to 7.6% of the units required to attain the same target.

Several surrogates for ichthyoplankton diversity were tested and found to protect 32.0% to 88.0% of the ichthyoplankton to the required conservation target. Each surrogate varied in the coverage provided to each ichthyoplankton element and between surveys. When 10% of each 'seascape' was protected, 44.5% to 66.7% of the ichthyoplankton elements were also protected to 10%. The 10% target of 'commercial species' protected 83.3% to 86.0% of the ichthyoplankton elements to the 10% target, 10% target of 'higher taxa' protected 64.0% to 75.0% of the elements to the target and 10% target of ichthyoplankton 'assemblages' protected 41.7% to 64.0% of ichthyoplankton elements to the 10% target.

It was found that incorporating measures to force the selection of clustered networks using summed rarity produced PA networks that were well connected. This technique may provide a more realistic opportunity to increase persistence with little loss in efficiency.

Several issues have been raised during the research and are discussed in the following sections. Section 11.2 is a discussion of possible improvements to the methods. Section 11.3 is a

description of the applicability of the methods to conservation planning in other areas. Section 11.5 outlines suggestions for promoting the wider adoption of selection algorithms into conservation planning.

11.2 Improvements to the methods

The ichthyoplankton database provided information on the abundance of biodiversity elements and included records of the absence of elements from samples. The data were collected using a systematic methodology and ichthyoplankton identified by trained and experienced personnel. The sampling, however, introduced some sampling bias. The abundances of the earlier and later stages of development may have been under-sampled (Koubbi pers comm.), but this is assumed to be continuous throughout the sampling. Subsequent versions of the summed rarity software will enable the conservation target of each biodiversity element to be set individually. The undersampled elements should have a higher conservation target to counteract such bias.

A wide range of factors are included in the PA planning process. Factors that could be incorporated into the algorithm are also wide ranging. It has been recognised that if available, criteria for persistence of species should be incorporated (Araújo & Williams, 2000). Where species distribution or abundance has been modelled, it may be advantageous to include a measure of the confidence of the results. This should not be given a high enough priority to select preferentially the units at the sampled (un-modelled) points. Areas where the confidence levels are higher should, however, be preferentially chosen when other factors provide a similar score and ties occur. This measure is available in the interpolation methods applied. An error map of each model can be generated. This measure will be incorporated into the summed rarity software.

A measure could also be incorporated according to the proportion of total species distribution occurring in the area under consideration. This would alter the conservation score of selection units, according to the proportion of the elements ranges within the selection unit. The score could also be incorporated by adjusting the conservation target, so that those species with ranges entirely within the study area are given higher proportional targets. This, like any other additional score in the algorithm, incorporates an extra element that may reduce transparency of the method. In addition, the future of habitat outside the planning area can not be guaranteed, so persistence in these areas cannot be relied upon.

11.3 Applicability of the methods

One of the main problems concerning the applicability of these methods is the general lack of good quality consistent biodiversity data. The methods can be used on many forms of data. Methods to gain relevant data are discussed in section 11.4. The costs of obtaining data are prohibitive to all but well funded organisations and those that can rely on sources such as volunteer groups. The

present research used previously collected data. There are no costs involved with the selection algorithm softwares used. C-Plan software is freely available via download from the internet (C-Plan, 2002) and it is intended that the summed rarity algorithm will be available in a similar manner. Several software packages are available for applying various selection algorithms, with varying costs. The irreplaceability-based C-Plan software is comprehensive, interactive, and contains many features that were not utilised during this research, due to data availability or applicability. It integrates with ArcView software that is available to conservation organisations, without charge, through a specified conservation programme. The costs of softwares should therefore not be preventative in the application of these methods in practical planning situations.

Environmental variables are suggested as surrogates due to the perceived ease of data collection. Reassessment is also rapid should conditions change sufficiently to necessitate relocating PAs. Those utilised in this research, however, were collected during a sampling survey. Some variables such as salinity need direct measurement. They were of a high resolution and such data cannot be obtained by remote methods that provide large quantities of easily obtainable data over large areas. It is not known to what extent reassessment of MPA position is possible given the complex process required for designation. Advances in information technology and data dissemination should facilitate such a scheme, but legislation is required to underpin such flexibility. These processes could also be difficult given the advanced planning required for activities that might necessitate such a change, for example infrastructure construction. This can affect habitats directly, or indirectly through hydrological disturbance (Chapter Two). The process to allow flexibility should perhaps be encouraged if the purpose of such protection is to be fulfilled successfully through time.

The analyses have identified many selection units directly within shipping and ferry lanes. Although this is a surprising result, such a position could be advantageous for seasonal MPAs. These areas are unlikely to be utilised for aggregate extraction or other related activities due to the heavy traffic. Stakeholder resistance would also be expected to be low in such cases, and consideration need only to be made to factors influencing the hydrography (such as infrastructure construction 'up current') or water quality (such as pollution).

Terrestrial PA networks designed for 'preservation' are evolving to allow more sustainable use of biodiversity and encourage benefits to local communities. MPAs in contrast, have often been designated as a direct response to collapsed or declining fish stocks. Their creation is primarily due to the need to protect and replenish fish stocks. These are fished in adjacent areas or at unrestricted times of the year (Kelleher, 1999). Managers of marine resources are beginning to appreciate the methodologies developed and tested in the terrestrial environment for selecting PAs (Pressey & McNeil, 1996). Managers of terrestrial resources are beginning to appreciate the benefits of sustainable biodiversity utilisation for the local communities often seen in MPAs.

11.4 Scale and biodiversity surrogates

The ichthyoplankton dataset was recorded at a scale that enabled identification of priority areas on a scale relevant to practical protection measures. Coarse scale analyses have identified many areas of the world that need concentrated effort to protect their biodiversity. Many methods have identified similar regions (Myers et al., 2000; Williams et al., 2000). These analyses have limited practical application due to the scale of the data available. Although algorithms are being improved, the quality of biodiversity distribution data needed for applying these methods remains poor (Cabeza & Moilanen, 2001). In Great Britain for example, several analyses have utilised datasets at a scale of 100km². Unfortunately most nature reserves in the UK are an order of magnitude smaller (Hopkinson, 1999). Fine scale data are needed to refine the results of such coarse scale analyses and identify PA networks that can practically be used to protect species and populations, and exclude unsuitable areas such as highly transformed habitat (Wessels et al., 2000). Some of the methodologies reported in the literature are increasing in sophistication to overcome problems that are generated by the coarse scale approach (Smith, 2001). These problems include selection units containing unsuitable habitat or species at the edge of their range. This may also be a by-product of using presence / absence data (Nicholls, 1998; Williams, 1998b). The additional costs of capturing abundance data may be balanced by the additional benefit of increased probability of identifying the best sites for viable populations (over using presence / absence data) and so increase the likelihood of population persistence (Nicholls, 1998; Rodrigues et al., 2000a). Proportional area within selection units can be useful when abundance data are not available. Selection units must be larger than the resolution of the underlying data to utilise this method.

There is a necessity to improve the methods used both to derive data for conservation planning, to supplement existing data by surveys and to enhance existing data, rather than re-analysing coarse scale data. Methods for surveying terrestrial habitats cost effectively are more difficult to utilise in the marine environment. One of the most popular is the use of datasets collected by volunteers, especially for taxa such as birds and butterflies. These type of datasets are available but not common for the marine environment, especially sub littoral (e.g. see JNCC, 2002).

These type of data are sometimes liable to contain biases as a product of the methods by which they are collected, such as non random samples, or presence only information. Errors can be inherent in the data especially when collating information from different sources and surveys. Different scientists will have slightly different sampling techniques and even use different taxonomies. These are problems associated with all dataset collation. If sampling bias can be identified, an attempt can be made to reduce its effects (e.g. Freitag *et al.*, 1998). The method developed by Smith (2001) identified a surrogate subset of the biodiversity dataset less subject to bias than the whole dataset. The subset of the bird dataset were 'distinctive birds'. These were successfully

used as a surrogate for all birds in South Africa. This approach was unfortunately not appropriate here, since the ichthyoplankton possess great similarity in superficial examination (Koubbi, pers comm.). Other marine datasets, however, may be able to utilise these methods to reduce bias in datasets such as those collected by volunteers, where sampling may be opportunistic in nature.

Climatic data and those collected by remote sensing could form a very useful source of data, but are often at a coarse scale. Data such as sea surface temperature (SST) are freely available, but have a resolution of 1km² at best, and are often supplied at 16 km². The spherical projection in which these data are supplied, is designed for continental scale analyses and not accurate at scales relevant for local scale PA identification.

It was difficult to quantify the applicability of the surrogates. Most other studies have used presence / absence data and reported the proportion of the species represented by the surrogates rather than the proportion of the species represented to the relevant target as conducted here. Seascape surrogate protected 44 to 67% of the ichthyoplankton stages to the relevant conservation The seascape categories were not, however, derived independently and relied on an arbitrary number of classifications. This relieves the risk of relying on expert perceptions. The underlying data were also interpolated. The resolution of sampling, however, was at a finer scale than environmental variables obtained by methods such as remote sensing and had been derived independently. A system that relies on two surrogates independently derived may be more appropriate if the data are available (Smith, 2001). This can involve characteristics such as landcover and species associations. Species distributions can then be modelled on the underlying landcover. This system is more reliable as species may be associated with more than one type of landcover. It could be adopted where the data are available on marine habitats but not on the more elusive species distribution data. The problem of scale is relevant again, however, as much marine habitat mapping is at a coarse scale (see JNCC, 2002). This may, nonetheless, often be a more reliable alternative to decisions based on subjectivity and arbitrary scoring systems.

The goal of PA networks in both terrestrial and marine environments is to sustain the persistence of biodiversity. As has been discussed, detailed biodiversity distribution datasets are scarce. There is also insufficient understanding of the requirements and surrogates of ecological and evolutionary processes thought to be necessary to include in PA networks. Consequently there is also a lack of methods for comparing the conservation value or irreplacability of these phenomena (Cowling, 1999).

11.5 Facilitating wider adoption of selection algorithms into conservation planning methods

Despite the large amount of theoretical work on PA network selection methods, the majority of conservation planning is carried out without reference to them (Pressey, 1994). There are five principle reasons why quantitative selection procedures have not been universally adopted when planning MPAs (Prendergast et al., 1999). It is often thought that the systematic procedures require large quantities of site specific data and that existing biological data are too incomplete or biased to support their use. The methods are viewed as data-driven and unable to capture in-depth personal experience and expertise (Davis et al., 1999). For this reason much marine conservation planning has instead used a type of scoring analysis (Kelleher et al., 1994; Jamison & Levings, 2001). For marine environments, these methods have been criticised for reasons outlined earlier. Conservation planning must always be based on the information available, but can be more efficient and effective if the data-driven systematic methods employed in the present research are used. A second reason may be a disinclination to apply the methods in the marine environment since they are mostly developed and tested in the terrestrial environment. These criticisms are being re-evaluated by some marine conservation planners (Pressey & McNeill 1996; Pressey, 1999b). A third reason may be that practitioners often believe that costs far outweigh the benefits of the methods (Pressey, 1999a) despite the proven advantages (Pressey, 1994). Fourthly, the approaches are often considered simplistic because they are thought not to address complex socioeconomic and political realities of site planning and acquisition. The algorithms can increasingly incorporate information on the huge range of factors involved in decisions between flexible sites (Pressey, 1999b; Balmford, 2000). When these additional factors are incorporated, selection algorithms actively assist in complex situations where it is difficult to decide on the merits of one site above another.

A final, related, reason may be the poor transfer of knowledge about these procedures to conservation planners and managers. Many of the procedures have been researched and tested by academics and managers. Conservation planners may not be aware of them (Prendergast *et al.*, 1999). They could be unaware of the recent improvements, for example to include additional non biological factors. There is a need for a range of adaptations to be made for the wider appreciation and understanding of the methods. Researchers need to make concerted efforts to collaborate with practitioners in applying systematic approaches to real planning exercises to advance their practical usefulness.

To enable this, there is a need for free, widely available and user friendly software that incorporates complimentarity and irreplacability with the range of non-biological factors necessary for the decision process. The software must facilitate the use of the methods by local communities and other stakeholders in addition to conservation planners. Only this coordination will enable analysis

of all the factors involved. The internet is a utility with many possibilities for distribution of the software, help and updates. It, however, remains inaccessible to some conservation organisations situated where internet availability is poor. It should also be capable of integrating with a GIS. There are several softwares, including C-Plan, that answer many of these needs and it is hoped that the summed rarity algorithm will be available in a similar manner. The softwares, however, largely remain in the academic domain. Several are mentioned in the scientific literature, but the availability and means by which they can be obtained are often not detailed. There is a need to widely publicise these softwares in literature relevant to conservation planners.

The C-Plan software, for example, is extremely sophisticated and allows a high level of user interaction, providing huge amounts of information concerning each selection unit. This can be invaluable in situations where the number of selection units is not prohibitive to individual investigation of each flexible unit. It is less relevant, however, when decisions are being made on a large number of selection units of a smaller size, where the number of flexible units can be a large proportion of the total.

The softwares also need to provide very simple means of data input. The data should be available to view for errors, rather than held in a complex database. Only one software known, 'Marxan' (Ball & Possingham, 2002), includes measures to increase the clustering of selection units, by aiming to minimise the boundary length to area ratio. Increasing clustering or reducing the distance between selected units is an extremely important component of PA network design. The software uses a 'simulated annealing' algorithm and integrates with a GIS. It is hoped that these softwares, offering a range of methods, will be aided by wider publicity in relevant literature. This will help their integration into practical conservation planning. Other mechanisms to increase the awareness of their availability and appropriateness should be utilised. These include communication mediums such as the internet and discussion groups. Conservation training courses are integrating PA planning methodologies into their theory and should encourage practical PA selection exercises.

To begin the process of selecting MPAs in the Dover Strait using the selection algorithms used in this study, it is recommended that:

- Appropriate and available biodiversity surrogates are selected;
- Appropriate conservation targets (e.g. 10%, 20%, 50%) are selected;
- Appropriate selection algorithm software, applicable to the data and GIS software available is selected;

- Appropriate and available socio-economic, political and ecological factors are selected, that can be incorporated into the algorithm and the planning discussions;
- A panel of experts, comprising of conservation experts, policy makers, selection procedure professionals and other stakeholders are assembled, and
- An interactive computer based planning process is established.

Key points for the panel of experts will be to:

- Test MPA network scenarios with the selection algorithm software and discuss alternative minimum sets.
- Decide on the network that protects the biodiversity elements to the required conservation target whilst minimising cost, maximising connectivity and best incorporating the additional biological and non-biological factors.

MPAs are not a panacea for the conservation of marine biodiversity, but can compliment the suite of measures necessary to reduce the crisis in marine ecosystems. The likelihood of their success can be increased by the application of methods explored and tested in this research. Softwares such as C-Plan allow conservation planners to utilise GIS and selection methods involving complimentarity and irreplacability or summed rarity, to investigate planning scenarios and build a network of integrated MPAs. With the incorporation of socio-economic and political factors it is anticipated these methods will lead to a wider knowledge, acceptance and use of the approaches advocated in this research, in both the marine and the terrestrial environments.

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APPENDIX: Fish Species

Information sources:

FIGIS: The FAO Fisheries Global Information System. URL: http://www.fao.org/fi/figis

MarLIN: Marine Life Information Network for Britain and Ireland. URL: < http://www.marlin.ac.uk >

Fishbase. URL: http://www.fishbase.org> Larvalbase. URL: http://www.larvalbase.org>

Agonus cataphractus (Hooknose)

Distribution: Eastern Atlantic: English Channel to Finmarken and Murman coasts and White Sea, also the Shetlands, the Faroes and southern and southwestern coasts of Iceland; southern part of Baltic.

Features: Unpaired breast row of plates absent, but paired plate rows cover whole breast. Snout with a pair of strong spiny hooks; numerous barbels on branchiostegal membranes. Spiny and soft dorsal fins almost fused. No spines on the hind part of the head.

Biology: Demersal; marine; depth range 1 - 270 m. Inhabits inshore waters, deeper waters in winter in Skaggerak, preferring sandy bottoms, rarely with stones. Temperature range: 4.0-8.0 °C. Feeds on bottom crustaceans and polychaetes. Matures after about 1 year; a few spawning in the second year. The eggs are laid in seaweed. Spawns in February - April, female laying 2,500 - 3,000 yellow eggs with a diameter of 2 mm. Period of development is very long and 6-8 mm long pelagic larvae hatch after 10-11 months.

Size: Maximum 21cm.

Blennius gattorugine (Tompot blenny)

Distribution: Northeast Atlantic: Atlantic coast from Ireland to Morocco; also in the Mediterranean Sea and the Sea of Marmora.

Features: Gill membranes not forming fold across isthmus. Tentacles on nasal openings and above eyes. No canine teeth in upper jaw. Dentaries joined by ligament. Frontals not covered by parietals. Spawning males chocolate-brown, with bulb glands on spiny anal finrays. Lateral line continuous with branches but discontinuous posteriorly.

Biology: Demersal; non-migratory; marine; depth range 3 - 32 m. Active mainly during dusk and dawn. Adults live in rocky while young are found in shallow water in the seaweed zone. Spawns in March - May. Male guards the eggs from several females, until larvae about 1 month.

Size: 30cm.

Buglossidium luteum (Solenette)

Distribution: Eastern Atlantic (Iceland and Scotland southward, also North Sea, Kattegat and Baltic) and Mediterranean (including Adriatic, Sea of Marmara, Bosphorus).

Features: Anterior nostril on blind side not enlarged, anterior nostril on eyed side with a backward-pointing tube, reaching to vertical through front margin of lower eye. Pectoral fins on blind side reduced to a single long and 1-2 short finrays. The supra-temporal branch of lateral lie without tubular scales. Vertebrae 36-38. Scales rectangular, intercanalicular striae strongly curved.

Biology: Depth range 5 - 450 m. Demersal on sandy bottoms of continental shelf and slope. Feeds on a wide range of bottom-living organisms, mainly crustaceans (copepods, amphipods, cumaceans), bivalve molluscs, and polychaetes.

Size: Maximum 15cm.

Clupea harengus (Atlantic herring)

Distribution: Eastern Atlantic (northern Bay of Biscay northward to Iceland and southern Greenland, eastward to Spitzbergen and Novaya Zemlya, also Baltic; western Atlantic (southwestern Greenland, Labrador, southward to South Carolina).

Features: Body elongate and fairly slender, belly rather rounded, scutes without prominent keel. No median notch in upper jaw. Gill cover (operculum) without radiating bony striae. Hind border of gill opening evenly rounded. Pelvic fin insertion behind vertical from dorsal fin origin pelvic. No distinctive dark spots on body or fins.

Biology: Coastal, pelagic down to 200 m, schooling, with complex feeding and spawning migrations, whose times and extent correlate with the various more or less distinct razes which can be recognized on morphological grounds (mainly numbers of vertebrae, finrays, scales and gillrakers). Feeds on small planktonic copepods in the first year, and thereafter mainly copepods (especially *Calanus finmarchicus* and *Temora longicornis*), but also hyperid amphipods, euphausids, mysid shrimps, small fishes, arrow-worms, ctenophores and pteropods). At least one population is spawning in any one month of the year, each race

having a different spawning time and place (spring, summer, autumn and winter herrings; in 0 to 5 m off Greenland down to 200 m in autumn (bank) herrings of the North Sea; eggs laid on the sea bed, on rock, stones, gravel, sand or beds of algae or phanerogams. Has a wide range of spawning strategies.

Size: 20cm. Maximum 40 cm.

Dicentrarchus labrax (Bass)

Distribution: Relatively common in the sea around England and Wales, Ireland and the southern North Sea coasts; it becomes much rarer to the north. It is an active swimming, schooling fish in inshore waters, commonly entering estuaries and penetrating upstream into almost freshwater, a habit of the young especially.

Features: Two dorsal fins separated by a short space; the first fin is strongly spiny. Body streamlined, relatively shallow with large scales. Forward pointing spines on the lower edge of the preoperculum; no heavy ridge across gill cover. Greeny-grey on the back with brilliantly silvery sides, and silvery white belly. A dusky patch on the gill cover. Small fish are faintly dark spotted.

Biology: Feeds on a wide range of fishes, especially members of the herring family, sandeels and other small schooling fishes. Also eats squids and various crustaceans, graduating onto a fish diet.

Breeds from March to mid June, mostly in May in inshore waters. The eggs and larvae are pelagic. It is a long lived fish, some living longer than 20 years.

Size: 60cm. Maximum 100cm.

Diplecogaster bimaculata (Two-spotted clingfish)

Distribution: Eastern Atlantic: Norway and the Faroes to Gibraltar including western Mediterranean and Adriatic Sea.

Features: Sucker appears at 8 mm and is well developed at 10 mm length. At 7.0 mm, the head was noticeably flattened dorsoventrally. Pigmentation: About 4.8-4.9 mm long (soon after the yolk has been absorbed), postlarvae still resemble the newly hatched larva. At 5.5 mm, pigment begins to develop on top of the head. In specimens 7.5-10 mm long, the melanophores were arranged in four more or less regular longitudinal rows on the body. Sequence of fin development: pelvic fins developing into a sucker; unpaired fins (at about 7.0 mm, the dorsal and anal fin rays were developing). Adult: body elongated and flattened with red spot on each side, near the tip of dorsal fins. Minute gill openings

Biology: Trawled over soft mud bottom. Feeds mainly on benthic organisms. Inhabits shallow water on rocky bottoms and bivalve banks. Spawns in June - July, egg measures 1.5 mm. Larvae are pelagic.

Size: 6cm.

Labrus bergylta (Ballan wrasse)

Distribution: British and Irish coasts.

Features: heavy bodied wrasse with a broad head, small mouth and thick lips. The colouration of this wrasse is variable but there are no external differences between the sexes. The body, head and fins are often brownish red or reddish with numerous small white spots but can be greenish with white spots or irregular large vertical dark stripes. Young are often bright emerald green.

Biology: Found in inshore waters amongst weed covered rocks or in lower shore pools. It is also found in the algal zone on rocky coasts from 5-30 m.

Size: 30cm. Maximum 50cm.

Limanda limanda (Common dab)

Distribution: Eastern Atlantic

Features: Body rather deep, its depth 2 to 2.5 times in standard length. Mout rather small, reaching only to just in front of lower eye. Ctenoid scales on eyed side, cycloid scales on blind side. Coloration usually warm sandy-brown, varying from light brown to grey-brown with small darker freckles on the eyed side; on the blind side white.

Biology: Benthic, lives mainly on sandy bottoms, from a few meters to about 150 m. Feeds mainly on crustaceans, molluscs, worms and small fishes. Spawns from January to August; larvae settle at depths of 10-20 m.

Size: 30cm. Maximum 42cm.

Liparis liparis (Sea snail or lumpsucker)

Distribution: British Isles

Features: A small, round bodied, tadpole-like fish with a long based dorsal fin. Anal fin also long-based but shorter. Both fins join to the tail fin, the anal more noticably. Skin loose and flabby, covered with minute prickles. Sucker disc on belly well developed. Unusually dull brown above, lighter below; variably patterned with stripes, patches and bars of darker brown.

Biology: Found in shallow inshore waters of 5-150m. Lives on mud, muddy sand and also on rocky grounds. Breeds in winter (January to March), the eggs being laid in hazelnut-sized clumps along short algae or bryozoans. The eggs hatch in 6-8 weeks and the larvae are pelagic. The sea snail feeds mainly on crustaceans, especially shrimps and worms and small fish.

Size: 10-12cm.

Liparis montagui (Montagu's sea snail)

Distribution: Northeast Atlantic: North Sea, around the British Isles, Norwegian Sea, south-western Barents Sea and around southern Iceland.

Features: No overlap of dorsal and caudal fins, but rarely overlapping anal and caudal fins

Biology: Demersal; marine; Occurs from intertidal to 30 m, often under stones or clinging to algae. Feeds primarily on crustaceans, intertidally - gammarid amphipods, subtidally - shrimps and small crabs. Spawns in winter; young are also found in the Wadden sea.

Size: Maximum 12cm.

Merlangius merlangus (Whiting)

Distribution: European Atlantic

Features: Chin barbel absent or small. Upper jaw projecting slightly. Three dorsal fins separated by small spaces and two anal fins touching each other or nearly so; anterior anal fin base elongate, one-half or more of preanal distance; pectoral fin reaching well beyond origin of anal fin; pelvic fin with a slightly elongated ray. Lateral line continuous along its entire length. Lateral-line canals on head with pores. Colour: variable; often a small dark blotch at upper base of pectoral fin.

Biology: Benthopelagic at depths from 10 to 200 m, but more common from 30 to 100 m, mainly on mud and gravel bottoms, but also on sand and rock. The young are found in shallower waters, from 5 to 30 m depth. Whitings migrate only after the first year of life when they leave the nursery areas for the open sea. First maturity is attained at 3 or 4 years of age. The sex ratio averages 38.5% males and 61.5% females in the Irish Sea, and 32.2% and 67.8% respectively in the North Sea. Fecundity estimates range from 200 000 eggs in small females to over 1 million eggs in large individuals. Spawning occurs at 20 to 150 m depth, from January to September in the area between the British Isles and the Bay of Biscay, from January to spring in the Mediterranean, and throughout the year in the Black Sea. The eggs are pelagic, and the larvae and juveniles are associated with jellyfish, and do not become demersal until they reach 5 to 10 cm length. Growth is rapid; at one year of age, the size of fish ranges from 15 to 19 cm, at 2 years, from 22 to 5 cm, at 3 years, from 30 to 34 cm; females grow faster than males, life expectancy is about 10 years. The diet of adults includes shrimps, crabs, molluscs, small fish, polychaetes and cephalopods.

Size: 30cm. Maximum 45cm.

Microchirus variegatus (Thickback sole)

Distribution: Northeast Atlantic: British Isles south to Senegal (baie du Lévrier) and the Mediterranean.

Features: Upper eye less than its own diameter from dorsal profile of head. Anterior nostril on blind side not enlarged, its distance from front margin of head about twice in its distance from cleft of mouth. Anterior nostril on eyed side with backward-pointing tube reaching to front border of lower eye. Pectoral fin on eyed-side small, on blind side reduced.

Biology: Inhabits mud or sand bottoms. Feeds on a wide range of small bottom-living organisms, mainly crustaceans (amphipods, shrimps), also polychaete worms and bivalve molluscs.

Size: Maximum 35cm.

Microstomus kitt (Lemon sole)

Distribution: Atlantic and English Channel

Features: Body rather deep. Its depth two to three times in standard length. Mout very small, not reaching lower eye. Lateral line with a slight curve above pectoral fin; scales 110-125. First interhaemal spine not projecting in front of anal fin. Eyed side marbled with thick skin and partly embedded cycloid scales. Colour generally warm brown with irregular mahogany markings and flecks of yellow and green on the eyed side.

Biology: Benthic, lives on a wide range of bottoms from mud and sand, gravel, even rocky grounds, in depths of 20-200 m, particularly on offshore banks. Feeds on a variety of small invertebrates, but worms seem to dominate. Apparently they do not feed in wintertime. It spawns in spring and summer in depths of 100 m. It becomes sexually mature at 3-4 years (males), 4-6 years (females), and may live for 17 years.

Size: 30cm. Maximum 45cm.

Molva molva (Ling)

Distribution: Northeastern Atlantic

Features: Jaws subequal; barbel longer than eye. Second dorsal fin with 59 to 70 rays; anal fin with 57 to 66 rays; pelvic fin not reaching beyond end of pectoral fin. Colour: dorsally reddish brown, shading to white ventrally; posterior areas of vertical fins dark with pale margins.

Biology: Demersal on rocky bottoms at depths of 15 to 600 m or more, commonly from 100m to 400m. Young up to 1-2 years of age are coastal (15-20 m depth) and pelagic; fish of 3 years migrate to greater depths. First maturity is reached at 5 years for males (80 cm) and 5-6 years for females (90-100 cm). Spawning occurs from March to July and eggs are pelagic. Fecundity may reach 20 to 60 million eggs per female. Major spawning grounds are located at 200 m depth from the Bay of Biscay to the Gulf of Norway at 100 to 300 m off southern Iceland, and at 50 to 300 m in the Mediterranean Sea. Growth is rapid (8-10 cm/year): at 1 year, 20 cm; 2 years, 31-35 cm; 3 years, 31-35 cm; 4 years, 73-83 cm. Females grow faster than males. The maxi-mum age is 10 years for males and 14 for females (ca. 200 cm total length). Feeds mostly on fish (cod, herring, flatfish) but also on crustaceans, cephalopods and echinoderms.

Size: 63 - 160cm. Maximum 200cm.

Platichthys flesus (Flounder)

Distribution: Eastern Atlantic, from the White Sea to Mediterranean and Black Sea.

Features: Body rather deep, about twice in standard length. Some scales much modified; normal scales cycloid in both sexes; lateral line almost straight. Often with the eyes on the left side (in certain areas one-third of population is reversed). Colour brownish, greyish or olivaceus, uniform or variously blotched and mottled with darker marks; fain red spots on the eyed side.

Biology: Benthic, at shallow depths with soft bottoms (to 55 m); often found in brackish water and in rivers and lakes. Feeds on a small fishes and invertebrates. The species is mainly nocturnal and burrowing. Spawns in February-June. In some areas, e. g. western Baltic, it hybridizes with the plaice (*Pleuronectes platessa*) and the hybrids are very common.

Size: 30 cm. Maximum 52 cm.

Pleuronectes platessa (European plaice)

Distribution: Western Mediterranean and along European coasts to White Sea (including Iceland); occasionally off Greenland.

Features: Body oval, compressed. Upper profile of head distinctly concave. Snout (in adults) longer than eye; lower eye a little in advance of upper. Interorbital ridge low, narrow, naked or with a few embedded scales; a bony prominence in front of lower eye and often a trace of another before upper eye. Scales mostly cycloid, but often more or less spinulate in the male; occasionally a few spinulate scales present in the female; 88 to 115 scales in a longitudinal series above lateral line. Dorsal fin origin above or a little in front of middle of eye; middle rays frequently with a series of embedded scales on ocular side. Pectoral of ocular side, length 2 to 3 in that of head. Caudal rounded or double-truncate. Colour brownish or greyish, with large, rounded, red or orange spots, sometimes margined with brown, scattered over the body; a series of similar spots along dorsal and anal fins and frequently 2 or 3 at base of caudal.

Biology: Lives on mixed bottoms, from a few metres to about 100 m, the older the deeper the occurrence. Prefers shallow water and small plaice are usually seen on bathing beaches. Occurs at a temperature range of 2-15° C. Feeds mainly on thin-shelled molluscs and polychaetes. Spawns when the temperature is about 6° C. **Size:** Maximum 75cm.

Pollachius pollachius (Pollack)

Distribution: Atlantic

Features: No barbel at tip of lower jaw. lateral line with a sharp dip between first and second do fins. Colour: variable, dorsally dark, sharply distinguished from silver-grey sides and belly, upper part of body with part of body with yellow to orange streaks or blotches. Fins uniformly dark except for yellowish pelvics. Lateral line greenish.

Biology: Pelagic to benthopelagic, mostly close to shore but up to 200 m depth over hard bottoms. Young are pelagic and live near the coast up to 3 years, then migrate to the open sea where they are found mostly between 40 and 100 m depth. Spawns in March in the Bay of Biscay, in February in Spain, and in May in Norway, at about 150 m depth. Ireland. Growth is rapid but slower in the north. Feeds mostly on fish and incidentally on cephalopods and crustaceans (shrimps and crabs).

Size: 50cm. Maximum 130cm.

Scomber scombrus (Atlantic mackerel)

Distribution: North Atlantic Ocean, including the Baltic Sea; eastern Atlantic including the Mediterranean and the Black seas; and western Atlantic from Labrador to Cape Lookout

Features: Palatine wide, teeth in two widely spaced rows. Space between first dorsal fin groove and second dorsal fin clearly greater (approximately 1.5 times) than length of groove; anal fin origin opposite that of second dorsal fin or nearly so; anal fin spine conspicuous, joined to the fin by a membrane but clearly independent of it. Swimbladder absent. Vertebrae 13 precaudal plus 18 caudal; first haemal spine anterior to first interneural process; 21 to 28 interneural bones under first dorsal fin. Colour: markings on back oblique to near vertical, with relatively little undulating; belly unmarked.

Biology: An epipelagic and mesodemersal species, most abundant in cold and temperate, shelf areas. Atlantic mackerel school by size. They overwinter in deeper waters but move closer to shore in spring when water temperatures range between 11° and 14° C. Two separate populations with little or no interchange seem to exist in the northwestern and northeastern Atlantic (including the Mediterranean). In the western population spawning takes place from Cheasapeake Bay to Newfoundland, initiating in the south in spring and progressively extending northward during the summer. Most of the spawing takes place within 10 to 30 miles from shore, but never in low-salinity estuaries. Large fish are the first to arrive at the spawning sites. The eastern population spawns from March to April in the Mediterranean, from May to June off southern England, northern France and in the North Sea, and from June to July in the Kattegat and Skagerrak. Fecundity, in a medium-sized female, fluctuates between 200 000 and 450 000 eggs per season and increases with size; spawning occurs in batches. Maturity is attained at an age of 2 or 3 years. Juvenile Atlantic mackerel feed on zooplankton (fish larvae, small crustaceans, pteropods). As they grow, they are in turn preyed upon by tunas, sharks and dolphins. Females grow bigger than males.

Size: 30 cm. Maximum 50cm.

Scophthalmus maximus (Turbot)

Distribution: Northeast Atlantic: throughout the Mediterranean and along the European coasts to Arctic Circle; also found in most of the Baltic Sea. Subspecies *P. m. maeotica* in the Black Sea. Asia.

Features: Body almost circular. Eye side scaleless but with large bony tubercles

Biology: Demersal; oceanodromous; brackish; marine; depth range 20 - 70 m. Lives on sandy, rocky or mixed bottoms; rather common in brackish waters. Feeds mainly on other bottom-living fishes (sand-eels, gobies, etc.), and also, to a lesser extent, on larger crustaceans and bivalves. Spawning season is between April and August; pelagic eggs.

Size: Maximum 100cm

Solea solea (Common sole)

Distribution: Eastern Atlantic (southward from Tronheim Fjord, also North Sea and western Baltic) and Mediterranean (also Sea of Marmara, Bosphorus and south-western Black Sea). Elsewhere, southward to Senegal.

Features: Body oval. Blind side of head covered with numerous small hair-like fringes; upper eye separated from dorsal profile of head by a distance distinctly greater than its diameter; anterior nostril of blind side surrounded by a small ridge but not enlarged, distance from this nostril to head profile contained 1.5 to 1.8 times in distance from nostril to mouth cleft; anterior nostril on eyed side with tube directed backwards, not reaching anterior margin of eye. Dorsal fin origin on dorsal profile of head before the eyes. Pectoral fins equally well developed on both sides, the fin on eyed side asymmetrical in shape. Base of caudal fin united by a membrane to last ray of dorsal and anal fins, but caudal peduncle still distinct. Lateral line supratemporal prolongation describing a smooth curve on head. Colour eyed side greyish brown to reddish brown; blind side white. Pectoral fin of eyed side with a black blotch restricted to distal end of fin; hind part of caudal darker than rest of fin.

Biology: Benthic species on sandy and muddy bottoms, from the shore down to 300 m. Usually solitary. Feed polychaete worms, small soft-shelled bivalves, small fishes and crustaceans. Reproduction: spawns January-April, with two peaks in February (Mediterranean), or December-May (Bay of Biscay), or April-June (North Sea).

Size: 30cm. Maximum 50cm.

Sprattus sprattus (Sprat)

Distribution: Northeast Atlantic (from North Sea and Baltic south to Morocco; also Mediterranean, Adriatic, Black Sea).

Features: Lower jaw slightly projecting, gill cover without bony radiating striae, teeth rarely present on vomer; belly with a strong keel of scutes; insertion of fin under or before the dorsal fin origin, last two anal finrays not enlarged. No dark spots on flanks.

Biology: Marine pelagic and usually inhore schooling fishes, sometimes entering estuaries (especially the juveniles) and tolerating low salinities; strong migrations between winter feeding and summer spawning grounds. Feeds on planktonic crustaceans. Some spawing almost throughout the year, near to the coast or up to 100 km out to sea, mainly in spring and summer, the young drifting inshore. Move to the surface at night.

Size: 12 cm. Maximum 16cm.

Taurulus bubalis (Longspined bullhead)

Distribution: Eastern Atlantic: Iceland, the Shetlands, from Murmansk southward to Portugal, also Baltic Sea northward to Gulf of Finland and northern Mediterranean coasts eastward to Gulf of Genoa.

Features: Longest spine on the front gill cover reaches backwards to a point below the foremost part of the dorsal fin. Gill membranes joined to the throat, no bony knobs above or under the rough lateral line.

Biology: A resident intertidal species with homing behaviour. Inhabits tidepools and inshore waters on rocky bottoms or among algae at 0-30 m. Can leave tidepools when conditions become inhospitable. Feeds on mysids, amphipods (gammarids), decapods, polychaetes, mollusks, ophiuroids and fishes. Breathes air when out of water.

Size: Maximum 17cm.

Trachinus vipera (Lesser Weever)

Distribution: Mediterranean, Atlantic and English Channel

Features: Body long and laterally flattened but the body is rather deeper than the other weevers, Mouth terminal and oblique, Spines their are no spines on the head only on the gill cover and dorsal fin. It has a large sloping mouth and pointed snout with eyes high on the head. The first dorsal fin is triangular and entirely black with an elongated first spine on the male. The second dorsal and anal fins extend almost to the tail and the pectoral fins are large and paddle shaped. The gill covers have a long spine pointing backwards. The fish is yellowish brown with a paler underside. No conspicuous patterning but their are small dark spots on the head and back. The spines of the first dorsal fin and gill covers release a poison that give an extremely painful sting to bathers or fishermen treading on the buried fish.

Biology: Common on clean sandy bottoms from the low water mark to the shallow sub-littoral down to 50m. The species lives buried in the sand with only the head and back uncovered. The species is most active at night.

Size: Maximum 14cm.

Trachurus trachurus (Atlantic horse mackerel)

Distribution: North-eastern Atlantic from Iceland to Senegal, included Cape Verde islands; Mediterranean and Marmara Seas, rare in Black Sea.

Features: Body elongate, fairly compressed. Head large; posterior end of upper jaw reaching anterior margin of eye; lower jaw projected. Maxilla large, wide, not covered by lachrymal. Adipose eyelid well developed. Small nostrils closely situated each other, anterior nostril oval and posterior nostril crescent. A distinct notch on posterior margin of opercle. Interorbital region slightly arched, its width usually slightly larger than eye diameter. Shoulder girdle (cleithrum) margin smooth, without papillae. Pelvic fin moderate in size, originating below end of pectoral fin base. Scales in curved lateral line, expanded dorsolaterally and scute-like; in straight lateral line. No distinctive markings except for a small, black opercular spot on edge near upper angle. Upper part of body and top of head dusky to nearly black or grey to bluish green; lower two thirds of body and head usually paler, whitish to silvery.

Biology: Benthopelagic species; usually over sandy bottom in 100-200 m, but reported to 1050 m, also pelagic and near surface at times; often shoals with juvenile herrings and other species of *Trachurus*. Feeding primarily on crustaceans (copepods), shrimps, but also small fishes and squids. Pelagic eggs and spawning generally occurs during the summer.

Size: 15 to 30cm. Maximum 60cm.

Taurulus lilljeborgi (Norway Bullhead)

Distribution: Scotland and Norway

Features: It is usually reddish in colour with similar markings to long-spined bullhead, and the long spines on each gill cover are almost identical.

Size: 30cm.

Trigla lucerna (Tub Gurnard)

Distribution: Eastern Atlantic: Norway to West African coast (Cape Blanc); not recorded at Madeira and the Azores. Also in the Mediterranean and Black Seas.

Features: Longest ray in the pectoral fin reaching the front part of the anal afin. Lateral line scales smooth. Reddish colour

Biology: demersal; marine; depth range 20 - 300 m Occurs at temperatures ranging from 8.0-24.0 °C. Inhabits sand, muddy sand or gravel bottoms. Feeds on fish, crustaceans and molluscs. Has three isolated rays on the pectoral fin which function as legs on which the fish rests and also help in locating food on the soft bottom.

Size: 40cm. Maximum 75cm.

Trisopterus luscus (Pouting)

Distribution: From the British Isles and Skagerrak to about 25°N along the West African coast, also at the offshore islands and in the western Mediterranean.

Features: Lower jaw shorter than upper. Greatest body depth greater than head length. Colour: light brown dorsally, sides greyish becoming silvery ventrally; four or five broad indistinct tranverse bars on the side; a dark blotch at the upper edge of the pectoral base.

Biology: A benthopelagic species living mostly on the outer shelf up to 100 m depth, but moving inshore to depths of 50 m or less for spawning. Found also in estuaries. Immatures form schools above sandy bottoms. First maturity is reached at the end of first year. Spawning occurs from December to April (mostly March-April) in the Atlantic and from January to July in the Mediterranean. Growth is rapid: at 1 year, 21-25 cm; 2 years, 23-27 cm; 3 years, 28-33 cm. Maximum age is 4 years. Feeds on benthic crustaceans but also on small fish, molluscs and polychaetes.

Size: 30cm. Maximum 45cm.

Trisopterus minutus (Poor cod)

Distribution: Eastern Atlantic: from the Trondheim Fjord and the Faeroe Islands to Portugal and along the Atlantic coast of Morocco; also in the Mediterranean.

Features: Chin barbel well developed. Body brownish yellow dorsally, becoming paler ventrally; a dark blotch is at the base of the pectoral fin. Occurs mostly from 15m to 200m in the Atlantic and to 120m in the Mediterranean on muddy or sandy bottoms. Feeds on crustaceans, small fish, and polychaetes.

Biology: benthopelagic; non-migratory; marine; depth range - 400 m.

Size: Maximum 40cm.

Trisopterus luscus (Pouting)

Distribution: Eastern Atlantic: British Isles and Skagerrak to the West African coast, including offshore islands. Also in the western Mediterranean.

Features: Chin barbel well developed. Pelvic fins with slightly elongated anterior rays. Body light brown dorsally, relatively tall, grayish on the sides becoming silvery ventrally, with four or five broad indistinct transverse bars on the sides; a dark blotch at the upper edge of the pectoral-fin base. Eye diameter as snout length. Anus lies below the middle of the first dorsal fin.

Biology: A benthopelagic species living mostly on the outer shelf up to 100 m depth, but moving inshore to depths of 50 m or less for spawning. Found also in estuaries. Immatures form schools above sandy bottoms. First maturity is reached at the end of first year. Spawning occurs from December to April (mostly March-April) in the Atlantic and from January to July in the Mediterranean. Maximum age is 4 years. Feeds on benthic crustaceans but also on small fish, molluscs and polychaetes.

Size: 30cm. Maximum 46cm.

Zeugopterus punctatus (Topknot)

Distribution: Northern Atlantic: from Trondheim to the Bay of Biscay, including Newfoundland, Canada **Features:** Dark coloration, marbled and with spots. Body oval, pelvic and anal fins used. Scales on the eyed side with fine spiny outgrowths, which are like rough fur to the touch.

Biology: Lives on stony or rocky ground in the algal zone, and feeds on small fishes and crustaceans. Spawns in March – June.

Size: 25cm.