# GIS Modeling Potential Marine Protected Areas in the Northwest Atlantic via Biological and Socioeconomic Parameters

by
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Overfishing of our national marine resources has degraded some of the most productive fishing regions in the Northwest Atlantic Ocean, most notably the Gulf of Maine and Georges Bank. These regions may have shifted from productive trophic regimes to a less than optimal state therefore reducing fishers' catches and associated revenue from commercially targeted species (Sinclair and Murawski, 1997, Jennings et al, 2001). Marine protected areas (MPAs) have been offered as an effective management tool to preserve biodiversity, enhance commercial fisheries, and protect against poor decisions in fisheries management (Bohnsack, 1999). Geographic information systems (GIS) bring together the fields of geography and fisheries management to help build a better understanding of the spatial interactions of complex marine environments (e.g., Kracker, 1999). Using GIS and spatial management such as MPAs can help fishery managers conserve and improve the population status of important biological resources while helping to preserve commercial fishing, an important social and political industry in New England.

Incorporating the needs of stakeholders in management decisions is necessary in order to implement an effective fisheries management strategy (e.g., Malakoff, 2002). This study used a weighted optimization raster model in a GIS to compare biological significant regions, which were composed of biodiversity estimates and spawning and juvenile habitats, to important commercial fishing grounds in the Gulf of Maine and Georges Bank. Biodiversity, spawning and juvenile data values were derived from fishery independent data collected by

the National Marine Fisheries Service in Woods Hole, MA. The essential commercial fishing zones were created from Vessel Trip Reports, which are derived directly from reports sent in by federally permitted fishers. The weighted model compares the biologically important resources from an area, or cell, to the level of commercial fishing occurring in the same cell using simple mathematically algorithms in map algebra. The model output shows where placement of MPAs might be most beneficial in order to conserve marine resources and enhance fisheries, as well as areas where fishing is more suitable. Output can be viewed in multiple ways, a spectrum of values ranging from negative numbers to positive ones or simply as areas important for the fishing community or potential MPA. The more negative the value in the spectrum output then the more important the area would be for fishers and conversely the more positive the output then the more suitable the area would be for possible MPA designation.

The optimization model can be tuned to meet management goals and objectives by adjusting the weighting scenarios for the input variables. The model design can be used for multiple species and ecosystem management or to protect specifically targeted species of particular concern. Managers may use the output to delineate MPAs in a variety of ways depending on the conditions of the resources and the prospects of the fishing community. Managers will enjoy greater success as the needs of both fishers and biological resources are met.

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APPROVED:

Major Professor, representing Geography

Chair of the Department of Geosciences

Dean of the Graduate School

I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request.

Charles M. Keith, Author

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## Introduction

The Gulf of Maine (GOM) and Georges Bank (GBK) regions of the Northwest Atlantic Ocean have been heavily exploited over the last century, and overfishing has limited and/or closed many traditional commercial fisheries in these once productive regions (Sinclair and Murawski, 1997). Although extinction of species is relatively rare in marine systems overfishing can cause shifts in the trophic structure of the ecosystem leading to multiple stable states of community structure, which may be irreversible (Jennings, 2001; Gabriel, 1992). These shifts can cause a system once dominated by high level trophic species, which are typically more commercially valuable, to become over run with lower level trophic species of less commercial importance (Pauly et al, 1998; Murawski et al, 2000). Trophic shifts caused by excessive fishing can create cascading effects throughout the food chain that alters both the genetic biodiversity of a species and the species biodiversity of the region.

Marine protected areas (MPAs), areas with little or no fishing pressure, have been offered as an effective management tool to preserve biodiversity and enhance fisheries (Bohnsack, 1999). Combining traditional fishery management, such as effort/gear restrictions and catch quotas, with MPAs may have a significant positive impact on marine biodiversity and fisheries management.

Geographic information systems (GIS) bring together the fields of geography and fisheries science, as they are both interested in the spatial and temporal extent of biological and physical resources within a landscape or, in the case of fisheries science, a seascape (e.g., Kracker, 1999). The goal of this study is to create a GIS for the GOM and GBK, that combines biological and socioeconomic fishery parameters to optimize where MPAs will best serve to protect biodiversity, enhance fisheries, and minimize impacts to fishing communities within the study area (Figure 1). GIS was used to create a series of raster data sets to delineate biodiversity “hotspots,” critical spawning and nursery habitats, and essential commercial fishing zones.  A weighted model assembled these rasters into optimized MPA output.  In discussing the model and output, this thesis outlines some of the major problems that impact marine biodiversity in fisheries science management, explains how MPAs may enhance biodiversity and fisheries management, and details how using GIS may identify potential MPAs with the use of biological and socioeconomic parameters, (Figure 2).

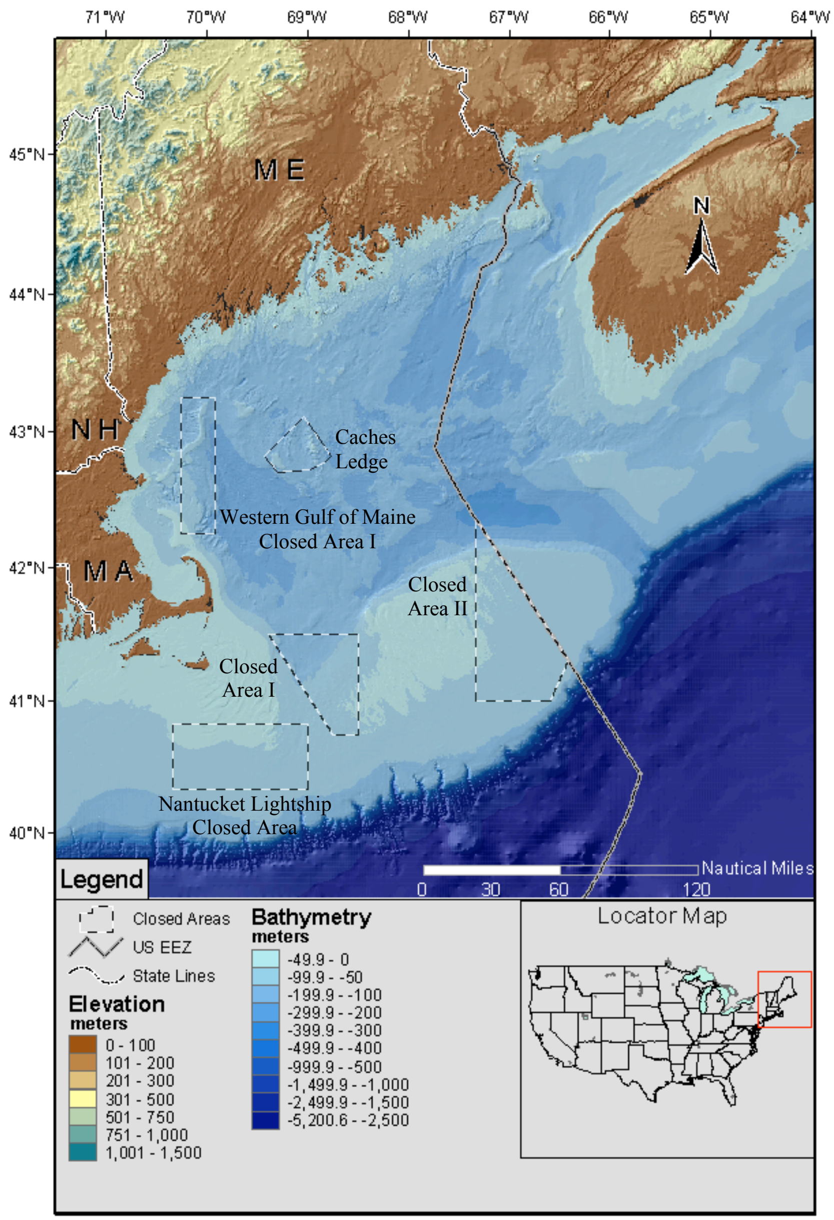



Figure 1. Study area located in the Gulf of Maine and Georges Bank regions of the Northwest Atlantic Ocean. Bathymetry and elevation data from USGS, (Roworth and Signell, 1999).

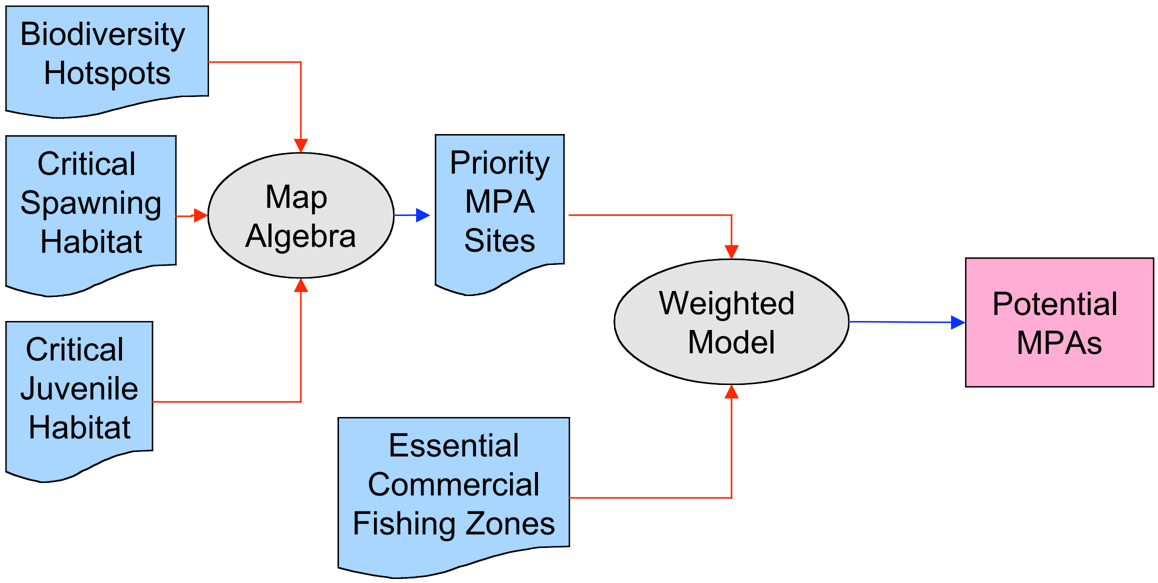



Figure 2. A simple GIS flowchart of the steps needed to delineate potential MPAs in the Gulf of Maine.

## Literature Review

### Fishery Management Problems

Little is known about the extent of global biodiversity, and even less is known about what species exist in the world's marine habitats. The biosphere is defined as the portion of Earth in which species may live. The amount of living space in the Earth's biosphere is quite disproportionate. By surface area land occupies 29% and ocean 71%, and by volume the differences are even more staggering: upper ocean 21%, deep ocean 78.5%, and land 0.5% (Childress 1983). Current estimates of the total number of species living in the Earth's biosphere range from 5 million to 80 million or possibly more (Lawton and May, 1995). Of the 1.75 million species cataloged to date, only 15% are from marine environments (Lawton and May, 1995). Considering the amount of possible niche space in the marine environment, scientists still have much to learn about these systems.

Over-exploitation is one of the primary threats to the biodiversity of marine species and given that we have explored and studied only approximately 5% of the world's oceans we must preserve these species diverse regions of the Earth. It was Aldo Leopold who declared, "If the biota, in the course of aeons, has built something we like but do not understand, then who but a fool would discard seemingly useless parts? To keep every cog and wheel is the first precaution of intelligent tinkering" (Leopold, 1948).

Many problems exist in today's fishery management science as evidenced by the fact that 38% of managed species have been documented by NOAA Fisheries as overfished or approaching an overfished status (Okey, 2003). The complicated process of managing fisheries involves many useful, but incomprehensive laws and policies, conflicting goals and objectives, and spreads management responsibilities over federal and state agencies and Regional Fishery Management Councils.

Fishery management in federal waters is governed by the Magnuson-Stevens (M-S) Act and its' various amendments (Christie and Hildreth, 1999). Individual state laws and policies regulate between the coast and 3 miles offshore, while the M-S Act manages from beyond the 3-mile line to 200 miles from the coastline. This is the first problem facing fisheries management. Federal and state policies do not necessarily work together to protect marine resources. Federal and state regulations that restrict gear type or amount of effort can be dissimilar within different jurisdictions, which can negate management goals (Christie and Hildreth, 1999). Many commercial fisheries and biological resources cross these arbitrary political boundaries and fish species are obviously unconcerned if they are in federal or state waters. This can lead to problems interpreting commercial landings data by fishery managers, which may lead to inaccurate population estimates and exploitation rates. As stated previously, over-exploitation of fisheries is one of the primary threats to preserving marine biodiversity.

The M-S Act outlines that fisheries should be managed to produce optimal yield, which has been defined as (Christie and Hildreth, 1999):

> the amount of fish which—
>
> A. will provide the greatest overall benefit to the Nation, particularly with respect to food production and recreational opportunities; and taking into account the protection of marine ecosystems;
>
> B. is prescribed as such on the basis of the maximum sustained yield from the fishery, as reduced by any relevant economic, social, or ecological factor; and
>
> C. in the case of an overfished fishery, provides for rebuilding to a level consistent with producing the maximum sustained yield in such fishery.

Problems occur because of the inherently different goals of optimal yield (OY) and maximum sustained yield (MSY). The goal of MSY is to allow the fishery to take the maximum amount of fish each year while ensuring that the population will produce enough young fish to sustain the fishery in the next year. When the population size is half as large as the carrying capacity (K), the population's rate of change is at its maximum and declines thereafter, reaching zero when the population reaches carrying capacity (Figure 3). In theory,

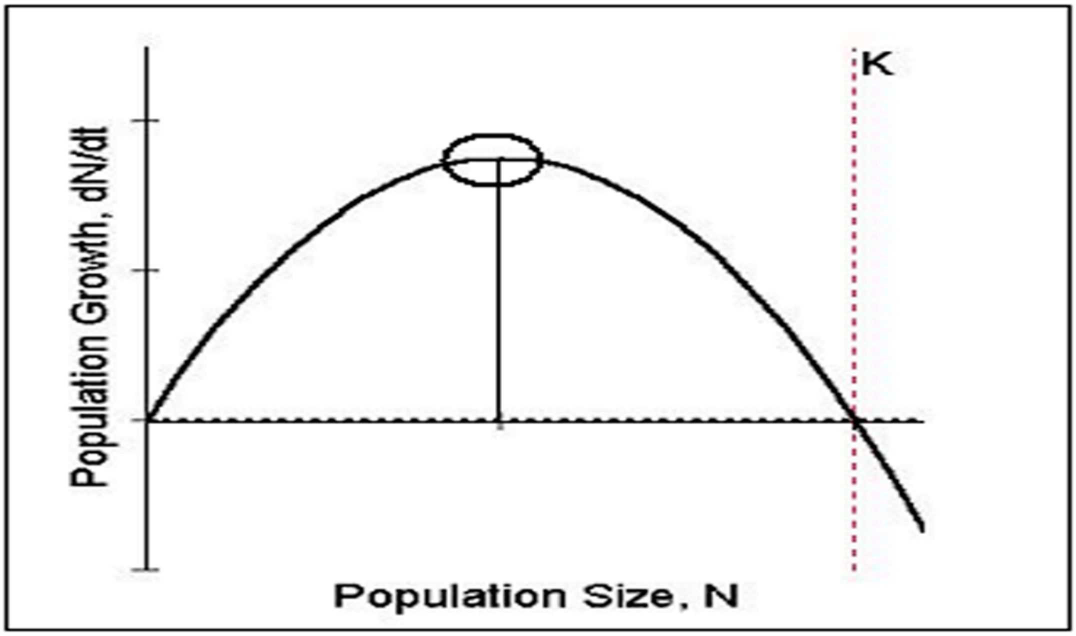



Figure 3. An example of MSY (Sampson, 2002)

such a population could be continuously harvested to one-half of its carrying capacity, thereby producing a perpetual, maximum yield without compromising the ability of the population to be replenished (Sampson, 2002). MSY does not incorporate needs for a healthy marine ecosystem. All surplus fish are allocated to the fishery and theoretically the number of fish allocated to the ecosystem for foodweb interactions or other needs is zero (Goldberg, 2002). Fishery managers tend to focus management on producing MSY because it is a number that can be calculated somewhat precisely and easily. Taking ecosystem and socioeconomic needs into consideration complicates fishery equations and adds uncertainty to estimates of OY. Other problems of MSY and its derivative biological reference points are (Sampson, 2002):

- Fishing at MSY is not cost effective. The economically optimal yield is generally less than MSY.
- The MSY values for different stocks may not be independent. Species are not ecologically isolated, and as a consequence changes in the biomass of one may affect the intrinsic growth rates and carrying capacity for other species.

- Fishing at the $F_{msy}$ rate, as opposed to any lower rate, implies a younger average age and a reduced number of age classes, which may lead to greater variability in recruitment.

- In multispecies fisheries, the stocks with lower productivity may end up being eliminated if the rate of fishing mortality is maintained at $F_{msy}$ (Sampson, 2002).

OY considers the social and economic needs of a community, whereas MSY does not. This is apparent when observing a small boat fishing community. Small boats have a limited fishing range and capacity and the greater in situ biomass created by optimal yield allows small boats to produce a higher catch in the vicinity of their homeport, therefore minimizing their costs (Goldberg, 2002).

Fishery management is plagued by the over-capitalization of fishing fleets through open access fisheries, which encourages overfishing (Ludwig et al, 1993). This occurs when catches are good, or artificially inflated by high catch quotas, and other fishers want to begin

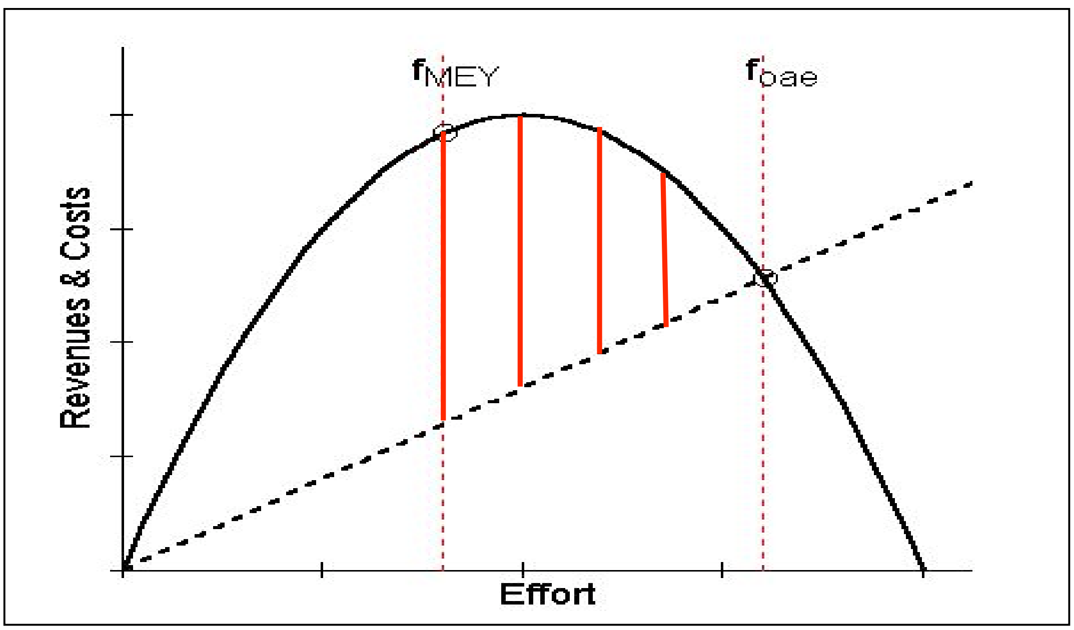
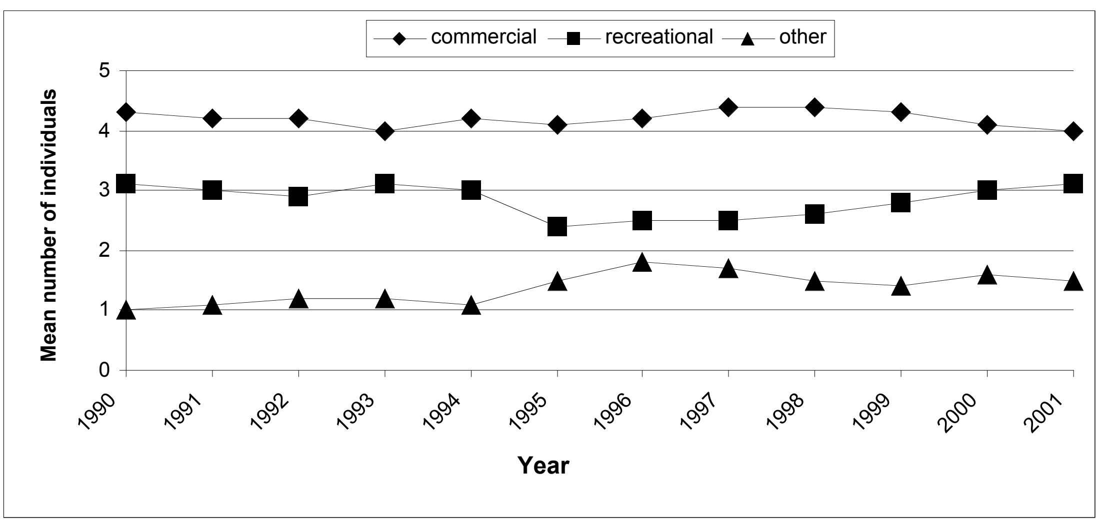



Figure 4. A hypothetical open access fishery (Sampson 2002).fishing for the abundant

species. Red lines on the Figure 4 represent economic benefits and they are reduced as more effort enters the fishery. Regulations often do not limit access to a fishery and governments may provide incentives such as low interest loans for buying and building boats. This frequently occurs when other fisheries have been limited because they are considered overfished and economic opportunities for fishers are limited. Fishing effort has now increased and will lead to further depleted fisheries and sacrificed future economic returns (Ludwig et al, 1993).

Eight regional councils across the U.S. determine the management strategies of commercial fisheries. The councils are comprised of state and federal representatives and appointed members who have fishery management and conservation knowledge (Okey, 2003).

The fishing industry plays an influential role in the management process, as they are often the appointees on the council (Allison, 2002). Fishing interests have at times made up 80% of the regional councils (Figure 5). Ideally industry representatives would favor




conservation in order to ensure long-term economic stability of fisheries and improve

Figure 5. Appointees on RegionalCouncils (Okey, 2003)

the likelihood of regulatory compliance by creating reasonable and effective policies (Allison, 2002). This has led many critics to declare that we have “left the fox to guard the henhouse” (Goldberg, 2002). The regional councils have ultimately lived up to this reputation by favoring short-term economic gains by limiting restrictive management (Rosenberg, 2003). Fisheries are considered a common or public resource and as such each person in the U.S. is entitled to the marine resources found within the U.S jurisdictional waters. Fisheries are then subject to the “Tragedy of the Commons” as outlined by Hardin (1968), where no individual or group is responsible for the common good and that resource is eventually overexploited. Obviously not everyone can be a fisher but luckily we have many fishing communities who do the work, reap the economic benefits, and provide a valuable commodity to the public. Interest groups other than fishing are not represented on the councils even though they have an interest in them. If the councils were democratic in function all interested groups would be represented (Rosenberg, 2003). These other interested groups might lack some of the technical expertise of immediate stakeholders but could bring a more sustainable approach to fishery management that seems to be lacking (Okey, 2003).

The over-representation of fishing industry in the regional councils leads to another problem, the tendency to quickly remove policy that restricts fishing and the slow process of establishing new restrictive measures on the fishing industry (Rosenberg, 2003). This occurs when new information shows an increasing trend in population biomass, numbers, etc., so managers immediately ease restrictions in order to make short-term profits. On the other hand, councils tend to take their time and typically request that more information be collected or contend that the data are flawed in some aspect when population trends show a decline (Figure 6). In essence, managers believe that increasing trends deserve swifter action and have more meaning than declining trends. This has been termed, “managing to the margins,” where the resource is exploited at every marginal opportunity regardless of the uncertainty associated with the data (Rosenberg, 2003). In direct contrast to the theory that marine fishes are highly resilient to large population reductions, is the fact that there is little evidence to prove that fishes experience rapid recovery from prolonged declines, which exacerbates overfishing problems and lack of swift management (Hutchings, 2000).

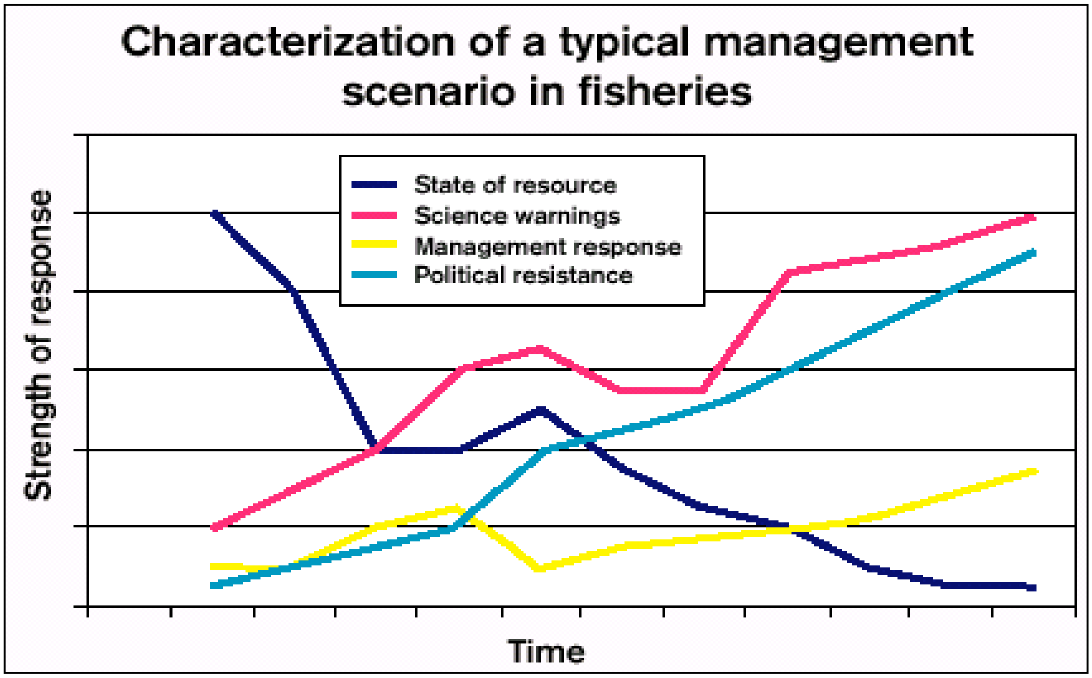



Figure 6. Management response to overfishing (Rosenberg, 2003)

Currently stock assessment scientists are tasked with the responsibility of proving that the species or stock being assessed is being overfished or is at the risk of being overfished. The "burden of proof" must show that the species is in jeopardy; many scientists have suggested reversing the burden of proof to show that the species is not in jeopardy and that fishing may continue at the appropriate level (Dayton, 1998). This shift would incorporate a precautionary approach to fisheries management, where error would be on the side of conservation rather than increasing exploitation (Ludwig et al, 1993; Rosenberg, 2003). Increases in population size would enact slight increases in catch until the trend is confirmed with subsequent data and decreases in population size would require immediate reductions in catch and fishing effort (Rosenberg, 2003).

The ocean is home to an amazingly dynamic and diverse assortment of resources. Single species management dominates how we evaluate the health of individual stocks, but it cannot incorporate all of complicated parameters involved in real world fish population interactions. Single species assessments and management tell managers how species abundance compares to recent historical levels, and then estimates how much surplus production, via MSY, is available to harvest. What it does not include are ecosystem interactions between foodwebs, symbiotic relationships between species and habitat, and many other parameters that science does not yet understand. Single species management has encouraged the fishing down of the food web (Pauly et al, 1998). Fisheries, in general, target large, predatory species upsetting the natural balance of predators and prey within the ecosystem and associated foodweb (Meyers and Worm, 2003). Fishing down foodwebs removes the large piscivorous fish and allows for zooplanktivorous ones to become increasingly abundant, reducing the future benefits provided from a balanced ecosystem (Pauly et al, 1998). Incorporating ecosystem management would include key parameters currently ignored by single species assessments.

## Marine Protected Areas: No Take

### *Definitions*

MPAs have a variety of definitions depending on the extent of management and the reasons for protecting a specific geographic area. The official federal definition of an MPA is (Executive Order 13158):

> any area of the marine environment that has been reserved by Federal, State, tribal, territorial, or local laws or regulations to provide lasting protection for part or all of the natural and cultural resources therein

Often MPAs allow for limited use of the region but no-take marine reserves do not allow the extraction of any type of resource from the region and also protect the area from controllable sources of pollution, i.e. dredge spoils (Murray et al, 1999). MPAs, and especially no-take marine reserves, are promising management tools for rebuilding overfished populations (Pauly et al, 1998).

**Function and Utility of No-Take MPAs**

Direct benefits to fisheries have been well documented through increases in biomass, density, size classes, and increased production of eggs and larvae. Removal of fishing effort within the no-take reserve provides refuge for exploited and non-targeted species alike (Allison et al, 1998). Because destructive fishing practices have been disallowed, essential fish habitat is permitted to recover and the area can support more individuals and greater numbers of species, increasing biodiversity of the reserve (Allison et al, 1998; Bohnsack, 1999).

Individuals can grow larger and thus more fecund in the no-take reserve. Fish fecundity has an exponential relationship between the size of the fish and the number of viable eggs or sperm that it produces. An example of vermillion rockfish illustrates that a 23-inch female fish will produce seventeen times more offspring than a 14-inch fish (PISCO, 2002). The eggs and subsequent larvae then have a more suitable area to settle to because of the protected habitat within the reserve (Bohnsack, 1999).

Spillover affects also occur, enhancing fisheries permitted outside the no-take marine reserve and providing for the more rapid recovery of overfished stocks (PISCO, 2002; Bohnsack, 1999; Roberts et al, 2001). Spillover is the process where adults emigrate, and eggs and larvae disperse via ocean currents to other areas. This increase in dispersal improves the chances of settlement even in heavily fished areas (Murawski et al, 2000). No-take marine reserves are therefore considered a precautionary management tool because they offer a bet-hedging strategy against poor management and environmental variation (Bohnsack, 1999). The export of adult fish also stabilizes fishery landings by providing a consistent source of biomass to the fishery, which can help prevent over-capitalization of fishing fleets (Bohnsack, 1999).

No-take reserves offer genetic protection for species. Species that are exploited can undergo shifts in life history, changing the size and age of maturity (Ernande et al, 2002). As the adult fish are heavily fished, genetic shifts force younger, less productive individuals to develop somatic tissue to ensure that a portion of the population will reproduce (Ernande et al, 2002). As stated earlier younger fish produce fewer, less viable eggs and sperm. Genetic variability is also important for stock persistence when environmental perturbations occur (Bohnsack, 1999).

Other indirect fishery benefits are produced by the creation of no-take marine reserves. Reserves provide important baseline scientific data for determining the impacts of fisheries on marine ecosystems, monitoring areas for understanding differences between natural environmental variability and human-induced influences on populations, and experimental areas to improve our understanding of fish behavior, species interactions, and natural mortality, which is a key parameter in virtual population analyses and stock assessments (Bohnsack, 1999; Murray et al, 1999). No-take reserves are also easier to enforce, especially when aided by vessel monitoring systems (VMS) that automatically track vessel location and speed, because no type of fishing is allowed and violations are easy to spot by VMS (Rago et al, 2000). No-take marine reserves can protect ecosystems and the rare species and habitats contained within, improve non-consumptive recreational opportunities, diversify coastal economies, and facilitate public appreciation and protection of marine resources (Sobel, 1996).

## Methods

### Sources of Data

The NOAA Fisheries Northeast Fishery Science Center (NEFSC) collects and maintains a variety of fisheries data and databases. The primary sources of information in this analysis can be broken into two groups, fishery independent data and fishery dependent data. Fishery independent data are collected aboard NOAA research vessels, i.e. independent of commercial harvest, and fishery dependent data are data directly derived from reports sent in by commercial fishers. Fishery independent databases used in the analyses are SVSTA - the bottom trawl survey) station database, SVCAT – the bottom trawl survey catch database, and SVBIO – the bottom trawl survey biological database. The fishery dependent database used in this analysis is comprised of three tables of Vessel Trip Reports, the first being the gear type used (VTRxxxxG, where the xxxx is the particular year), the second is VTRxxxxS (the species catch information), and the third is the VTRxxxxT (the trip information).

The NEFSC conducts fishery independent surveys for marine resources for six reasons: to examine the recruitment of marine resources, to monitor abundance and survival of harvestable sizes, to observe the geographic distribution of species, to examine ecosystem changes, to monitor biological rates of the stocks, and to collect environmental data. The NEFSC maintains the longest continuous time series of research vessel (R/V) sampling in the world. Fall and spring resource surveys began in 1963 and 1968 respectively. These surveys have been conducted with two NOAA vessels, the *R/V Albatross IV* (AL IV) and the *R/V Delaware II* (DE II), both which operate out of Woods Hole, MA. Sampling locations or "stations" are allocated to the ocean bottom from Cape Hatteras, NC to Nova Scotia, Canada at depths ranging from 10 to 400 m through a stratified-random sampling design. The NEFSC stratified the northeastern U.S. continental shelf into regions; known as strata, that share similar depth characteristics (Figure 7). The number of sampling points per strata is proportional to the area occupied by the strata; so larger regions will be allocated more sampling stations. Approximately 350 sampling locations are chosen randomly per spring and fall cruises so that statistical analyses can be performed on the data collected. This type of sampling design is intended to provide a representative sample population of the species that occupy the strata. Sampling is usually conducted with a Yankee 36 bottom survey trawl with the following dimensions: a headrope of ~18.3 m, footrope of ~24.4 m and lined with ~1.25 cm mesh material. The trawl is rigged with roller gear (~41 x 13 cm), sweep cookies (~10.0 x 2 cm) for sampling in hard bottom habitat, 9.1 m legs and 450 kg polyvalent doors.

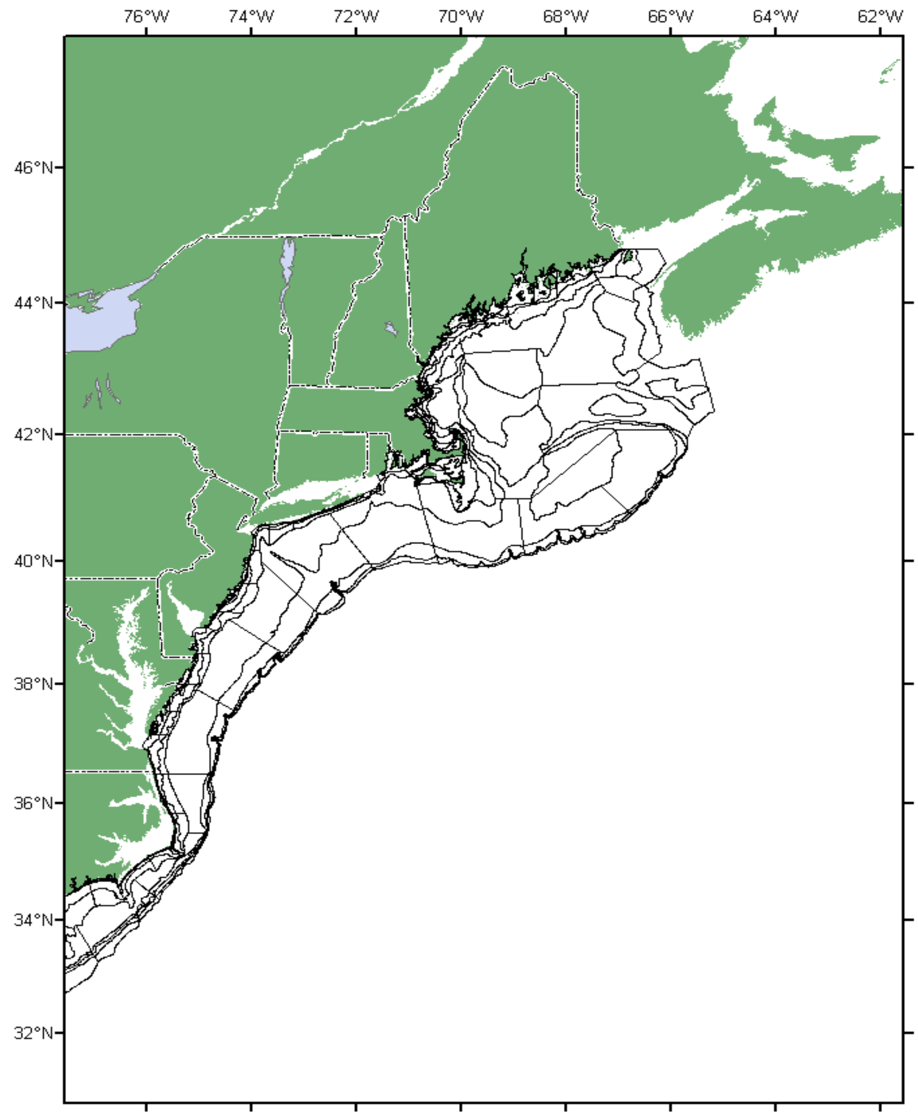



Figure 7. NEFSC inshore and offshore survey strata for bottom trawl surveys.

Standardized sampling protocols are followed while occupying a sampling station during a research survey. The trawl is towed for 30 minutes at 7.0 km per hour (3.8 kts) speed over ground using a DGPS navigation system. An average station will cover approximately 3.5 km (1.9 nm) distance over the ocean bottom. Sampling duration begins at the point of locking the ships trawl winches at the appropriate wire scope. Scope of the trawl warp is set according to the depth of the sampling station and maintains a 4:1, 3:1, or 2.5:1 ratio for depth ranges of 18-27 m, 28-183 m, and >= 184 m respectively.

The catch is brought on board, sorted into species and a total weight for each species is then recorded to the nearest 0.1 kg. Individuals of each species are then weighed and measured, the sex and maturity of the individual are determined, stomach contents are analyzed, and scales, otoliths, or vertebrae are preserved for subsequent aging. All data are recorded digitally into a shipboard, networked computer system, the Fishery Science Computer System (FSCS). All sampling stations and individual fish records have unique ID numbers for querying and analysis.

Vessel trip reports (VTR), also known as logbooks, are the primary source of fishery dependent data. Fishers with federal fishing permits are required to fill out a VTR upon completion of a fishing trip conducted in state or federal waters. A fisher is also required to fill out an individual VTR if they change gear type, area fished, or mesh size. VTR's provide information regarding vessel name and permit number, dates fished, area fished, latitude and longitude where fishing was concentrated, pounds of species kept and discarded, gear type, and effort information. The resolution of these data is kept relatively imprecise in order to keep an individual fishers favorite fishing grounds from becoming public knowledge. Data can be reasonably aggregated to a 10-minute square fishing area, approximately 343 $km^2$. These data can then be aggregated into total landings per 10-minute square per year.

**Identifying Biodiversity Hotspots**

The purpose of this analysis is to create a raster data set highlighting areas of high biodiversity, a key element in the MPA delineation process, (Figure 8). Data analyzed were from the spring and fall bottom trawl surveys for the years 1994-2003. Data auditing was necessary in order to remove errors in the bottom trawl survey station and catch databases. Only those stations meeting minimum NEFSC survey-haul-gear (SHG) requirements for a valid standardized tow were used in this analysis. A total of 3,070 stations met the minimum

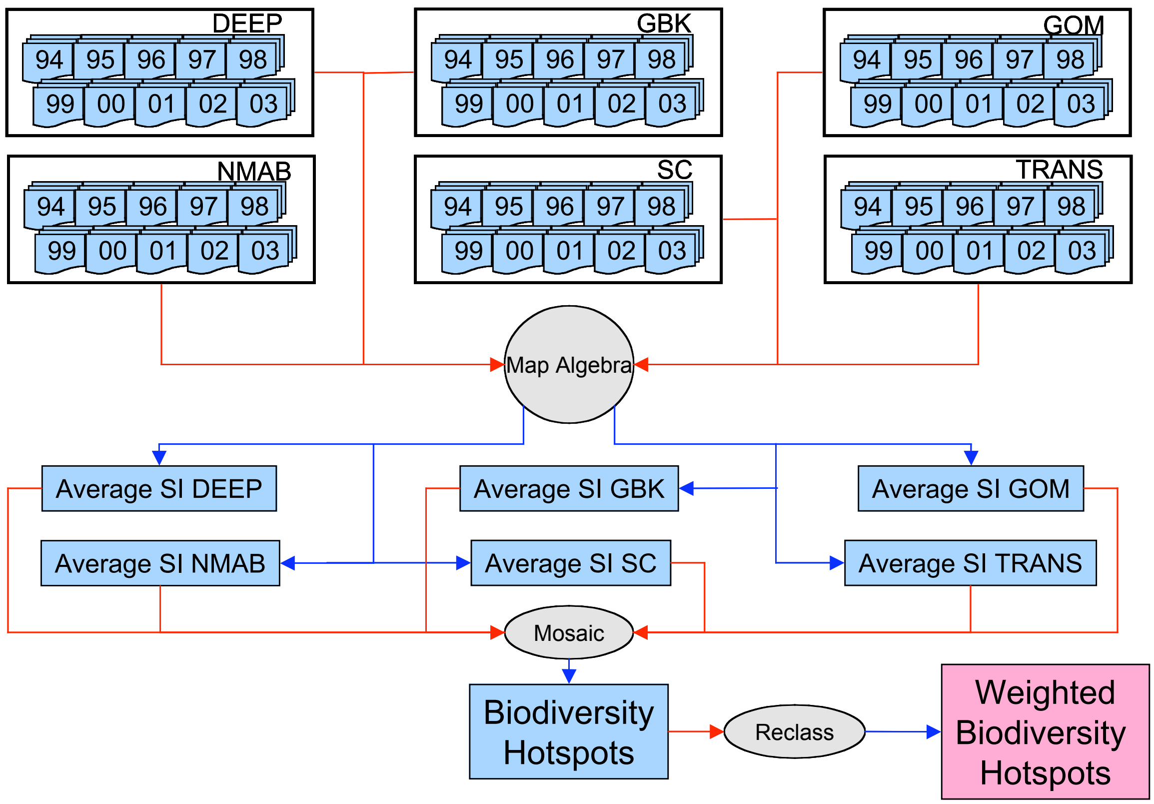



Figure 8. A GIS flowchart for the creation of the weighted biodiversity hotspots raster data set.

requirements. An average of 306 stations were conducted per year in the study area, 147 in the spring and 160 in the fall surveys. Catch records with zero or blank fields for the number of individuals caught were removed. Some zero or blank fields were updated using species length-weight regression formulas when total weight for a species was provided but individual numbers of the species were missing. A total of 43,678 species records remained upon completion of the data audit (Tables 1 and 2). Two R/Vs were used to conduct the surveys; the DE II completed three surveys and the AL IV completed the remaining seventeen. Although the relative fishing power of the two vessels is likely different, species abundance data were not adjusted for these differences. Data were not adjusted because significant differences were not found for individual species abundances but existed for total numbers and total weight caught (Byrne and Forrester, 1991).

Table 1. Summary of survey station data used in analysis after auditing procedures.

| Year | Cruise Code | Season | Vessel | Gear | Stations |
|---|---|---|---|---|---|
| 1994 | 199402 | Spring | DE II | Yankee 36 | 144 |
| 1994 | 199406 | Fall | AL IV | Yankee 36 | 147 |
| Sum | | | | | 291 |
| 1995 | 199503 | Spring | AL IV | Yankee 36 | 143 |
| 1995 | 199507 | Fall | AL IV | Yankee 36 | 175 |
| Sum | | | | | 318 |
| 1996 | 199602 | Spring | AL IV | Yankee 36 | 136 |
| 1996 | 199604 | Fall | AL IV | Yankee 36 | 170 |
| Sum | | | | | 306 |
| 1997 | 199702 | Spring | AL IV | Yankee 36 | 153 |
| 1997 | 199706 | Fall | AL IV | Yankee 36 | 180 |
| Sum | | | | | 333 |
| 1998 | 199802 | Spring | AL IV | Yankee 36 | 171 |
| 1998 | 199804 | Fall | AL IV | Yankee 36 | 193 |
| Sum | | | | | 364 |
| 1999 | 199902 | Spring | AL IV | Yankee 36 | 139 |
| 1999 | 199908 | Fall | AL IV | Yankee 36 | 162 |
| Sum | | | | | 301 |
| 2000 | 200002 | Spring | AL IV | Yankee 36 | 144 |
| 2000 | 200005 | Fall | AL IV | Yankee 36 | 143 |
| Sum | | | | | 287 |
| 2001 | 200102 | Spring | AL IV | Yankee 36 | 146 |
| 2001 | 200109 | Fall | AL IV | Yankee 36 | 146 |
| Sum | | | | | 292 |
| 2002 | 200202 | Spring | AL IV | Yankee 36 | 150 |
| 2002 | 200209 | Fall | AL IV | Yankee 36 | 142 |
| Sum | | | | | 292 |
| 2003 | 200303 | Spring | DE II | Yankee 36 | 142 |
| 2003 | 200306 | Fall | DE II | Yankee 36 | 144 |
| Sum | | | | | 286 |
| Grand Total | | | | | 3070 |

Table 2. Summary of species catch records used in analysis after auditing procedures.

| Year | Cruise Code | Season | # of Species Records |
|---|---|---|---|
| 1994 | 199402 | Spring | 1,770 |
| 1994 | 199406 | Fall | 2,111 |
| 1995 | 199503 | Spring | 1,879 |
| 1995 | 199507 | Fall | 2,411 |
| 1996 | 199602 | Spring | 1,616 |
| 1996 | 199604 | Fall | 2,388 |
| 1997 | 199702 | Spring | 1,845 |
| 1997 | 199706 | Fall | 2,553 |

| | | | |
|---|---|---|---|
| 1998 | 199802 | Spring | 2,226 |
| 1998 | 199804 | Fall | 2,925 |
| 1999 | 199902 | Spring | 1,824 |
| 1999 | 199908 | Fall | 2,502 |
| 2000 | 200002 | Spring | 2,081 |
| 2000 | 200005 | Fall | 2,302 |
| 2001 | 200102 | Spring | 2,128 |
| 2001 | 200109 | Fall | 2,356 |
| 2002 | 200202 | Spring | 2,413 |
| 2002 | 200209 | Fall | 2,309 |
| 2003 | 200303 | Spring | 2,087 |
| 2003 | 200306 | Fall | 1,952 |
| Grand Total | | | 43,678 |

A set of subregions was used to group data in the time series based on cluster analyses of species assemblages from NEFSC survey data (Gabriel, 1992). Gabriel's (1992) analysis showed persistent spatial boundaries among groundfish species assemblages between the following subregions; deepwater, Georges Bank, Gulf of Maine, northern Mid-Atlantic Bight, southern Mid-Atlantic Bight, and the Scotian shelf. A spatially persistent boundary also occurred in some years for a transitional zone separating the GBK and the GOM and was included in the analysis. Some of these subregions were slightly modified in this analysis to include only those strata that occur in the study area, this excluded the southern Mid-Atlantic Bight entirely and portions of the northern Mid-Atlantic Bight and deepwater subregions, (Figure 9, Table 3).

Subregions are important in the analysis because they group similar species assemblages into areas with comparable depth zones allowing for analysis and comparisons of community structure between the subregions.

Table 3. List of NEFSC offshore strata by subregion included in analysis.

| Subregion | Strata Included |
|---|---|
| Deepwater | 11-12, 14-15, 17-18 |
| Georges Bank | 13, 16, 19-21 |
| Gulf of Maine | 24, 26, 27-30, 36-40 |
| N. Mid-Atlantic Bight | 9-10 |

| | |
|---|---|
| Scotian Shelf | 33-35 |
| Transitional zone | 22-23, 25 |

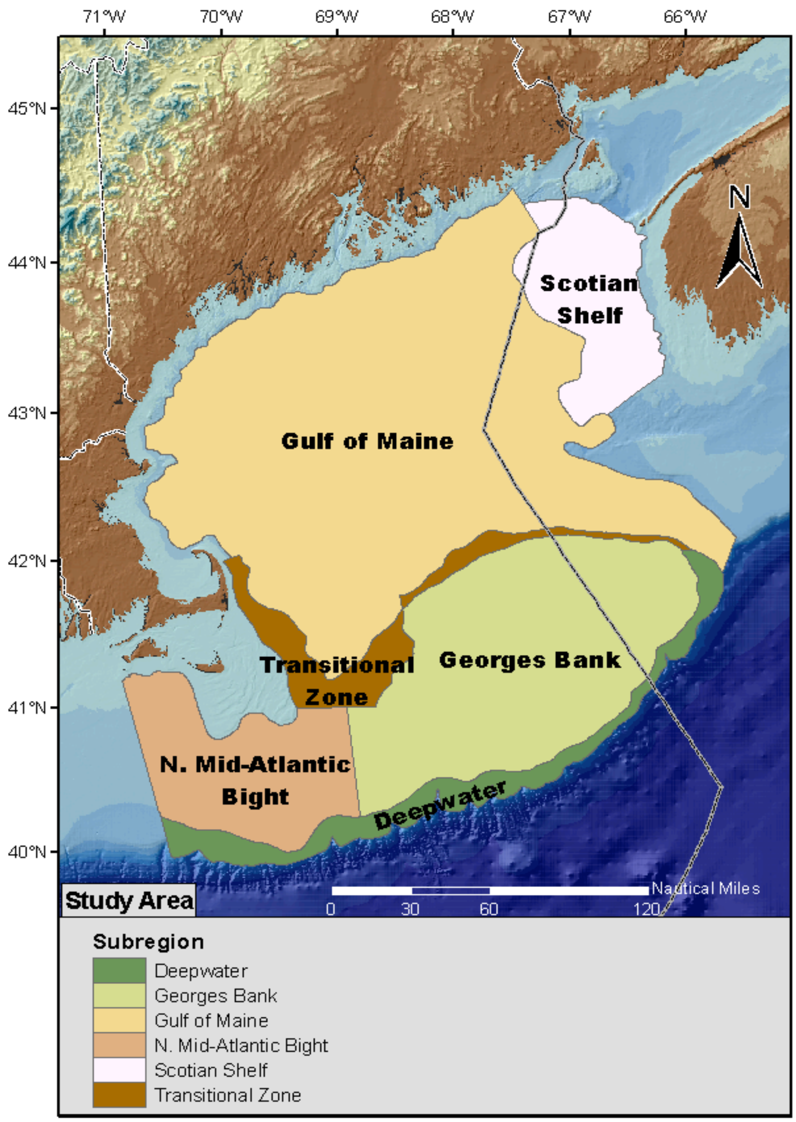



Figure 9. Subregions of study area based on persistent spatial boundaries of fish assemblages (Gabriel, 1992). Closed fishing areas and the U.S. EEZ are also shown.

Biodiversity was then calculated for each of the 3,070 sampling stations from the catch record data using the Shannon index of diversity (Magurran, 1988):

$$H = \sum_{i=0}^{n} - p_i \ln p_i$$

The Shannon index of diversity accounts for both species richness and evenness of a sampling location and is often considered a measure of heterogeneity. The derived index indicates the level of uncertainty that the next species observed would differ from those found before it. The index can be interpreted as the greater the level of uncertainty, the higher the diversity (Jennings et al, 2001). Values from the Shannon index are typically between 1.5 and 3.5 (Magurran, 1988). The Shannon index assumes random sampling from an infinitely large population and that all species at a sampling location are represented in the sample. These assumptions are met through the design of the stratified random bottom trawl survey and the fact that the trawl catches a representative sample of the community structure.

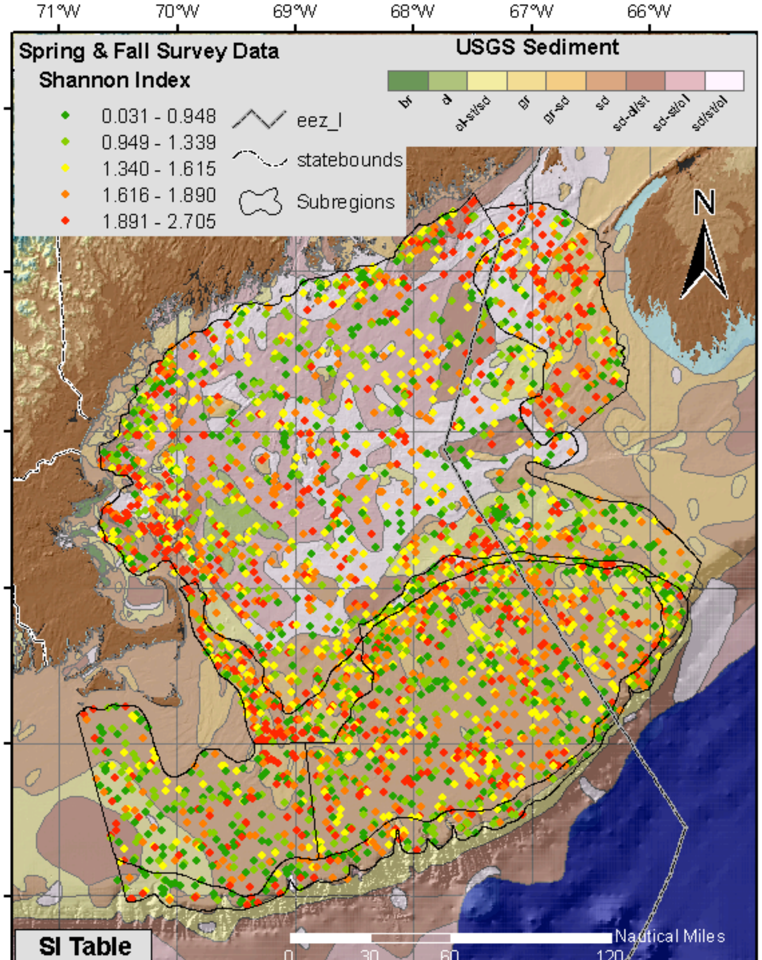
Shannon index calculations were accomplished by joining two tables in the NEFSC bottom trawl survey database: the station records database and the catch records database. The key fields needed from the databases were the unique ID fields from both databases, the spatial coordinates of the sampling locations from the station database and the species caught at a sampling location along with abundance of each species from the catch database. The ID field linked the databases together. Table 4 shows how the Shannon index was calculated for three stations. All species that were caught during a station were included when calculating the Shannon index. A few species could not be identified by scientific personnel aboard the R/V but were kept in the analysis and assigned a code of unknown 1 through unknown x. Catchability of different species and diel adjustments were not made to abundances due to a lack of information for all species in the analysis.

Table 4. An example of the Shannon diversity index calculation for three individual stations.

| Station | Latitude | Longitude | # Caught | Species | Total Ind # | *pi* | *pi ln pi* |
|---|---|---|---|---|---|---|---|
| 243 | 42.191000 | -68.073000 | 93 | *Merluccius bilinearis* | 250 | 0.372 | 0.368 |
| 243 | 42.191000 | -68.073000 | 4 | *Melanogrammus aeglefinus* | 250 | 0.016 | 0.066 |
| 243 | 42.191000 | -68.073000 | 10 | *Urophycis tenuis* | 250 | 0.040 | 0.129 |
| 243 | 42.191000 | -68.073000 | 32 | *Urophycis chuss* | 250 | 0.128 | 0.263 |
| 243 | 42.191000 | -68.073000 | 1 | *Enchelyopus cimbrius* | 250 | 0.004 | 0.022 |
| 243 | 42.191000 | -68.073000 | 2 | *Macrouridae* | 250 | 0.008 | 0.039 |
| 243 | 42.191000 | -68.073000 | 1 | *Peprilus triacanthus* | 250 | 0.004 | 0.022 |
| 243 | 42.191000 | -68.073000 | 29 | *Sebastes fasciatus* | 250 | 0.116 | 0.250 |
| 243 | 42.191000 | -68.073000 | 3 | *Helicolenus dactylopterus* | 250 | 0.012 | 0.053 |
| 243 | 42.191000 | -68.073000 | 2 | *Pasiphaea multidentata* | 250 | 0.008 | 0.039 |
| 243 | 42.191000 | -68.073000 | 16 | *Dichelopandalus leptocerus* | 250 | 0.064 | 0.176 |
| 243 | 42.191000 | -68.073000 | 43 | *Pandalus propinquus* | 250 | 0.172 | 0.303 |
| 243 | 42.191000 | -68.073000 | 12 | *Crustacea shrimp* | 250 | 0.048 | 0.146 |
| 243 | 42.191000 | -68.073000 | 2 | *Octopoda* | 250 | 0.008 | 0.039 |
| **243** | **42.191000** | **-68.073000** | | | $\sum -pi(\ln pi)$ | | **1.913** |
| 244 | 42.230500 | -67.976167 | 1 | *Clupea harengus* | 308 | 0.003 | 0.019 |
| 244 | 42.230500 | -67.976167 | 96 | *Merluccius bilinearis* | 308 | 0.312 | 0.363 |
| 244 | 42.230500 | -67.976167 | 5 | *Urophycis tenuis* | 308 | 0.016 | 0.067 |
| 244 | 42.230500 | -67.976167 | 5 | *Urophycis chuss* | 308 | 0.016 | 0.067 |
| 244 | 42.230500 | -67.976167 | 1 | *Urophycis chesteri* | 308 | 0.003 | 0.019 |
| 244 | 42.230500 | -67.976167 | 10 | *Urophycis sp* | 308 | 0.032 | 0.111 |
| 244 | 42.230500 | -67.976167 | 4 | *Macrouridae* | 308 | 0.013 | 0.056 |
| 244 | 42.230500 | -67.976167 | 11 | *Sebastes fasciatus* | 308 | 0.036 | 0.119 |
| 244 | 42.230500 | -67.976167 | 1 | *Helicolenus dactylopterus* | 308 | 0.003 | 0.019 |
| 244 | 42.230500 | -67.976167 | 3 | *Crangon septemspinosa* | 308 | 0.010 | 0.045 |
| 244 | 42.230500 | -67.976167 | 4 | *Pasiphaea multidentata* | 308 | 0.013 | 0.056 |
| 244 | 42.230500 | -67.976167 | 1 | *Lebbeus polaris* | 308 | 0.003 | 0.019 |
| 244 | 42.230500 | -67.976167 | 9 | *Dichelopandalus leptocerus* | 308 | 0.029 | 0.103 |
| 244 | 42.230500 | -67.976167 | 46 | *Pandalus propinquus* | 308 | 0.149 | 0.284 |
| 244 | 42.230500 | -67.976167 | 1 | *Homarus americanus* | 308 | 0.003 | 0.019 |
| 244 | 42.230500 | -67.976167 | 109 | *Crustacea shrimp* | 308 | 0.354 | 0.368 |
| 244 | 42.230500 | -67.976167 | 1 | *Bathypolypus arcticus* | 308 | 0.003 | 0.019 |
| **244** | **42.230500** | **-67.976167** | | | $\sum -pi(\ln pi)$ | | **1.752** |
| 245 | 42.190667 | -67.738667 | 2 | *Malacoraja senta* | 205 | 0.010 | 0.045 |
| 245 | 42.190667 | -67.738667 | 18 | *Clupea harengus* | 205 | 0.088 | 0.214 |
| 245 | 42.190667 | -67.738667 | 51 | *Merluccius bilinearis* | 205 | 0.249 | 0.346 |
| 245 | 42.190667 | -67.738667 | 3 | *Gadus morhua* | 205 | 0.015 | 0.062 |
| 245 | 42.190667 | -67.738667 | 4 | *Melanogrammus aeglefinus* | 205 | 0.020 | 0.077 |
| 245 | 42.190667 | -67.738667 | 6 | *Pollachius virens* | 205 | 0.029 | 0.103 |
| 245 | 42.190667 | -67.738667 | 6 | *Urophycis tenuis* | 205 | 0.029 | 0.103 |
| 245 | 42.190667 | -67.738667 | 14 | *Urophycis chuss* | 205 | 0.068 | 0.183 |
| 245 | 42.190667 | -67.738667 | 13 | *Urophycis chesteri* | 205 | 0.063 | 0.175 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 245 | 42.1906667 | -67.7386667 | 1 | *Hippoglossoides platessoides* | 205 | 0.005 | 0.026 |
| 245 | 42.1906667 | -67.7386667 | 3 | *Glyptocephalus cynoglossus* | 205 | 0.015 | 0.062 |
| 245 | 42.1906667 | -67.7386667 | 5 | *Helicolenus dactylopterus* | 205 | 0.024 | 0.091 |
| 245 | 42.1906667 | -67.7386667 | 1 | *Lebbeus polaris* | 205 | 0.005 | 0.026 |
| 245 | 42.1906667 | -67.7386667 | 1 | *Spirontocaris liljeborgii* | 205 | 0.005 | 0.026 |
| 245 | 42.1906667 | -67.7386667 | 2 | *Dichelopandalus leptocerus* | 205 | 0.010 | 0.045 |
| 245 | 42.1906667 | -67.7386667 | 55 | *Pandalus propinquus* | 205 | 0.268 | 0.353 |
| 245 | 42.1906667 | -67.7386667 | 19 | *Crustacea shrimp* | 205 | 0.093 | 0.220 |
| 245 | 42.1906667 | -67.7386667 | 1 | *Bathypolypus arcticus* | 205 | 0.005 | 0.026 |
| **245** | **42.1906667** | **-67.7386667** | | | $\sum -pi(\ln pi)$ | | **2.183** |

At present biodiversity could be modeled using subregion, which inherently includes information pertaining to similar species assemblages and similar depth strata. Other factors likely influence the spatial distribution of biodiversity, such as season, sediment type and year. Season and year were linked to the geographic data through a table join in ESRI ArcMap 9.0. ESRI ArcMap 9.0 and ArcInfo Workstation 9.0 were used exclusively for mapping geographic data and for some spatial analyses. A table join allows for linking additional attribute data from an external table to geographic features based on a common ID field. Sediment type attributes were added to the spatial locations of the Shannon index using the Identity command on a sediment shapefile created by the USGS (Hastings et al, 2000) in ArcToolbox. The Identity command computes the geometric intersection of the input coverage (the Shannon index of diversity), and the identity coverage (the USGS sediment polygon coverage), to produce an output coverage that contains attributes from both the input and the identity coverages, (Figure 10).




| YEAR | ID | DD_LAT | DD_LON | SI | REGION | SEDIMENT |
|---|---|---|---|---|---|---|
| 1996 | 199604284 | 44.433333 | -67.483333 | 2.346117 | GOM | sd-cl/st |
| 1997 | 199702312 | 44.416667 | -67.5 | 2.484342 | GOM | sd-cl/st |
| 2002 | 200202290 | 44.398833 | -67.169333 | 2.433176 | SC | sd/st/cl |
| 2001 | 200102264 | 44.395035 | -67.013252 | 2.119977 | SC | sd/st/cl |
| 2000 | 200002308 | 44.387167 | -66.899667 | 1.793470 | SC | sd/st/cl |
| 2003 | 200303287 | 44.376862 | -67.564637 | 2.210797 | GOM | sd-cl/st |
| 1996 | 199604285 | 44.366667 | -67.666667 | 1.443499 | GOM | sd-cl/st |
| 2003 | 200303286 | 44.361873 | -67.089272 | 2.704916 | SC | sd/st/cl |
| 2002 | 200202291 | 44.360667 | -67.662333 | 0.859466 | GOM | sd-cl/st |
| 1999 | 199908275 | 44.3535 | -66.7165 | 0.591841 | SC | sd/st/cl |

Figure 10. Spatial locations of stations with an example of Shannon index, subregion, season, sediment type and year attribute information. The U.S. EEZ is also shown.

The four variables of subregion, season, sediment type and year, were all believed to have influenced the spatial distribution of biodiversity within the study area. Significance of these variables was tested though stepwise linear regression model selection in S-Plus 6.2. The stepwise regression aided in the determination of what variables to include in the interpolation of biodiversity by considering two models: a full model with a response variable and all potentially influential factor variables, and a simple model with a single response and factor variable. The two models are shown in Table 5.

Table 5. Linear regression models used in the stepwise regression analysis.

| **Model** | **Response Variable ~ Explanatory Variables** |
|---|---|
| Full Model | Shannon Index ~ Subregion + Season + Sediment Type + Year |
| Simple Model | Shannon Index ~ Subregion |

The stepwise model selection indicated that only two of the factor variables included were significant in modeling the Shannon index, subregion and year.

The Shannon index point data, shown in Figure 10, were then subset according to the statistically significant explanatory factors, subregion and year, from the stepwise linear regression model. Data were then examined for trends, outliers, and spatial autocorrelation. To visually examine the Shannon index for trends or potential outliers, histograms and normal QQ plots were created using S-Plus statistical software.

Spatial autocorrelation is derived from the first law of geography, which is the expression of spatial dependence that "everything is related to everything else, but near things are more related than distant things" (Tobler, 1970). Spatial autocorrelation is a measure or index of spatial dependence, and is therefore interested in two aspects of the data, the similarity of the attribute of interest and similarity of the locations of the attribute of interest (e.g., Longley el al, 2001). The Moran index (which calculates the products of values in neighboring objects) was used to test if the Shannon index attributes showed a systematic pattern in its spatial distribution. In general, results from the calculation of Moran's index range from –1 to +1, where negative values are unalike, positive values are alike, and zero values show no spatial autocorrelation at all. Spatial autocorrelation was measured for the biodiversity index with the Moran's I utility in the ArcToolbox Spatial Statistics Tools. This tool measures spatial autocorrelation (feature similarity) based on both feature locations and feature values simultaneously (ESRI, 2001). Graphical output evaluates whether the pattern expressed within the data are clustered, random, or dispersed. Again the numeric output of the Moran's I value ranges from –1.0 to +1.0. An index value near -1.0 indicates a dispersed pattern and a value of +1.0 indicates a clustered pattern. A Z-Score is also calculated to assess whether the observed pattern is statistically significant or not. Data were grouped by subregion and year.

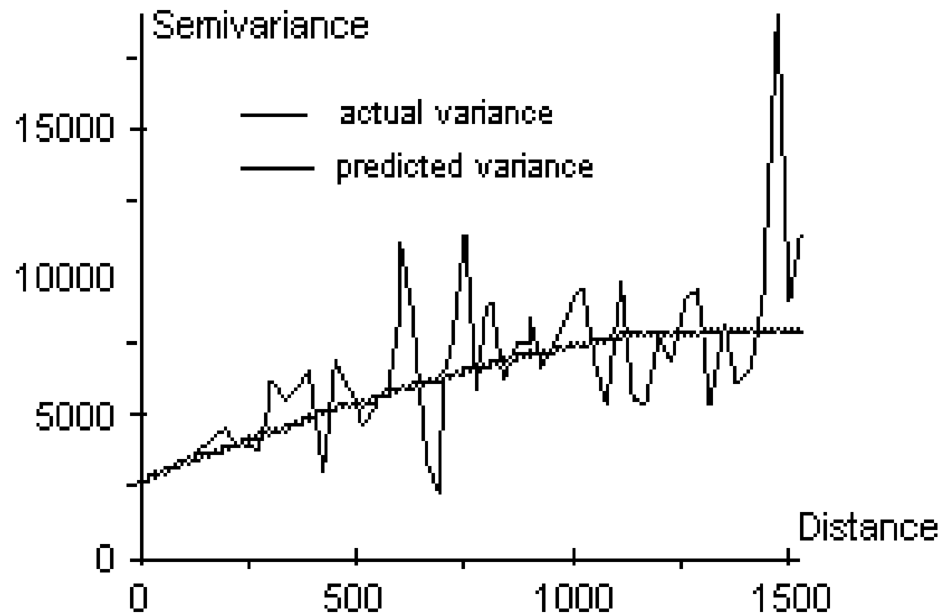



Figure 11. An example of an semivariogram used to interpolate known values to areas where sampling did not occur.

Interpolation of the Shannon index point data to a continuous surface was performed with ordinary kriging. Kriging is a spatial interpolation technique that estimates an unknown point value from neighboring points with known values and applies a weighting function that is based on the semivariogram. A major advantage of kriging is the ability to output a measure of uncertainty of estimates, which can be used to identify locations where additional sampling would make a significant difference in decreasing uncertainty. Ordinary kriging was chosen because all regions expressed some spatial dependence, even though it was usually not statistically significant. The semivariogram is a statistical model that summarizes the similarity between pairs of points with increasing distance, and is thus the descriptor of the amount and form of spatial autocorrelation in the kriging process. The y-axis, semivariance (often denoted as gamma), is one half the average square difference between samples separated by a common distance, the x -axis (Figure 11). There are two components of the semivariogram, the empirical values, the jagged black line, and the theoretical model, the smooth black line. The empirical semivariogram plots the semivariance between a pair of points binned to similar distance ranges, known as the lag distance. Points within the distance range are then averaged and the theoretical semivariogram is fit to the averaged semivariance for the distance bins. Lag size in this analysis was set to one half the largest distance among all points divided by the number of lags, twelve in all cases. This is a general rule of thumb for estimating lag size for data acquired in a random sampling scheme (ESRI, 2001). Plotting all points and manually measuring the two points furthest apart estimated the largest distance. If the first law of geography is true then the semivariance values on the left of Figure 11 will be low and increase as distance between data points increases. Empirical and theoretical spherical semivariograms were created for the Shannon index point data by subregion and year along with the associated kriged surfaces of biodiversity.

The kriged surfaces of biodiversity were then converted into raster representations of biodiversity. In general, the raster representation of the kriging output converts a temporary surface into a permanent one with an appropriate cell size. Each cell of any raster coverage contains only one value. In this analysis, cell size was based on the dimensions of the swept area of a standard bottom trawl survey tow. The standard bottom trawl tow is usually conducted for 30 minutes, (0.5 hours), at 7.0 kts producing a nominal distance of 3.5 km or

3,500 m. Area of the tow was therefore approximated by multiplying the distance, 3,500 m, times 25 m, the width of the bottom trawl, producing an area of 87,500 $m^2$. Cells in a raster feature are limited to a square configuration and do not represent the dimensions of a trawl accurately. Taking the square root of the trawl area resulted in a square cell size of 296 $m^2$, keeping the area swept by the trawl consistent. Cell size was increased by 40% to 500 $m^2$, which will account for some of the dimensional differences and aid computation speed of making the biodiversity raster images.

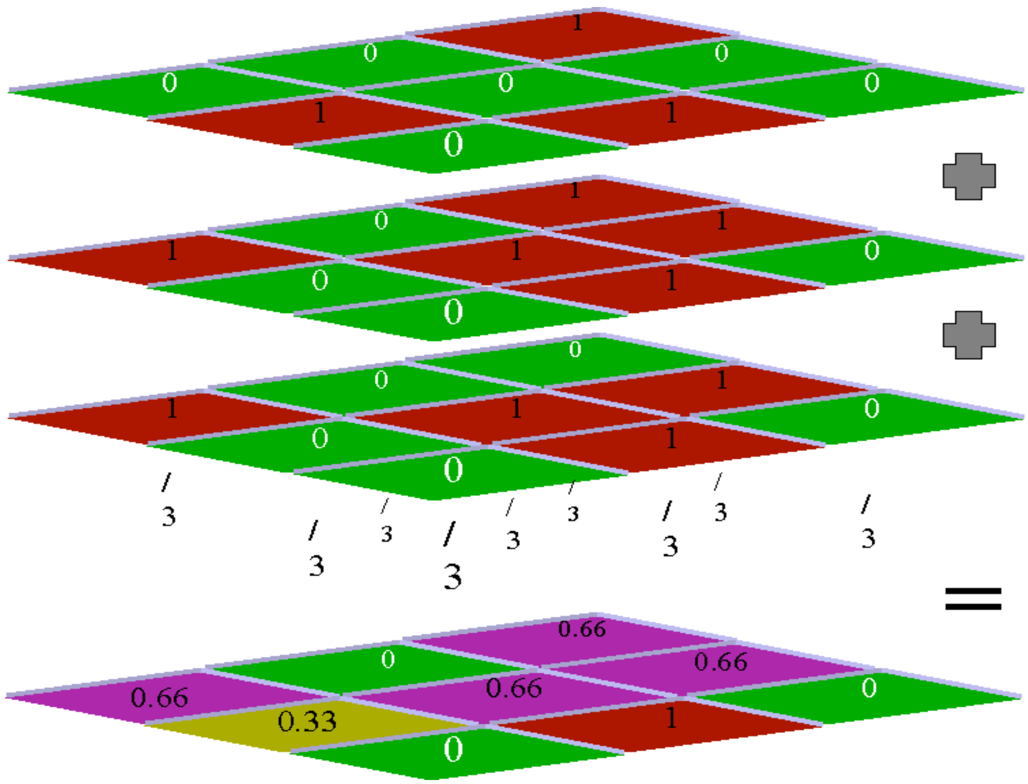



Figure 12. An example of map algebra using the raster calculator to create a biodiversity hotspot map.

The kriged surfaces were interpolated for the entire study area. If the kriged surface only interpolated to the extent of the sampling points significant gaps would occur. These large raster biodiversity coverages were clipped using the ArcMap Raster Calculator to the spatial extent of the subregion. Fine scale raster coverages were created from the subregion polygons shown in Figure 9. The raster coverages of subregion contain a value of 1 if it is within the subregion and a 0 if outside. By multiplying the large biodiversity raster coverages to the fine scale subregion raster, values inside the subregion remain unchanged and those outside become 0 and were essentially removed.

Averaging the yearly biodiversity raster coverages for each subregion creates Biodiversity "hotspots". The average biodiversity raster was created using the ArcMap Raster Calculator (Figure 12). The raster calculator added the value of the Shannon index from each cell, producing a cumulative biodiversity, and then divided this value by 10, the number of years in the time series. Combining the yearly biodiversity smoothed the year-to-year variation per cell and provided a representation of the central tendency of biodiversity. This process was conducted for each region.

The six separate subregion rasters were combined into one raster data set using the mosaic command in Raster Calculator. Mosaicking allows adjacent grids to be merged together, thereby minimizing abrupt changes along the boundaries of different grids, and should thus be used only with continuous surfaces. Because the spatial extent of the subregions did not overlap, the mosaic process did not modify cells along the boundaries. The symbology of the mosaic data set was classified into deciles, categorizing the histogram of data values into percentiles so that 10% of the data fell into each category. The compiled biodiversity raster grid was then reclassified into values ranging from 1 to 10 to represent the appropriate percentile group. Reclassify is a command that modifies the INFO table of the raster data set from the original data values to a new value symbol. These reclassified biodiversity data were then used in the weighted raster model for optimizing potential MPAs.

**Spawning and Nursery Area Habitats**

Analyses were performed to create a priority spawning and nursery habitat raster data set for inclusion in the selection of potential MPAs, (Figure 13). Similar databases were used to conduct the spawning and nursery area habitats analyses as were utilized in the biodiversity

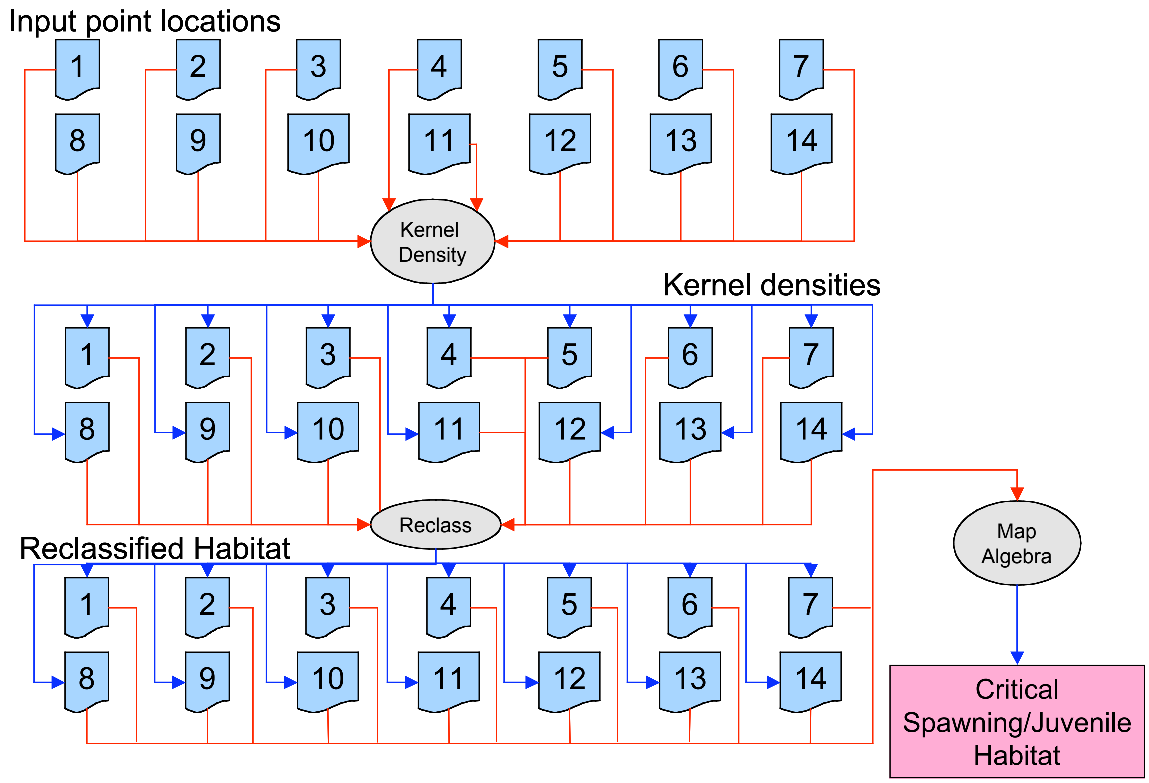



Figure 13. A GIS flowchart for the creation of the weighted juvenile and spawning habitat raster data sets.

analyses. Station records were pulled from the bottom trawl survey station database and the biological records were accessed from a new table, the bottom trawl survey biology database. This database contained information concerning the lengths, weights, and maturity stages of individual fish. NOAA Fisheries biologists assess the maturity stage of a particular fish aboard the R/V by dissecting and examining gonad tissue. Assessment of the gonad results in a maturity code for the individual of immature, developing, ripe, ripe and running, spent, or resting. An additional time series of data was added to the analyses (the winter BTS) so that winter, spring, and fall cruises for the years 1994 – 2003 were included. The strata set that was used for the biodiversity hotspot analysis was also used for the spawning and nursery area habitat analysis.

Fourteen select species were used in the analysis due to their importance as commercial species targeted by fishers, and because information concerning their maturity were available from the NEFSC BTS, as well as detailed records of their life history information from literature, and (Table 6). Life history information normally pertains to specific spawning seasons and maximum size of juvenile animals. These values were gleaned from Essential Fish Habitat Source Documents for each species.

Table 6. Spawning and juvenile life history information of selected species in GIS analysis.

| Species | Species Name | Common Name | Stock Region | Max Size of Juvenile | Spawning Season (Peak) |
|---|---|---|---|---|---|
| 1 | *Clupea harengus* | Atlantic herring | GOM & GBK | 24 | Autumn |
| 2 | *Gadus morhua* | Atlantic cod | GOM | 35 | Winter / Spring |
| | *Gadus morhua* | Atlantic cod | GBK & south | 35 | Winter / Spring |
| 3 | *Glyptocephalus cynoglossus* | witch flounder | GOM & GBK | 30 | Spring / Summer |
| 4 | *Hippoglossoides platessoides* | American plaice | GOM & GBK | 27 | Spring (Mar-May) |
| 5 | *Limanda ferruginea* | yellowtail flounder | GBK | 26 | Spring / Summer (May) |
| | *Limanda ferruginea* | yellowtail flounder | SNE | 26 | Spring / Summer (May) |
| | *Limanda ferruginea* | yellowtail flounder | Cape Cod | 26 | Spring / Summer (May) |
| 6 | *Lophius americanus* | monkfish | GOM & GBK | 43 | Spring / Autumn |
| 7 | *Macrozoarces americanus* | ocean pout | GOM | 29 | Autumn |
| | *Macrozoarces americanus* | ocean pout | SNE | 29 | Autumn |
| 8 | *Melanogrammus aeglefinus* | haddock | GOM | 32 | Winter / Summer (Mar-April) |
| | *Melanogrammus aeglefinus* | haddock | GBK | 32 | Winter / Summer (Mar-April) |
| 9 | *Merluccius bilinearis* | silver hake | GOM & N GBK | 23 | Spring / Summer |
| | *Merluccius bilinearis* | silver hake | S GBK & south | 23 | Spring / Summer |
| 10 | *Peprilus triacanthus* | butterfish | GOM & GBK | 11 | Summer |
| 11 | *Pseudopleuronectes americanus* | winter flounder | GOM | 27 | Winter |
| | *Pseudopleuronectes americanus* | winter flounder | GBK | 27 | Winter |
| | *Pseudopleuronectes americanus* | winter flounder | SNE & Mid Atlantic | 27 | Winter |
| 12 | *Scomber scombrus* | Atlantic mackerel | Labrador to NC | 25 | Spring / Summer |
| 13 | *Scophthalmus aquosus* | windowpane flounder | GOM & GBK | 22 | Summer (July-August) |
| | *Scophthalmus aquosus* | windowpane flounder | SNE & Mid Atlantic | 22 | Spring (May) / Autumn (October) |
| 14 | *Sebastes fasciatus* | Acadian redfish | GOM & GBK | 22 | Spring / Summer |

* GBK = Georges Bank, GOM = Gulf of Maine, SNE = Southern New England, NC = North Carolina

Data were accessed for each species individually so that specific life history parameters could be applied to the data, which limited data selection to only spawning or juvenile fish. Individuals of a particular species were only considered spawners if the fish was greater than the maximum juvenile size and had a maturity code of ripe or ripe and running.

Juvenile parameters were fish less than or equal to the maximum juvenile size and a maturity code of immature. These queries resulted in a metric describing the number of spawning or immature individuals caught per station. From this point forward in the analysis the methodology for both spawning and juvenile data sets was identical.

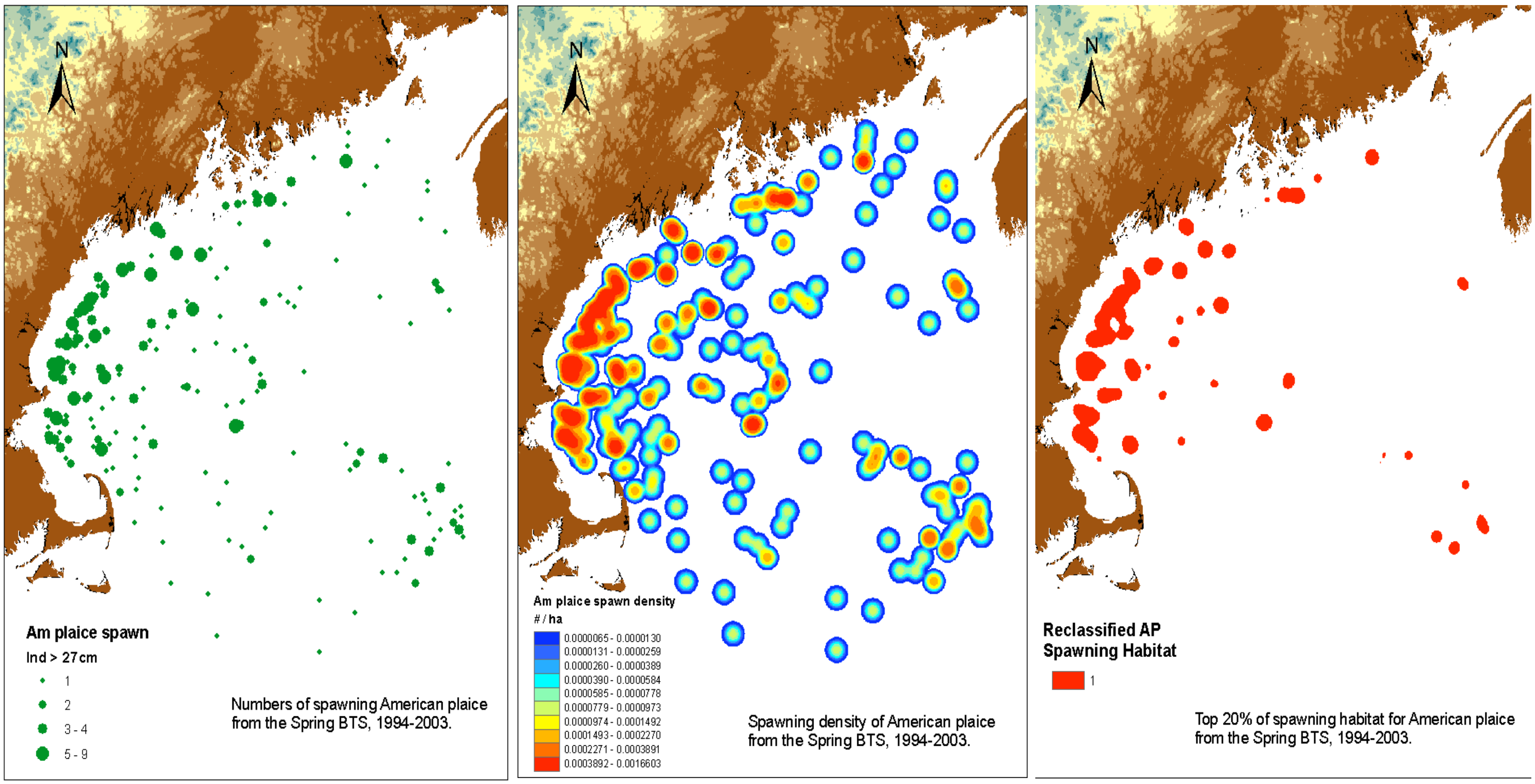



Figure 14. An example of transforming numbers per tow from fishery independent data (a) into kernel density estimates (b) and then reclassified spawning habitat (c).

Spawning/juvenile information was then linked to spatial locations in the station database via the ID field to create species-specific point shapefiles (Figure 14). The point data were then rasterized using the kernel density function in ArcMap - Spatial Analyst. Kernel density analysis took the known quantities of spawning/juvenile fish and spreads it across the seascape based on the quantity that was measured at each point, and the spatial relationship of the locations of the measured quantities. In general, the surface value of a kernel is highest at the location of the point and decreases to 0 at the extent of the search radius. The volume under the surface equals the population field value for the point, or 1 if none is specified. The density at each output raster cell is calculated by adding the values of all the kernel surfaces where they overlay the raster cell center. The search radius was set to 10,000 m, equivalent to an area of 314 km,, with spawning/juvenile density reported in numbers per hectare. This process was repeated for each of the fourteen species for the two data sets, spawning habitat and nursery habitat.

The density raster data sets were classified into deciles, the 10$^{th}$, 20$^{th}$,…100$^{th}$ percentiles so that 10% of the data would fall in each category. The reclassify command was used to change the density calculations into integers values, i.e. 1 = the 10$^{th}$ percentile, 2 = the 20$^{th}$ percentile, etc, for each species. Raster calculator was used to remove all values in the reclassified data set that were less than 9. This condensed data set was again reclassified from values of 9 and 10 to values of 1. The resulting data sets contained the areas with the highest density of spawning/juvenile fish, i.e. the top 20% of the spawning/juvenile habitat for each species.

Raster calculator was used to combine the fourteen spawning habitats into a single representative spawning habitat map by adding each raster together (Figure 15). Since each raster data set contained a value of 1 for a critical spawning area, the values in the output data set contained information on how many species share this critical habitat. The resulting number of species represented the weight during the optimization process for delineating potential MPAs.

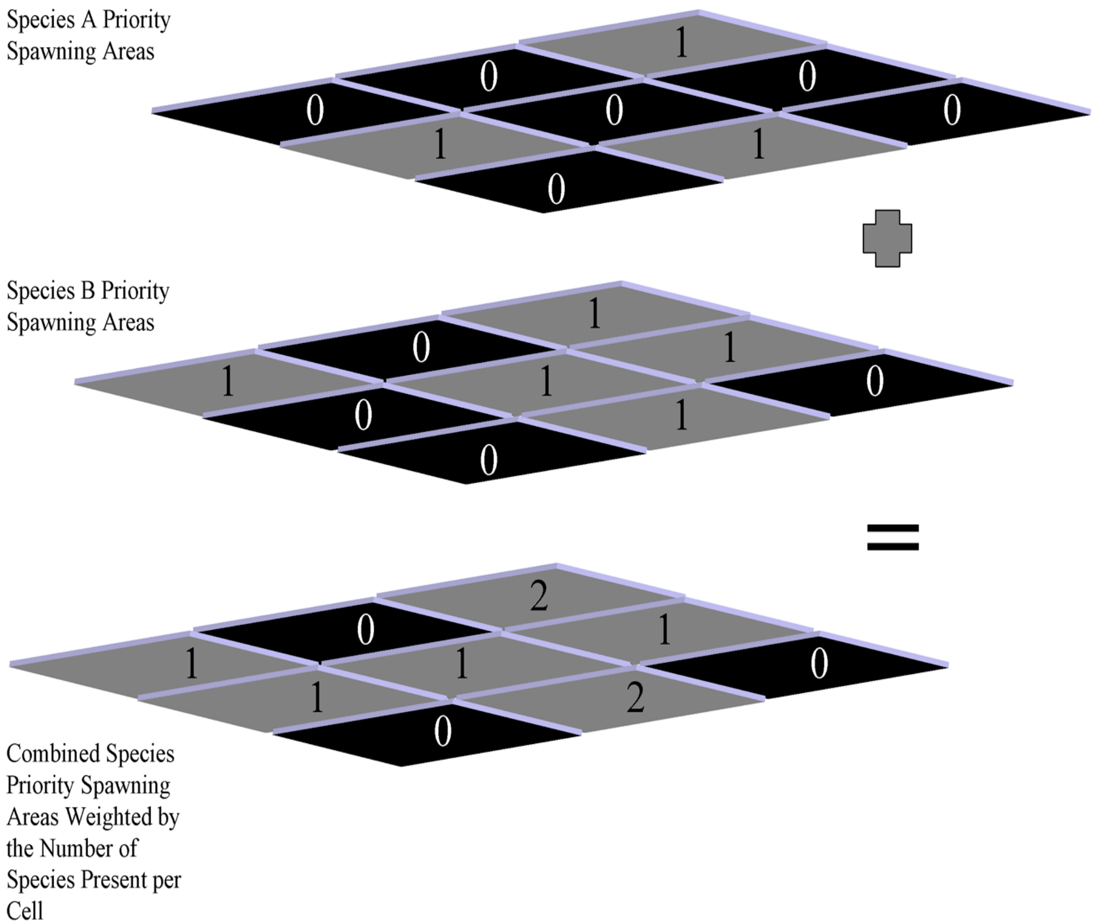



Figure 15. The process of combining spawning habitat for many species to get critical spawning areas.

**Essential Commercial Fishing Zones**

Fishery dependent data were analyzed from the VTR databases. The years used in this analysis ranged from 1994 – 2002, (Figure 16). 2003 had to be omitted because the data were incomplete. Data were limited to the same subregions used in the previous analyses. The VTR Gear, Species, and Trip databases were linked together with common ID fields, providing a table and point shapefile containing latitude and longitude, ID, species caught, quantity kept and discarded. Only those species for which spawning and juvenile habitat

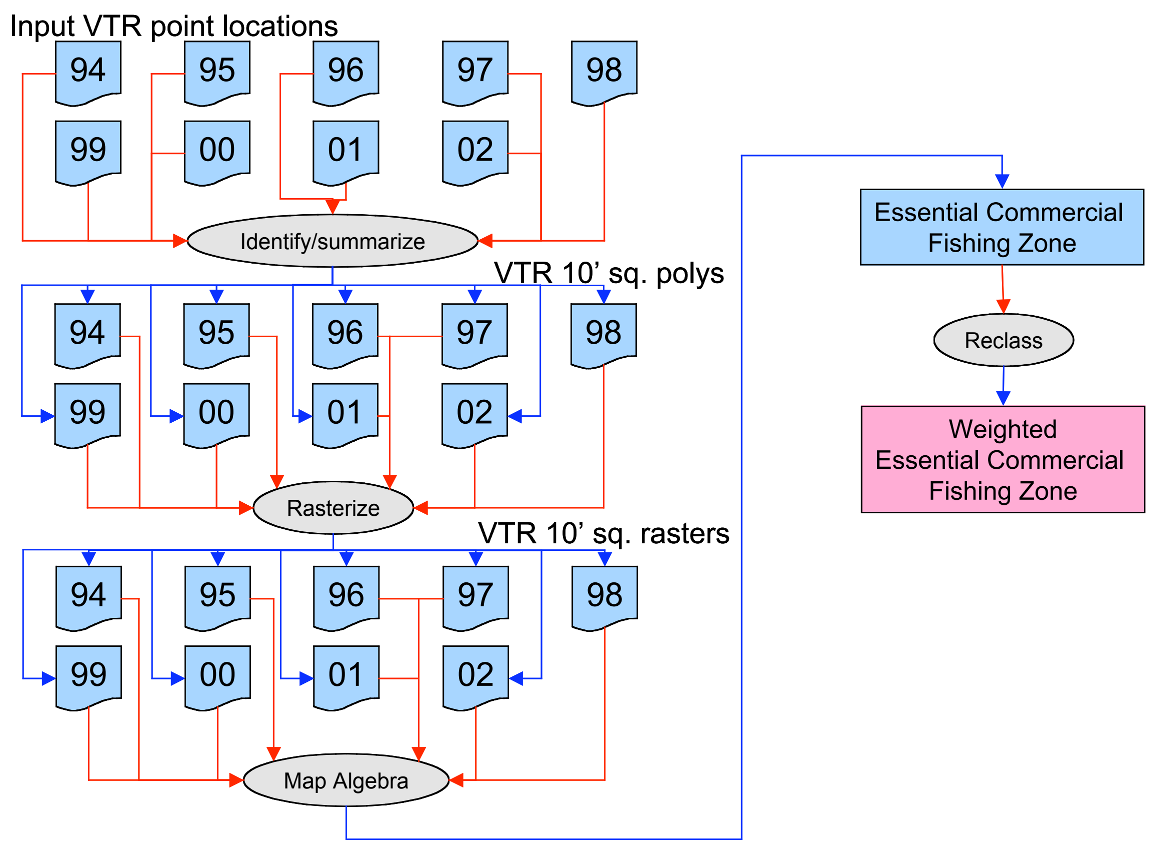



Figure 16. A GIS flowchart for the creation of the weighted essential commercial fishing zone raster data sets.

analyses could be performed were included in this analysis. Species were kept consistent in both analyses to insure that some commercially important species would maintain viable and productive populations in the study area. An initial analysis was conducted to see what species were reported in the VTR database for the study area. Kept and discarded catches were reported in pounds and converted into metric tons (Table 7).

Table 7. Kept and discarded species (mt) from VTR data in the study area

| Common Name of Species | Kept mt Total | Discard mt Total | Common Name of Species | Kept mt Total | Discard mt Total |
|---|---|---|---|---|---|
| Alewife | 1 | 0 | Halibut, Greenland | 0 | 0 |
| Amber Jack | 0 | 0 | Herring, Atlantic | 434,715 | 993 |
| Angler (monkfish) | 38,430 | 564 | Herring, Blue Back | 74 | 41 |
| Bass, Striped | 23 | 17 | John Dory | 16 | 0 |
| Bluefish | 860 | 16 | Lumpfish | 1 | 0 |
| Bonito | 1 | 0 | Mackerel, Atlantic | 3,277 | 45 |

| | | | | | |
|---|---|---|---|---|---|
| Butterfish | 3,834 | 114 | Mackerel, Chub | 1 | 0 |
| Cobia | 0 | 0 | Mackerel, Frigate | 0 | 0 |
| Cod | 64,645 | 2,285 | Mackerel, King | 0 | 0 |
| Croaker, Atlantic | 39 | 8 | Mackerel, Spanish | 0 | 0 |
| Cunner | 18 | 2 | Marlin | 4 | 0 |
| Cusk | 1,960 | 22 | Marlin White | 1 | 0 |
| Dogfish (Nk) | 4,293 | 968 | Menhaden | 3 | 0 |
| Dogfish Chain | 14 | 0 | Mullets | 1 | 0 |
| Dogfish Smooth | 46 | 101 | Other Fish | 473 | 46 |
| Dogfish Spiny | 18,366 | 7,419 | Pollock | 20,688 | 115 |
| Dolphin Fish | 12 | 0 | Porgy, Red | 0 | 0 |
| Eel, American | 1 | 0 | Pout, Ocean | 42 | 75 |
| Eel, Conger | 5 | 0 | Puffer, Northern | 0 | 0 |
| Eel, Nk | 179 | 1 | Redfish | 2,004 | 117 |
| Flounder, Am. Plaice | 25,291 | 550 | Rosefish,Blk Bellied | 1 | 2 |
| Flounder, Fourspot | 14 | 5 | Scad, Rough | 0 | 5 |
| Flounder, Summer | 2,392 | 170 | Sculpins | 20 | 76 |
| Flounder, Windowpane | 2,646 | 140 | Scup | 148 | 19 |
| Flounder, Winter | 21,037 | 185 | Sea Bass, Black | 128 | 4 |
| Flounder, Witch | 14,544 | 304 | Sea Raven | 10 | 33 |
| Flounder, Yellowtail | 24,411 | 390 | Sea Robins | 4 | 7 |
| Flounders (Nk) | 3,279 | 23 | Shad, American | 40 | 4 |
| Gizzard Shad | 0 | 0 | Shark, Atl Sharpnose | 0 | 0 |
| Grouper | 4 | 0 | Shark, Basking | 0 | 4 |
| Grunts | 0 | 0 | Shark, Black Tip | 0 | 0 |
| Haddock | 15,758 | 612 | Shark, Blue | 3 | 35 |
| Hagfish | 8,439 | 112 | Shark, Dusky | 0 | 0 |
| Hake Mix Red & White | 4,795 | 29 | Shark, Hamerhd Great | 0 | 0 |
| Hake, Offshore | 584 | 16 | Shark, Hammerhead | 0 | 4 |
| Hake, Red | 4,041 | 200 | Shark, Mako | 5 | 2 |
| Hake, Silver | 37,978 | 524 | Shark, Mako Longfin | 1 | 0 |
| Hake, White | 8,924 | 73 | Shark, Mako Shortfin | 4 | 0 |
| Halibut, Atlantic | 44 | 3 | Shark, Nk | 23 | 2 |
| Shark, Porbeagle | 31 | 1 | Tilefish | 881 | 0 |
| Shark, Sandbar | 6 | 5 | Triggerfish | 0 | 0 |
| Shark, Thresher | 13 | 0 | Tuna Nk | 25 | 2 |
| Shark, Tiger | 0 | 1 | Tuna, Albacore | 100 | 0 |
| Shark, White | 1 | 6 | Tuna, Big Eye | 15 | 0 |
| Shark, Whitetip Oc | 10 | 0 | Tuna, Bluefin | 1,641 | 68 |
| Silverside, Atlantic | 0 | 0 | Tuna, Little | 0 | 0 |
| Skates | 23,722 | 6,344 | Tuna, Skipjack | 2 | 0 |
| Smelt | 0 | 0 | Tuna, Yellowfin | 119 | 1 |
| Spadefish | 1 | 0 | Wahoo | 0 | 0 |
| Spot | 5 | 1 | Weakfish, Spotted | 1 | 0 |
| Sturgeon, Atlantic | 0 | 0 | Weakfish, | 3 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| | | | Squeteague | | |
| Sturgeons | 0 | 0 | Whiting, King | 1,954 | 67 |
| Swordfish | 26 | 0 | Wolffishes | 1,346 | 11 |
| Tautog | 7 | 0 | Grand Total | 798,507 | 22,985 |

Many of these species comprised only a small percentage of the total catch. Table 8 shows the species included in the essential fishing zone analysis. Total kept and discarded catch for all species were compared to the total kept and discarded catch for the selected species for each year in the time series (Table 9). These selected species comprised the majority of fish landed in the study area, 89.5% over all years.

Table 8. Selected species list for VTR analysis and associated catch of kept and discarded (mts).

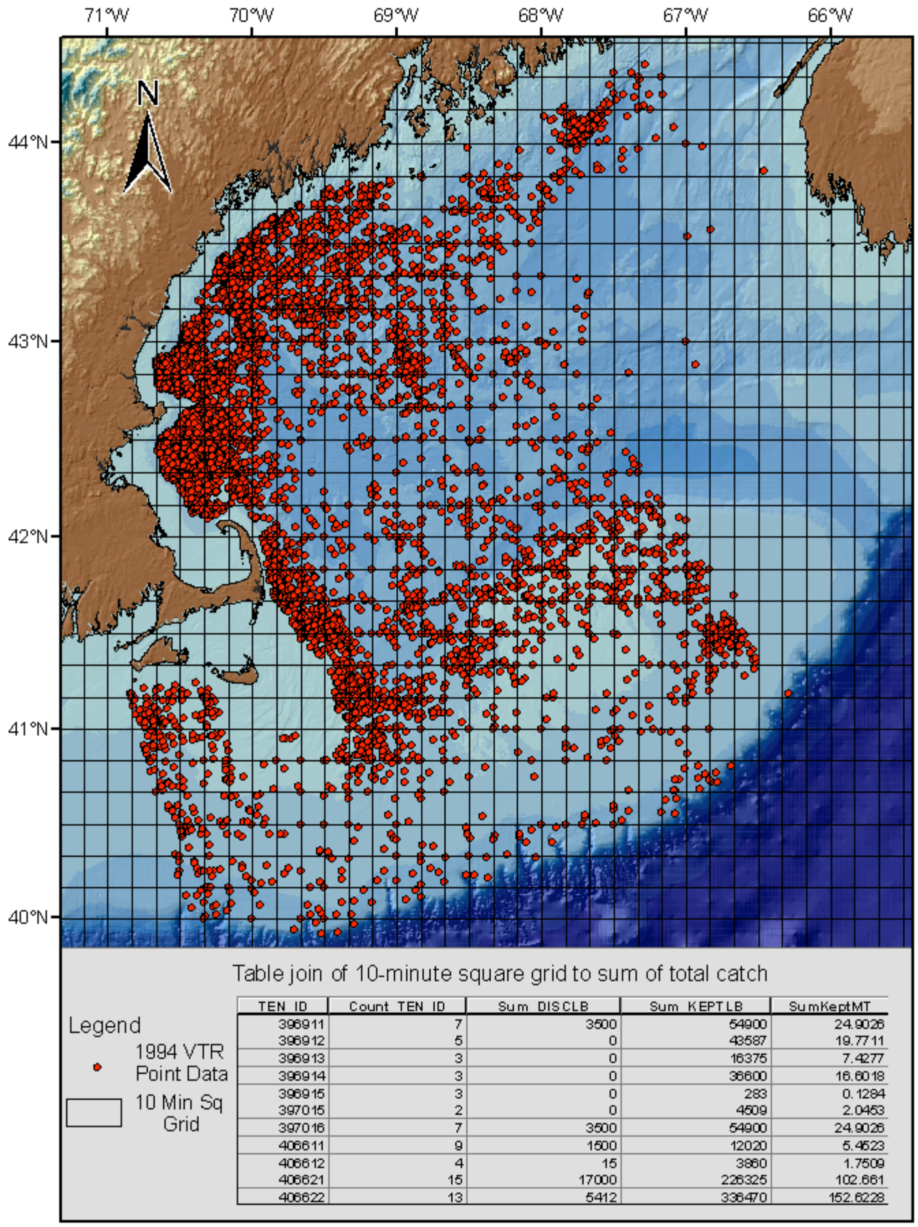
| Common Name of Species | Kept mt Total | Discard mt Total |
|---|---|---|
| Angler (monkfish) | 43,179 | 579 |
| Butterfish | 4,272 | 115 |
| Cod | 72,018 | 2,493 |
| Flounder, Am. Plaice | 28,909 | 611 |
| Flounder, Windowpane | 3,002 | 141 |
| Flounder, Winter | 22,109 | 216 |
| Flounder, Witch | 16,771 | 360 |
| Flounder, Yellowtail | 24,191 | 403 |
| Haddock | 17,547 | 770 |
| Hake, Silver | 40,606 | 554 |
| Herring, Atlantic | 436,243 | 894 |
| Mackerel, Atlantic | 3,885 | 50 |
| Pout, Ocean | 45 | 89 |
| Redfish | 2,539 | 162 |
| Grand Total | 715,315 | 7,440 |

Table 9. All species caught vs. select species caught and percent of total catch for VTR data.

| Year | VTR Data All Spp mt Kept | VTR Data Select Spp mt Kept | % Total |
|---|---|---|---|
| 1994 | 42,245 | 36,632 | 86.7 |
| 1995 | 82,530 | 75,706 | 91.7 |
| 1996 | 96,275 | 85,926 | 89.3 |
| 1997 | 98,931 | 88,120 | 89.1 |
| 1998 | 80,633 | 70,457 | 87.4 |
| 1999 | 117,522 | 95,502 | 81.3 |
| 2000 | 117,522 | 112,747 | 95.9 |
| 2001 | 94,016 | 87,485 | 93.1 |

| | | | |
|---|---|---|---|
| 2002 | 68,833 | 62,741 | 91.2 |
| Average % Total, 1994 - 2002 | | | 89.5 |

A 10-minute quadrilateral grid shapefile was created by the NEFSC to cover the commercial fishing grounds off of the Eastern U.S. Each cell in the grid is 10 minutes of latitude by 10-minutes of longitude. VTR point data per year for the selected species were overlain onto the 10-minute squares grid and the identity command was used in ArcToolbox (Figure 13). An identity overlay added an ID field of the 10-minute quadrilateral grid to the attribute information for the VTR point data. Kept pounds were then summed for each 10-minute quadrilateral in a summary table. A table join was then used to join the sum of kept metric tons to the spatial locations of the 10-minute quadrilaterals (Figure 17).




| TEN_ID | Count_TEN_ID | Sum_DISCLB | Sum_KEPTLB | SumKeptMT |
|---|---|---|---|---|
| 396911 | 7 | 3500 | 54900 | 24.9026 |
| 396912 | 5 | 0 | 43587 | 19.7711 |
| 396913 | 3 | 0 | 16375 | 7.4277 |
| 396914 | 3 | 0 | 36600 | 16.6018 |
| 396915 | 3 | 0 | 283 | 0.1284 |
| 397015 | 2 | 0 | 4509 | 2.0453 |
| 397016 | 7 | 3500 | 54900 | 24.9026 |
| 406611 | 9 | 1500 | 12020 | 5.4523 |
| 406612 | 4 | 15 | 3860 | 1.7509 |
| 406621 | 15 | 17000 | 226325 | 102.661 |
| 406622 | 13 | 5412 | 336470 | 152.6228 |

Figure 17. An example of the 1994 VTR point data, the 10-minute quadrilateral grid and how data were aggregated in a table join.

The VTR summary data of metric tons caught per 10-minute quadrilateral were summed for each year and polygon shapefiles were converted into raster data sets using the ArcToolbox Conversion Tools utility – Feature to Raster. The 10-minute quadrilateral cells in the raster data sets were summed across years for the time series and the average was computed with Raster Calculator. Data sets were averaged to show which fishing zones or 10-

minute quadrilateral regions have had the most productive landings for the time series. The averaged kept metric ton data was then classified into deciles showing the $10^{th}$, $20^{th}$…100th percentiles so that 10% of the catch data would fall in each category. The reclassify command was used to change the average kept metric tons into negative integer values, i.e. -1 = the $10^{th}$ percentile, -2 = the $20^{th}$ percentile, etc. These values were used in the weighted model for delineating potential MPAs.

**Weighted Optimization Model**

The weighted optimization model was a simple mathematical expression used to combine the various raster data sets into one output data set in order to optimize the conservation needs of marine biological resources and those needs of the fishing community. Weighted model analyses were restricted from the closed areas in the study area and from Canadian waters. Two steps were required to implement the model. The input rasters of the weighted model were the biodiversity hotspots, top 20% spawning habitats, top 20% juvenile habitats and the essential commercial fishing zones. The first step combined the three biological input rasters into a single data set with map algebra by adding the individual biological raster data sets together to produce a new priority MPA raster data set. This data set contained positive weights representing the components of the potential MPAs; the essential commercial fishing zones, which represented valuable regions to commercial fishers, have a negative weight value. The second step combined these two weighted elements with map algebra to determine which regions of the study area are optimal for MPAs or for fishing. The output was a raster data set contains a spectrum of values both positive and negative; values are positive where MPAs designation is suitable and negative where commercial fishing should be allowed to continue. The spectrum of positive and negative values can be used to evaluate the suitability of the cell for its purpose. Higher values, whether positive or negative, were expected to indicate a more suitable area for a specific type of management. Two models were run with slightly differing weighting schemes (Table 10).

Table 10. Weighted optimization model inputs using 2 scenarios of management goals.

**Weighted Model 1**

| | Inputs | Step | Weights | Based on |
|---|---|---|---|---|
| | Biodiversity Hotspots | 1 | 1-10 | Deciles |
| + | Top 20% Spawning Habitat | 1 | 1-4 | # of Species |
| + | Top 20% Juvenile Habitat | 1 | 1-9 | # of Species |
| = | Priority MPA sites | Output | 1-19 | Additive Model |
| | Reclassified Priority MPA sites | 2 | 1-10 | Deciles |
| + | | | | |
| | Essential Commercial Fishing Zones | 2 | -10- -1 | Deciles |
| = | Optimized MPA sites | Output | -9 - 10 | Final Weighted Output 1 |

**Weighted Model 2**

| | Inputs | Step | Weights | Based on |
|---|---|---|---|---|
| | Biodiversity Hotspots | 1 | 1-10 | Deciles |
| + | Top 20% Spawning Habitat | 1 | 1-4 | # of Species |
| + | Top 20% Juvenile Habitat | 1 | 1-9 | # of Species |
| = | Priority MPA sites | 2 | 1-19 | Additive Model |
| + | | | | |
| | Essential Commercial Fishing Zones | 2 | -10- -1 | Deciles |
| = | Optimized MPA sites | Output | -9 - 16 | Final Weighted Output 2 |

The only difference in the models was how the priority MPA output was handled. In model 1 the output was reclassified into deciles, values of 1 – 10, and then added to the essential commercial fishing zones giving equal weight to both input data sets. The second model skipped the reclassification of the priority MPAs into deciles and used the weights from the priority MPA data set directly. The second model gave a higher weighting scheme to the priority MPA data set than the essential commercial fishing zone data set.

# Results

## Biodiversity Hotspots

Results from the model selection using stepwise linear regression are shown in Table 11. Only two of the four variables in the model have a significant affect on modeling biodiversity. The Cp statistic is a measure of the trade offs between bias due to excluding important explanatory variables and extra variance because too many variables were included in the model. The output model has the lowest computed Cp statistic, indicating that the full model added extra variance because of season and sediment type and the simple model excluded an important explanatory variable year. Results from the linear regression model are shown below in Tables 12 and 13.

Table 11. Linear regression models used in the stepwise regression analysis.

| Model | Response Variable ~ Explanatory Variables | Cp Statistic |
|---|---|---|
| Full Model | Shannon Index ~ Subregion + Season + Sediment Type + Year | 871.51 |
| Simple Model | Shannon Index ~ Subregion | 875.95 |
| Output Model | Shannon Index ~ Subregion + Year | 871.13 |
| Residual standard error: 0.5314 on 3055 degrees of freedom<br>Multiple R-Squared: 0.04471<br>F-statistic: 10.21 on 14 and 3055 degrees of freedom, the p-value is 0 | | |

Table 12. ANOVA table from the linear regression model, SI ~ subregion + year.

| | Df | Sum of squares | Mean square | F value | p - value |
|---|---|---|---|---|---|
| SUBREGION | 5 | 30.48 | 6.096 | 21.59 | <0.000 |
| YEAR | 9 | 9.89 | 1.099 | 3.89 | <0.000 |
| Residuals | 3055 | 862.68 | 0.282 | | |

Multiple linear regression analysis results provided an F-statistic of 10.21 on 14 and 3055 degrees of freedom, with a p-value of <0.000. This indicates that it is unlikely that random chance led to this model outcome and that biodiversity is influenced by both subregion and year. P-values from the ANOVA table above also indicate that subregion and year influence the values of biodiversity. The $R^2$ and sum of squares values in the ANOVA table indicates that this regression equation poorly fits the values of biodiversity. This model only explains approximately 5% of the total variance in the model indicating that unknown parameters not included in the model heavily influence it.

Table 13. Linear regression model coefficients.

| Variable | Coefficient | Std. Error | t - statistic | p - value |
|---|---|---|---|---|
| (Intercept) | 1.417 | 0.012 | 117.705 | 0.000 |
| SUBREGION1 | 0.064 | 0.020 | 3.171 | 0.002 |
| SUBREGION2 | 0.036 | 0.008 | 4.258 | 0.000 |
| SUBREGION3 | -0.029 | 0.009 | -3.293 | 0.001 |
| SUBREGION4 | 0.068 | 0.008 | 8.928 | 0.000 |
| SUBREGION5 | 0.017 | 0.006 | 3.031 | 0.003 |
| YEAR1 | 0.049 | 0.022 | 2.257 | 0.024 |
| YEAR2 | 0.035 | 0.012 | 2.776 | 0.006 |
| YEAR3 | -0.005 | 0.009 | -0.630 | 0.529 |
| YEAR4 | -0.006 | 0.006 | -0.885 | 0.376 |
| YEAR5 | -0.005 | 0.006 | -0.976 | 0.329 |
| YEAR6 | -0.004 | 0.005 | -0.776 | 0.438 |
| YEAR7 | 0.009 | 0.004 | 2.042 | 0.041 |
| YEAR8 | 0.013 | 0.004 | 3.663 | 0.000 |
| YEAR9 | -0.005 | 0.003 | -1.484 | 0.138 |

The linear regression coefficient table (Table 12) explains the likely influence of each of the included explanatory variables showing that all subregions are significant but not for all years in the model. Visual analysis of the biodiversity data was conducted by inspecting histograms and normal QQ-plots. These graphs indicated that the data were relatively normally distributed and outlier’s were not a significant problem within the data set and no data transformations were unnecessary (Figures 18 and 19).

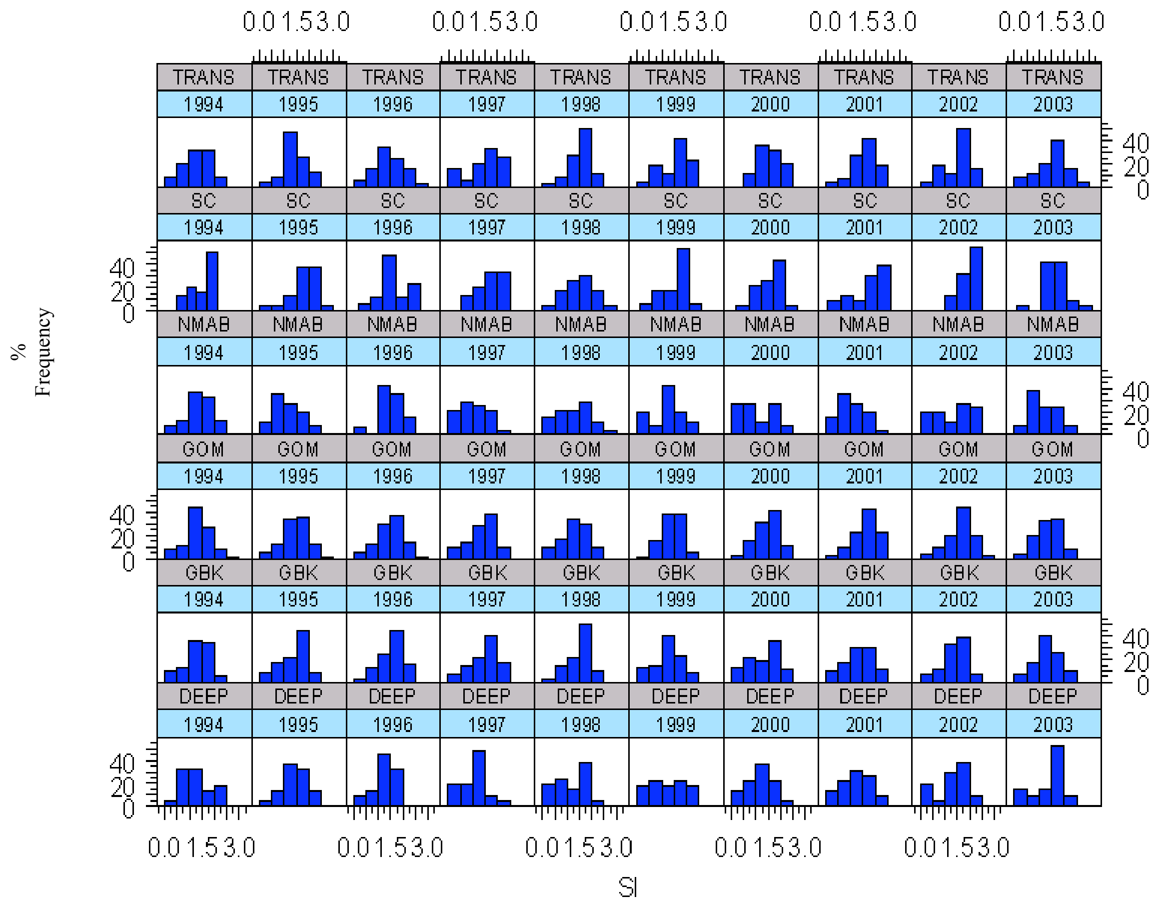



Figure 18. Percent frequency histograms of the Shannon index by subregion and year.

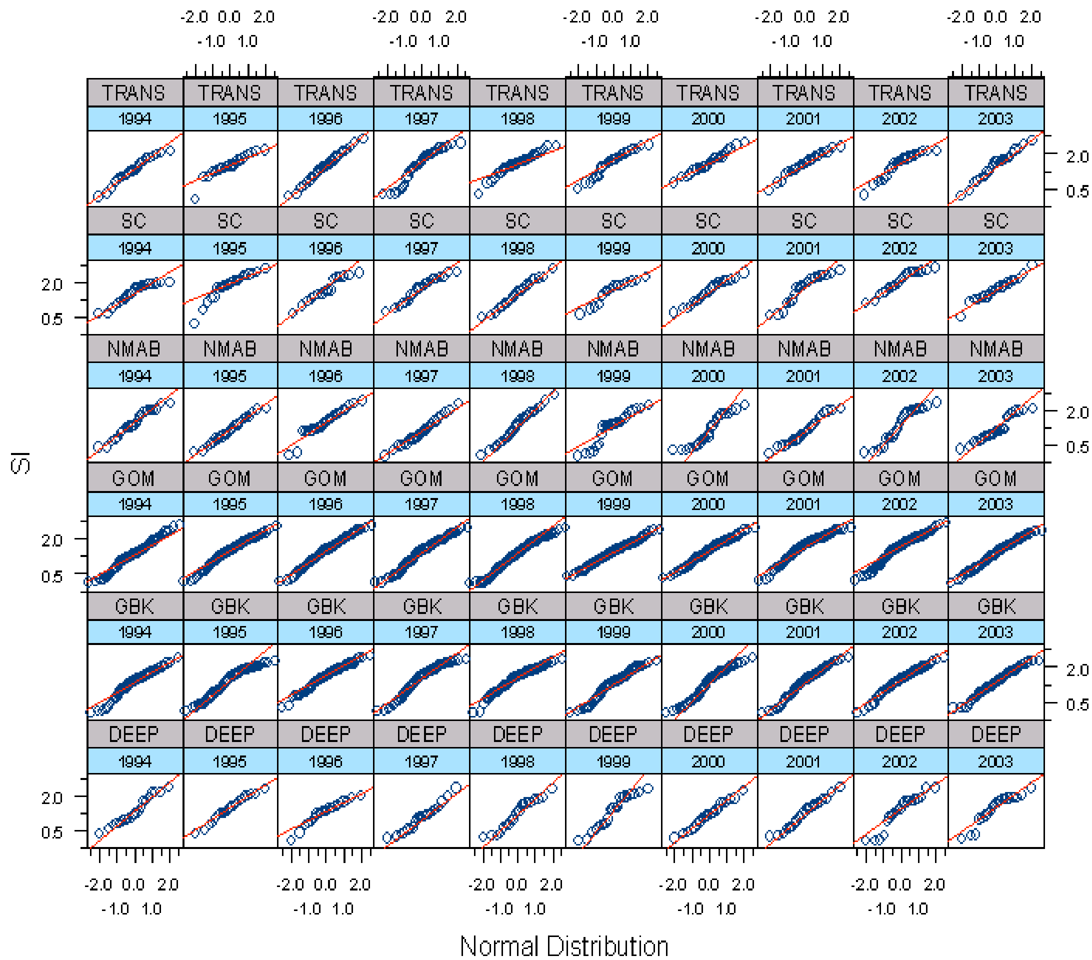
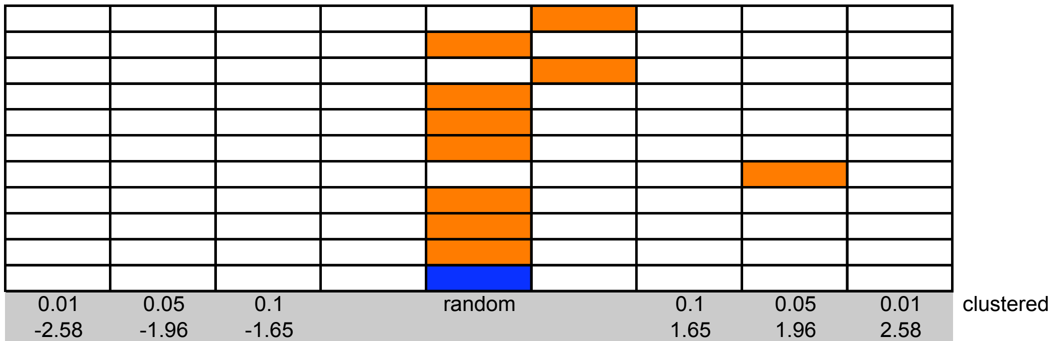



Figure 19. Normal QQ-plots of the Shannon Index by subregion and year.

Figures 20a, b, and c show the graphical and numeric results of the Moran's index calculations by subregion and year. Red squares indicate pattern and significance of the yearly Z scores and the blue squares show the mean for the subregion. Index values are shown in the tables to the right of the graphs. Random patterns or lack of spatial dependence were detected for the majority of the data analyzed in all regions except the GOM, as indicated by the blue square representing the mean value of the Moran's I. The GOM was the only region showing a marginally significant clustered pattern.

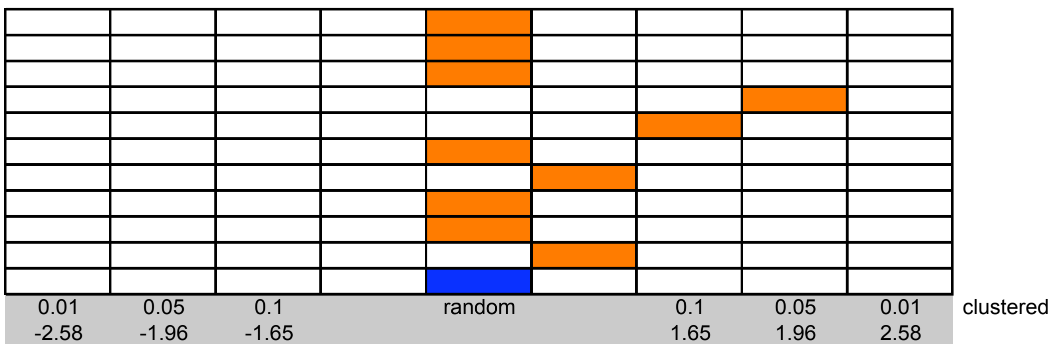
The results of interpolating the biodiversity point data into continuous surfaces using ordinary kriging, with the construction of empirical and theoretical spherical semivariograms for each subregion and year, are shown in Figures 21-26. Spherical semivariograms are variable between subregions and among years. Variation among subregions was expected because subregions were created based on differing depth zones and species assemblages. Variation among years indicates that biodiversity changes from year to year within each subregion, as evidenced by the semivariogram parameters summarized in Table 13.

**Moran's Index Table for the Deep Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | 0.113 | -0.050 | 0.016 | 1.274 |
| 2002 | -0.041 | -0.050 | 0.010 | 0.086 |
| 2001 | 0.310 | -0.045 | 0.093 | 1.167 |
| 2000 | 0.043 | -0.048 | 0.050 | 0.404 |
| 1999 | -0.100 | -0.048 | 0.066 | -0.204 |
| 1998 | -0.017 | -0.050 | 0.016 | 0.267 |
| 1997 | 0.378 | -0.050 | 0.042 | 2.096 |
| 1996 | -0.106 | -0.048 | 0.010 | -0.572 |
| 1995 | -0.170 | -0.048 | 0.017 | -0.947 |
| 1994 | 0.103 | -0.048 | 0.027 | 0.912 |
| mean | 0.051 | -0.048 | 0.035 | 0.448 |

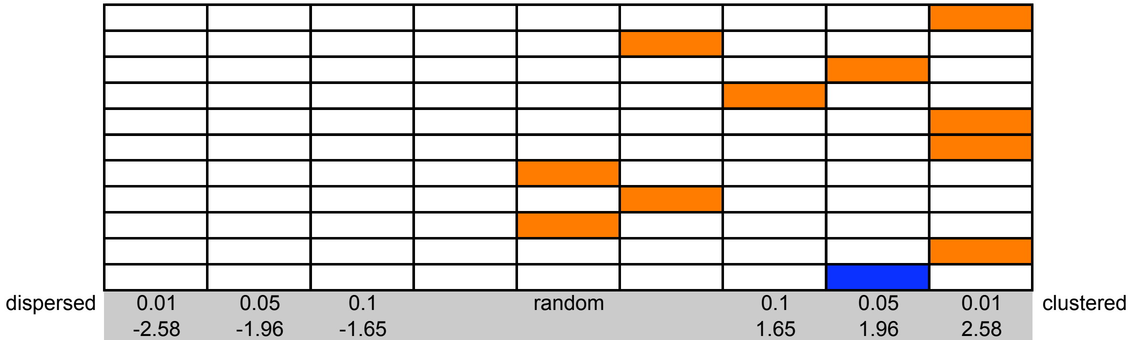
**Moran's Index Table for the Georges Bank Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | 0.004 | -0.014 | 0.000 | 0.850 |
| 2002 | -0.017 | -0.013 | 0.002 | -0.086 |
| 2001 | -0.005 | -0.013 | 0.000 | 0.404 |
| 2000 | 0.039 | -0.013 | 0.000 | 2.465 |
| 1999 | 0.023 | -0.013 | 0.000 | 1.680 |
| 1998 | -0.033 | -0.011 | 0.001 | -0.829 |
| 1997 | 0.019 | -0.011 | 0.000 | 1.338 |
| 1996 | 0.008 | -0.012 | 0.001 | 0.858 |
| 1995 | -0.004 | -0.010 | 0.000 | 0.341 |
| 1994 | 0.023 | -0.013 | 0.001 | 1.523 |
| mean | 0.006 | -0.012 | 0.001 | 0.854 |

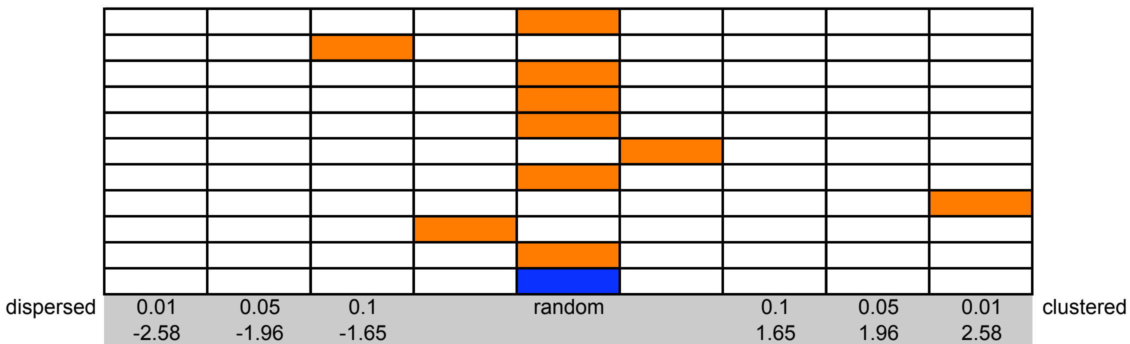
Figure 20a. Spatial autocorrelation values of the Shannon index (biodiversity) using the Moran's index by subregion and year.

**Moran's Index Table for the Gulf of Maine Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | 0.071 | -0.009 | 0.000 | 4.292 |
| 2002 | 0.042 | -0.008 | 0.002 | 1.161 |
| 2001 | 0.067 | -0.009 | 0.001 | 2.239 |
| 2000 | 0.024 | -0.009 | 0.000 | 1.917 |
| 1999 | 0.084 | -0.008 | 0.000 | 4.952 |
| 1998 | 0.058 | -0.006 | 0.000 | 5.159 |
| 1997 | -0.010 | -0.008 | 0.000 | -0.127 |
| 1996 | 0.011 | -0.008 | 0.000 | 1.400 |
| 1995 | 0.006 | -0.008 | 0.000 | 0.986 |
| 1994 | 0.042 | -0.009 | 0.000 | 2.713 |
| mean | 0.040 | -0.008 | 0.001 | 2.469 |

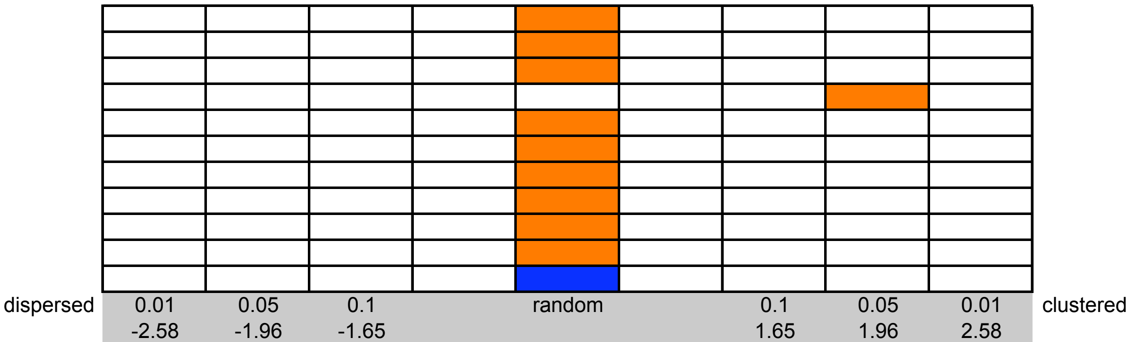
**Moran's Index Table for the N. Mid Atlantic Bight Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | -0.025 | -0.040 | 0.003 | 0.273 |
| 2002 | -0.249 | -0.040 | 0.013 | -1.842 |
| 2001 | -0.056 | -0.040 | 0.002 | -0.350 |
| 2000 | 0.096 | -0.040 | 0.019 | 0.977 |
| 1999 | -0.085 | -0.040 | 0.006 | -0.568 |
| 1998 | 0.053 | -0.037 | 0.003 | 1.643 |
| 1997 | -0.004 | -0.037 | 0.002 | 0.816 |
| 1996 | 0.079 | -0.037 | 0.002 | 2.891 |
| 1995 | -0.114 | -0.040 | 0.004 | -1.222 |
| 1994 | -0.067 | -0.042 | 0.004 | -0.384 |
| mean | -0.037 | -0.039 | 0.006 | 0.223 |

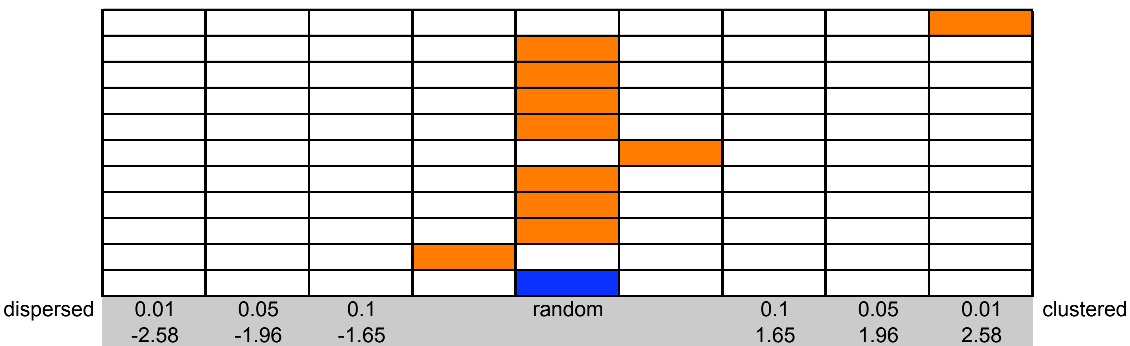
Figure 20b. Spatial autocorrelation values of the Shannon index (biodiversity) using the Moran's index by subregion and year.

**Moran's Index Table for the Scotian Shelf Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | -0.022 | -0.043 | 0.004 | 0.324 |
| 2002 | 0.023 | -0.048 | 0.006 | 0.889 |
| 2001 | -0.092 | -0.045 | 0.004 | -0.760 |
| 2000 | 0.074 | -0.045 | 0.003 | 2.143 |
| 1999 | -0.040 | -0.063 | 0.005 | 0.331 |
| 1998 | -0.103 | -0.045 | 0.004 | -0.946 |
| 1997 | -0.022 | -0.043 | 0.003 | 0.376 |
| 1996 | -0.026 | -0.063 | 0.006 | 0.457 |
| 1995 | -0.088 | -0.043 | 0.004 | -0.733 |
| 1994 | -0.028 | -0.043 | 0.004 | 0.251 |
| mean | -0.032 | -0.048 | 0.004 | 0.233 |

**Moran's Index Table for the Transitional Zone Subregion**




| | Moran's Index | Expected Index | Variance | Z Score |
|---|---|---|---|---|
| 2003 | 0.253 | -0.042 | 0.007 | 3.494 |
| 2002 | -0.145 | -0.040 | 0.009 | -1.108 |
| 2001 | 0.082 | -0.040 | 0.018 | 0.909 |
| 2000 | -0.165 | -0.042 | 0.016 | -0.985 |
| 1999 | -0.051 | -0.040 | 0.007 | -0.129 |
| 1998 | 0.033 | -0.029 | 0.002 | 1.308 |
| 1997 | -0.057 | -0.026 | 0.003 | -0.572 |
| 1996 | -0.061 | -0.032 | 0.002 | -0.612 |
| 1995 | -0.040 | -0.045 | 0.007 | 0.063 |
| 1994 | -0.143 | -0.042 | 0.007 | -1.258 |
| mean | -0.030 | -0.038 | 0.008 | 0.111 |

Figure 20c. Spatial autocorrelation values of the Shannon index (biodiversity) using the Moran's index by subregion and year.

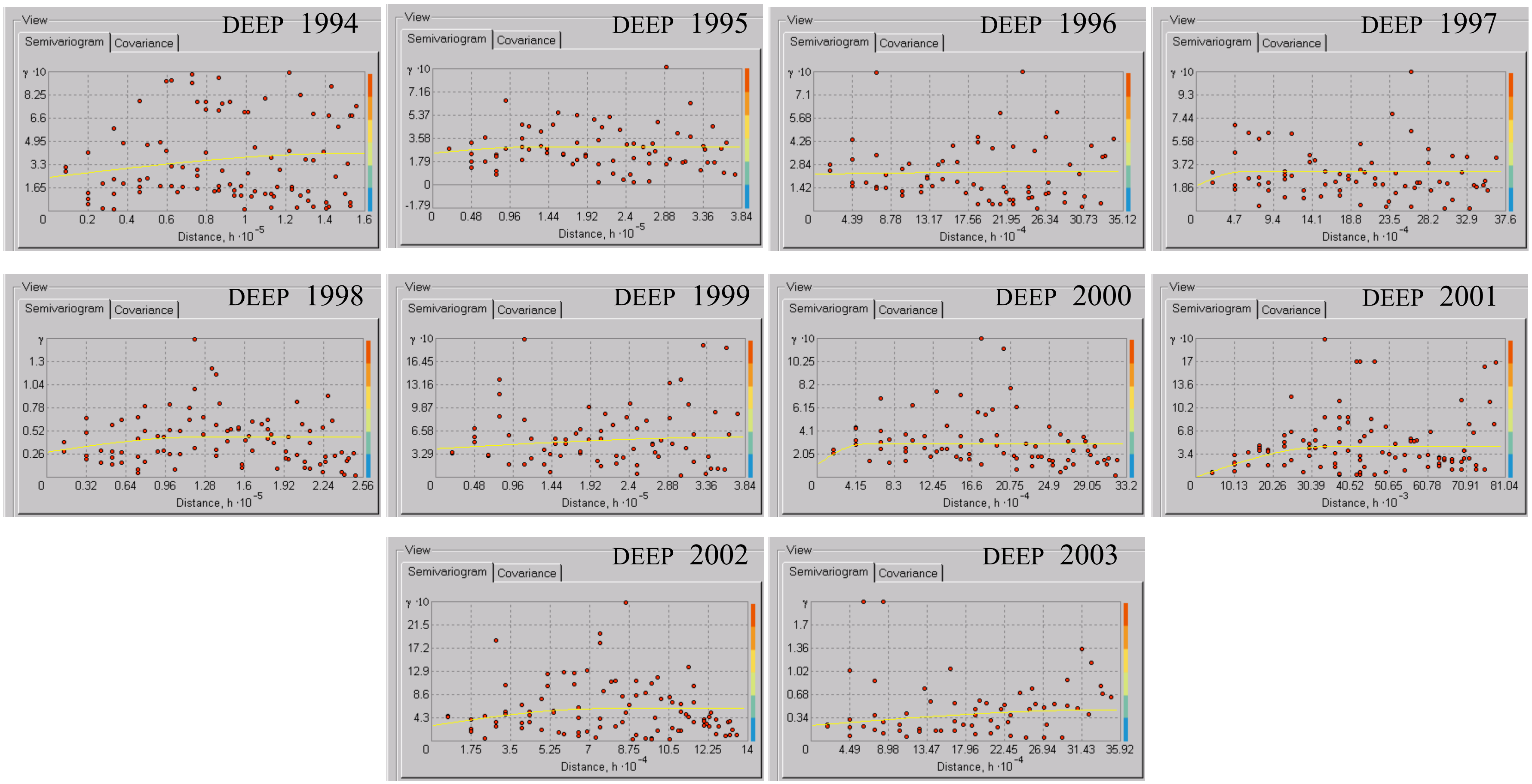



Figure 21. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

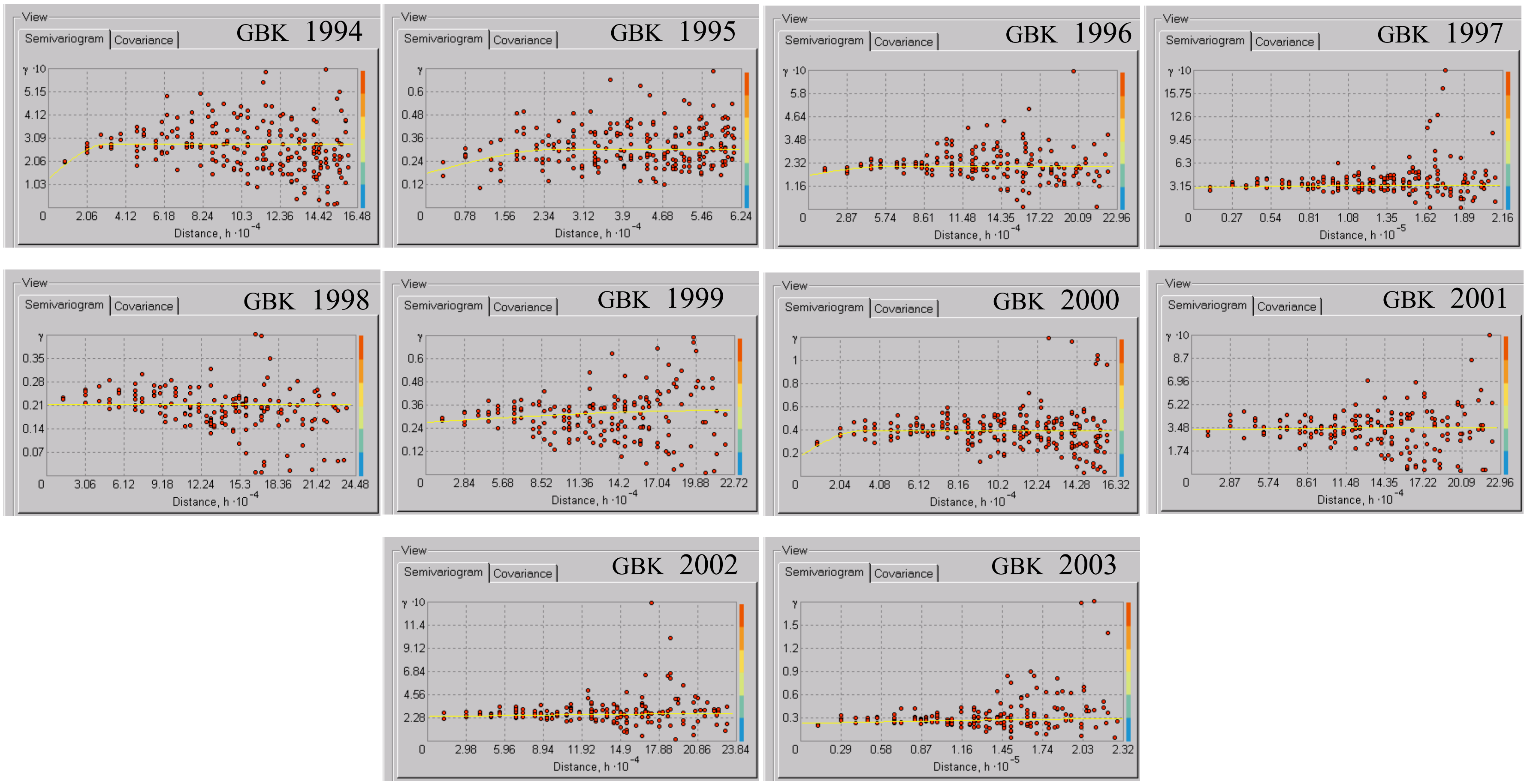



Figure 22. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

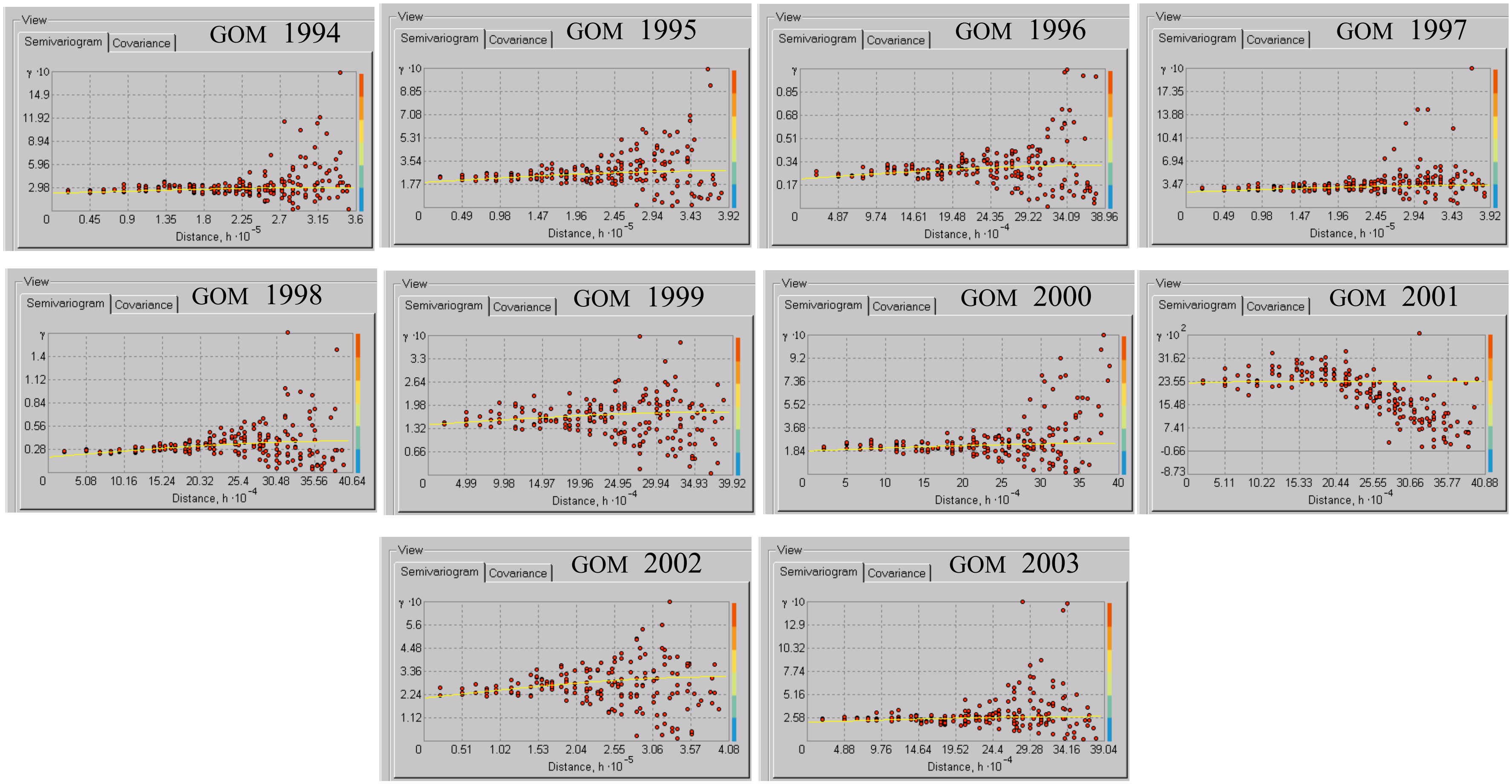



Figure 23. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

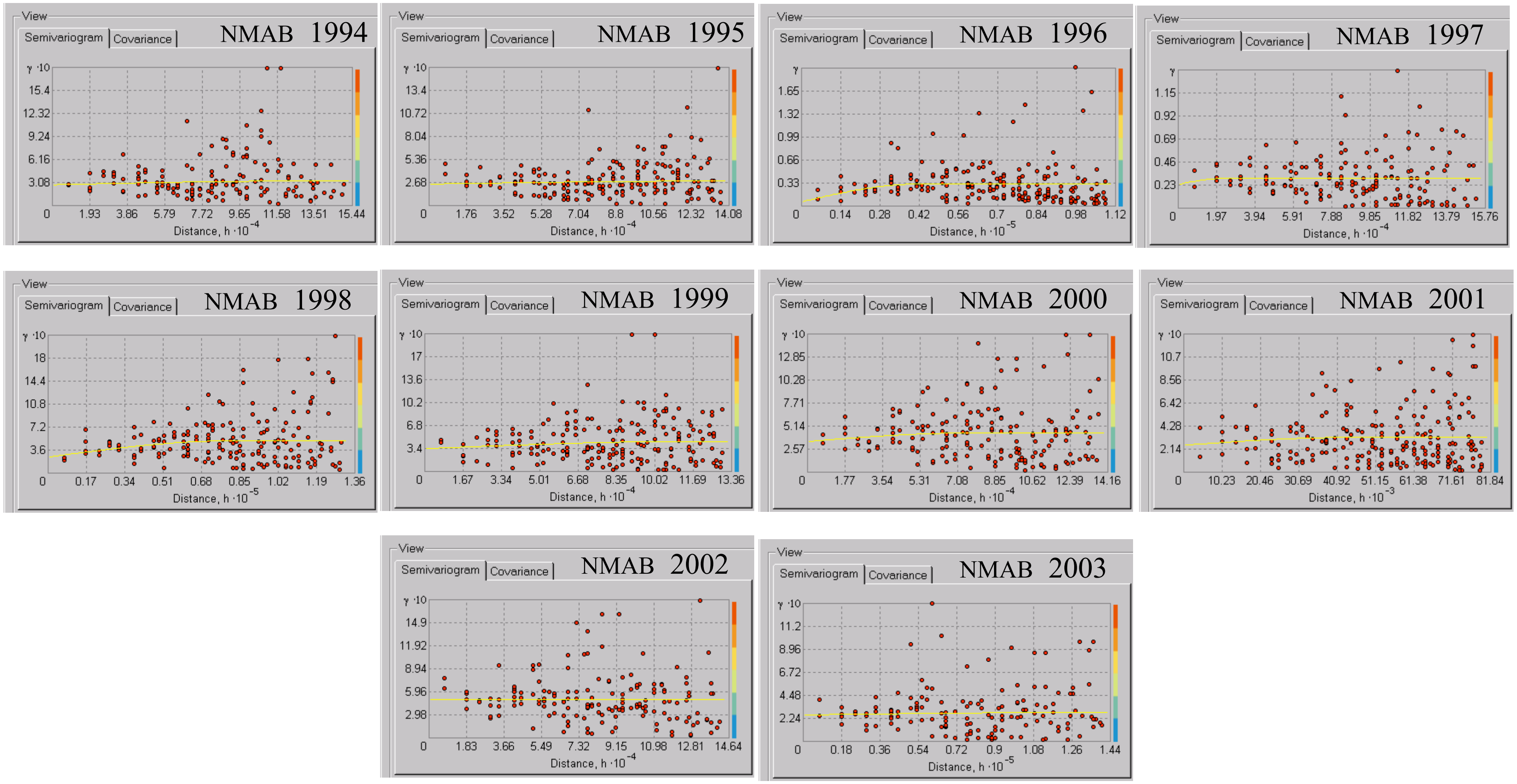



Figure 24. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

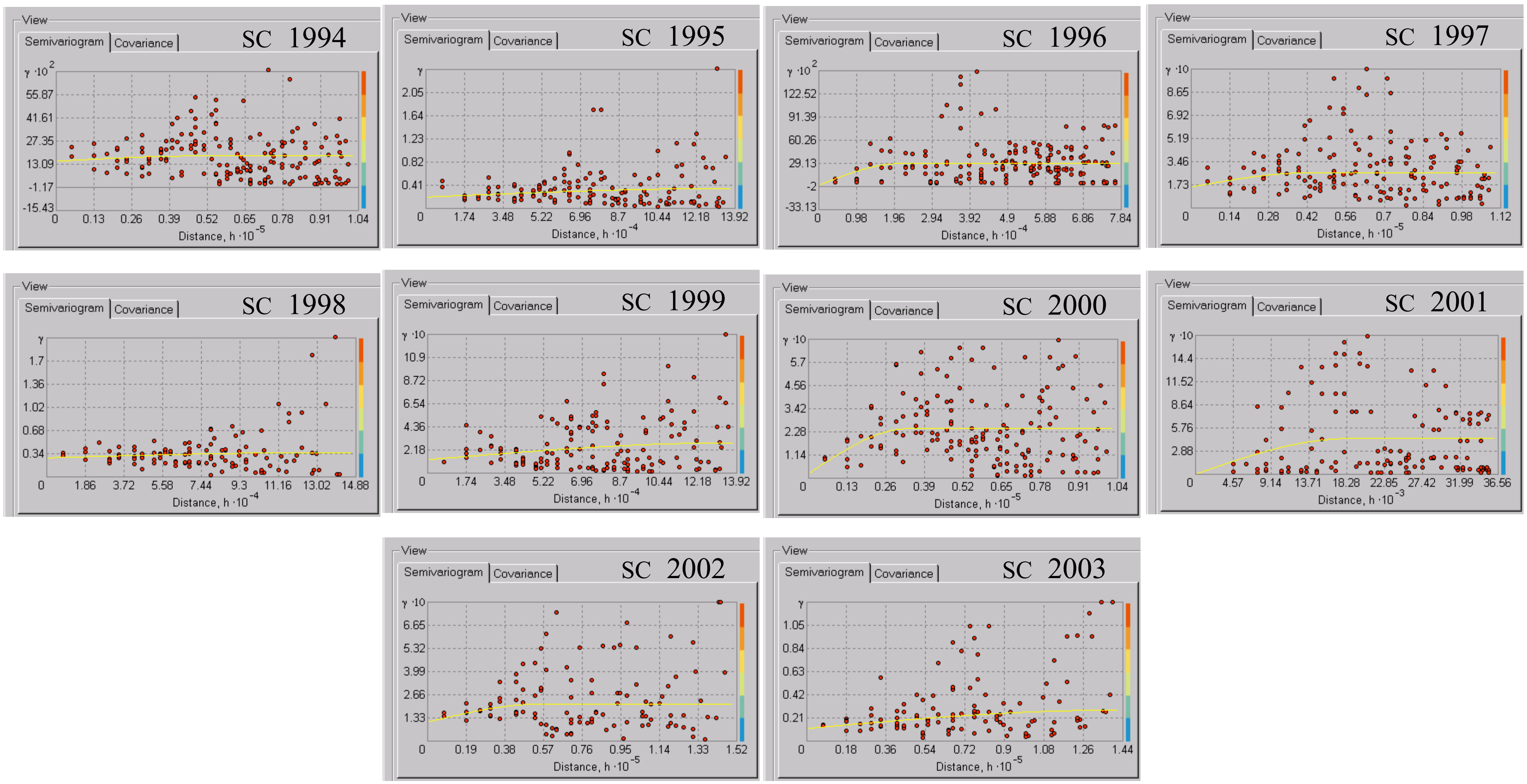



Figure 25. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

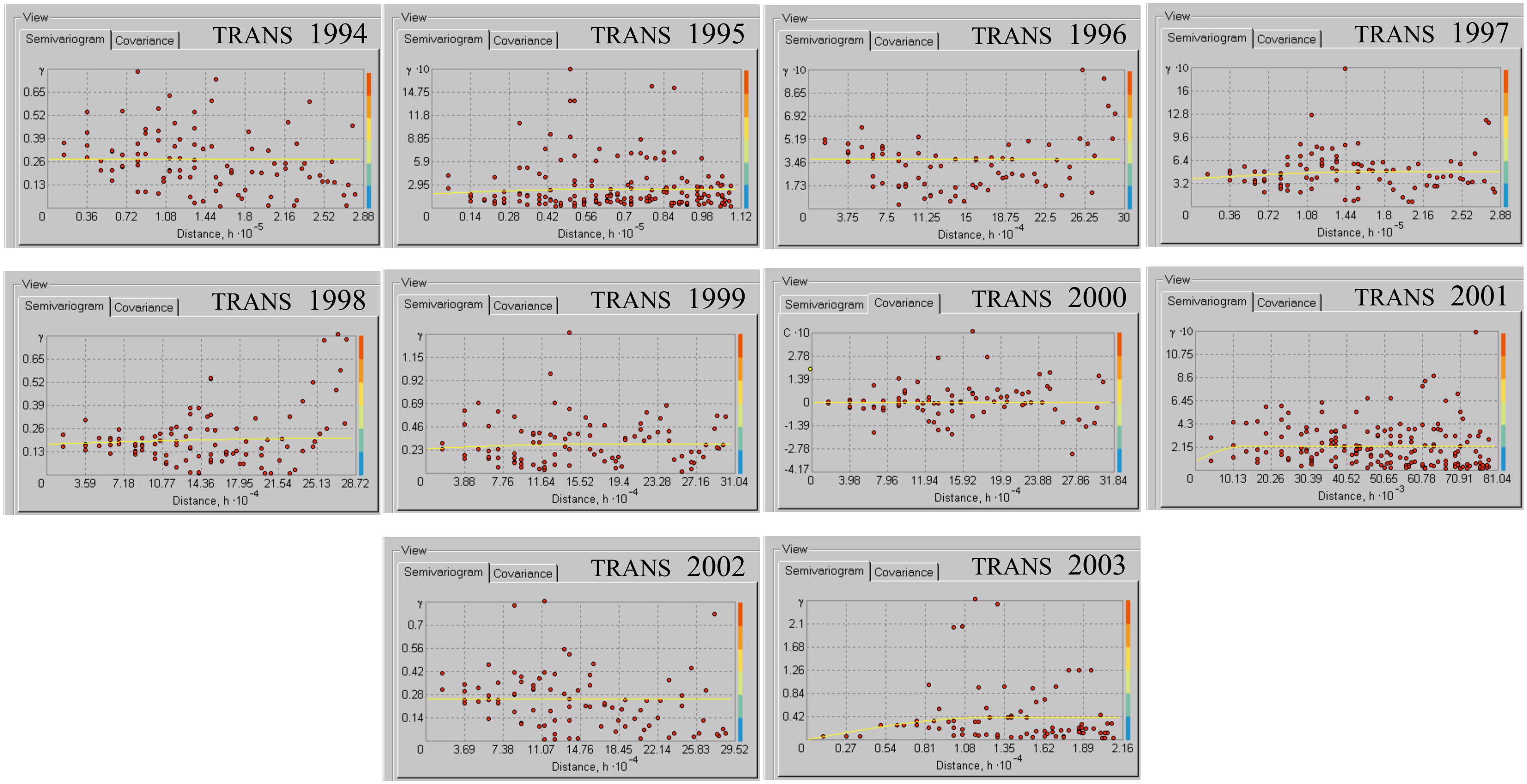



Figure 26. Spherical semivariograms of the Shannon Index data (biodiversity) for the deepwater subregion, 1994 – 2003

Table 14. Spherical semivariogram parameters for interpolating biodiversity with ordinary kriging.

| Sub-region | Year | Lag Size | Major Range | Partial Sill | Nugget | Sub-region | Year | Lag Size | Major Range | Partial Sill | Nugget |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Deep | 1994 | 13,318 | 156,730 | 0.174 | 0.239 | NMAB | 1994 | 12,735 | 131,010 | 0.051 | 0.278 |
| Deep | 1995 | 31,839 | 124,240 | 0.047 | 0.244 | NMAB | 1995 | 11,598 | 137,470 | 0.035 | 0.250 |
| Deep | 1996 | 28,882 | 342,350 | 0.016 | 0.226 | NMAB | 1996 | 9,194 | 41,121 | 0.254 | 0.060 |
| Deep | 1997 | 30,929 | 56,344 | 0.116 | 0.199 | NMAB | 1997 | 12,963 | 23,615 | 0.061 | 0.237 |
| Deep | 1998 | 21,193 | 124,900 | 0.172 | 0.281 | NMAB | 1998 | 11,030 | 81,976 | 0.257 | 0.251 |
| Deep | 1999 | 31,784 | 376,740 | 0.162 | 0.405 | NMAB | 1999 | 10,998 | 117,560 | 0.108 | 0.337 |
| Deep | 2000 | 27,337 | 49,800 | 0.182 | 0.111 | NMAB | 2000 | 11,654 | 76,510 | 0.096 | 0.342 |
| Deep | 2001 | 6,668 | 35,202 | 0.452 | 0.000 | NMAB | 2001 | 6,737 | 44,460 | 0.073 | 0.251 |
| Deep | 2002 | 11,542 | 75,320 | 0.318 | 0.281 | NMAB | 2002 | 12,022 | 136,470 | 0.000 | 0.491 |
| Deep | 2003 | 29,585 | 350,680 | 0.232 | 0.226 | NMAB | 2003 | 11,890 | 140,940 | 0.025 | 0.258 |
| | | | | | | | | | | | |
| GBK | 1994 | 13,544 | 32,202 | 0.155 | 0.128 | SC | 1994 | 8,514 | 49,136 | 0.033 | 0.149 |
| GBK | 1995 | 5,170 | 27,340 | 0.128 | 0.176 | SC | 1995 | 11,447 | 135,680 | 0.153 | 0.200 |
| GBK | 1996 | 18,876 | 62,751 | 0.046 | 0.171 | SC | 1996 | 6,513 | 21,627 | 0.290 | 0.000 |
| GBK | 1997 | 17,852 | 159,720 | 0.032 | 0.296 | SC | 1997 | 9,193 | 42,918 | 0.107 | 0.156 |
| GBK | 1998 | 20,127 | 228,480 | 0.000 | 0.213 | SC | 1998 | 12,215 | 141,660 | 0.079 | 0.280 |
| GBK | 1999 | 18,681 | 221,430 | 0.062 | 0.271 | SC | 1999 | 11,479 | 136,060 | 0.159 | 0.126 |
| GBK | 2000 | 13,424 | 31,243 | 0.215 | 0.176 | SC | 2000 | 8,514 | 33,871 | 0.223 | 0.021 |
| GBK | 2001 | 18,920 | 224,260 | 0.018 | 0.332 | SC | 2001 | 3,010 | 18,606 | 0.445 | 0.000 |
| GBK | 2002 | 19,625 | 232,620 | 0.029 | 0.240 | SC | 2002 | 12,503 | 56,239 | 0.105 | 0.109 |
| GBK | 2003 | 19,310 | 228,890 | 0.058 | 0.228 | SC | 2003 | 11,805 | 139,930 | 0.167 | 0.114 |
| | | | | | | | | | | | |
| GOM | 1994 | 29,792 | 353,130 | 0.076 | 0.226 | TRANS | 1994 | 23,765 | 269,770 | 0.000 | 0.274 |
| GOM | 1995 | 32,407 | 384,130 | 0.089 | 0.192 | TRANS | 1995 | 9,192 | 55,136 | 0.059 | 0.180 |
| GOM | 1996 | 32,066 | 380,090 | 0.100 | 0.215 | TRANS | 1996 | 24,675 | 280,100 | 0.000 | 0.374 |
| GOM | 1997 | 32,635 | 386,830 | 0.102 | 0.232 | TRANS | 1997 | 23,993 | 176,540 | 0.103 | 0.386 |
| GOM | 1998 | 33,431 | 396,270 | 0.193 | 0.187 | TRANS | 1998 | 23,652 | 280,350 | 0.033 | 0.174 |
| GOM | 1999 | 32,854 | 389,430 | 0.037 | 0.143 | TRANS | 1999 | 25,529 | 164,620 | 0.045 | 0.244 |
| GOM | 2000 | 32,947 | 390,530 | 0.061 | 0.185 | TRANS | 2000 | 26,227 | 295,600 | 0.000 | 0.197 |
| GOM | 2001 | 33,657 | 122,260 | 0.006 | 0.230 | TRANS | 2001 | 6,668 | 12,147 | 0.139 | 0.081 |
| GOM | 2002 | 33,700 | 396,600 | 0.103 | 0.207 | TRANS | 2002 | 24,275 | 275,560 | 0.000 | 0.256 |
| GOM | 2003 | 32,141 | 380,980 | 0.063 | 0.210 | TRANS | 2003 | 1,780 | 12,577 | 0.407 | 0.000 |

Figures 27 and 28 show biodiversity by subregion and biodiversity across the congruent study area. The range of biodiversity values vary between each subregion showing pockets of high diversity in each map, (Figure 27), but the same classification scale was used across the study area in Figure 28 reducing the appearance of patchiness in biodiversity. The deep subregion showed an area of high biodiversity near Oceanographer Canyon, as indicated by the red patch at approximately 68 W degrees longitude. In general diversity seemed to increase as latitude increased in this subregion. The GBK subregion had an hourglass shaped pattern of high diversity. Major portions of the red areas fell within the current closed area II on Georges Bank and outside the closed areas on the southern extent of the subregion. The GOM area displayed a pattern of diversity that radiated from high to low when moving east from the coast of Massachusetts. The NMAB subregion showed areas of high diversity on the east and west borders of the area. The Scotian shelf displayed highest diversity in the northern portion of the subregion. The last subregion, the transitional zone, showed the highest diversity in the Great South Channel which extents down from Cape Cod to the SW edge of Georges Bank.

The overall map was different than the subregion maps. The highest diversity was found in the Scotian shelf subregion, where it appeared completely red and the subregion with the lowest diversity values was seen in the NMAB area. High diversity was found in the GOM subregion, the transitional zones and sporadically on Georges Bank. Current closed areas in the Gulf of Maine offer protection for some biodiversity in the region. The closed area called Nantucket Lightship, which occupies much of the NMAB subregion, offers no protection of high biodiversity areas. The areas containing some of the highest biodiversity occur in Canadian waters across the EEZ.

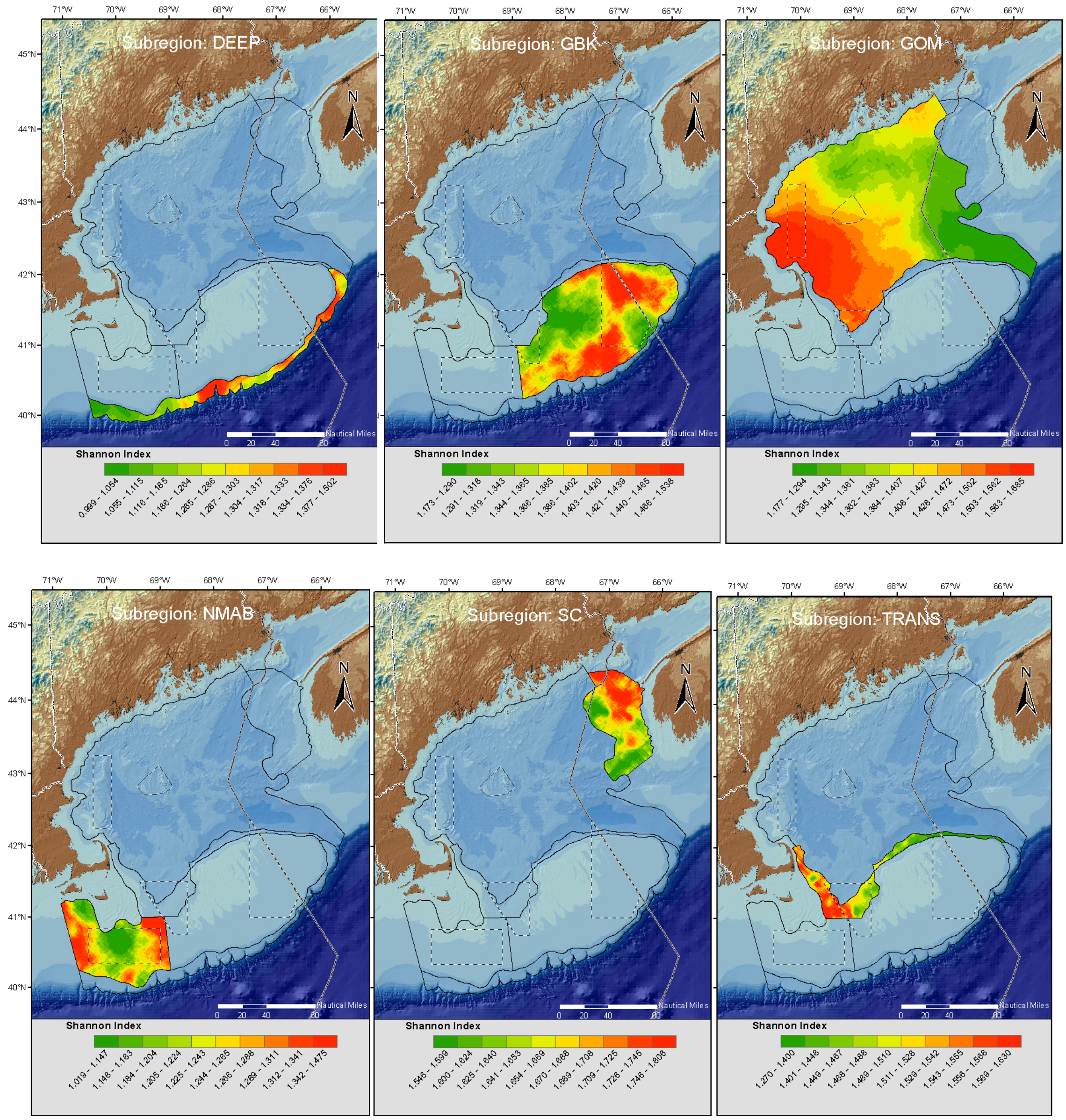



Figure 27. Biodiversity hotspots interpolated with ordinary kriging by subregion. From left to right, top to bottom: Deepwater, Georges Bank, Gulf of Maine, Northern Mid-Atlantic Bight, Scotian Shelf, and the Transitional Zone, green to red spectrum ramps from low to high.

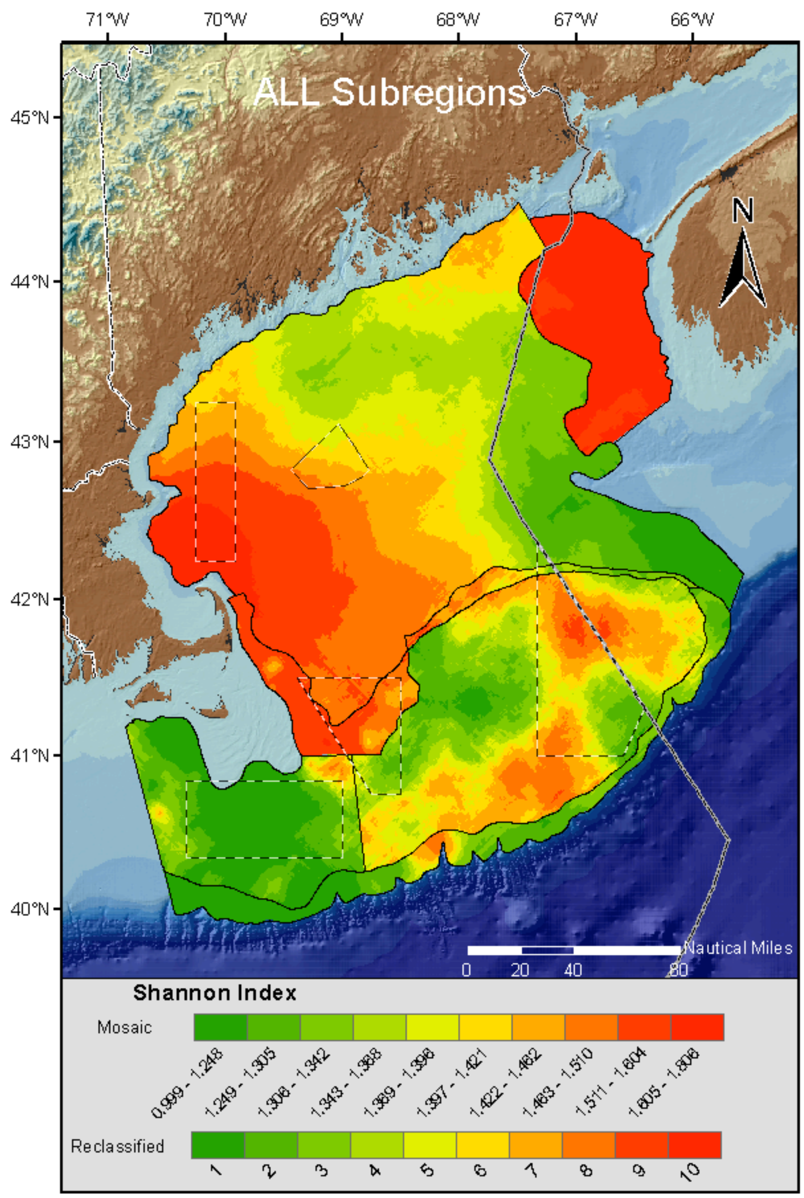



Figure 28. Mosaicked subregions of biodiversity for the study area, scale bars represent the data in decile categories for the Shannon Index (top) and the reclassified data set (bottom). Closed fishing areas and the U.S. EEZ are also shown.

**Spawning and Nursery Area Habitats**

Figures 29a & b and 30a & b show the reclassification of juvenile and spawning rasters to a value of 1 for the top 20% of densities for each species. Values of 1 were chosen specifically so that when the reclassified density maps are summed together the cumulative value is the weighting factor in the MPA optimization model indicating the number of species present in each cell (Figure 31).

The Nursery habitat maps indicated that the different species occupy a wide variety of the subregions but often can be found regionally concentrated in specific areas. For example juvenile haddock found on the Scotian shelf and in Great South Channel off of Cape Cod or juvenile redfish in the Western Gulf of Maine closed area near Jeffery's Ledge and also on the Scotian shelf.

Spawning habitat maps had less spatial diversity than the nursery habitat analysis, which resulted from fewer data points found when querying spawning individuals from the database. However spawning aggregations can be seen in several species such as redfish, American plaice, and yellowtail flounder. Spawning habitat for the selected species appeared more localized and clustered within a single subregion rather than spread out across several.

The cumulative maps for both spawning and nursery habitats highlight the critical areas for these selected species. Juvenile species shared more of the same habitat as indicated by the higher number of species occupying a single cell, maximum = 9. A large portion of the study area appears to be critical habitat for juvenile species. Because more data were found in querying the database for juveniles more overlap of species were found. Spawning habitat analysis showed as many as 4 spawning species occupying the same cell. Critical spawning areas were concentrated along the southern coast of Maine, New Hampshire and Massachusetts, the Great South Channel, closed area II on the eastern portion of Georges Bank and the Canadian side of the GBK subregion.

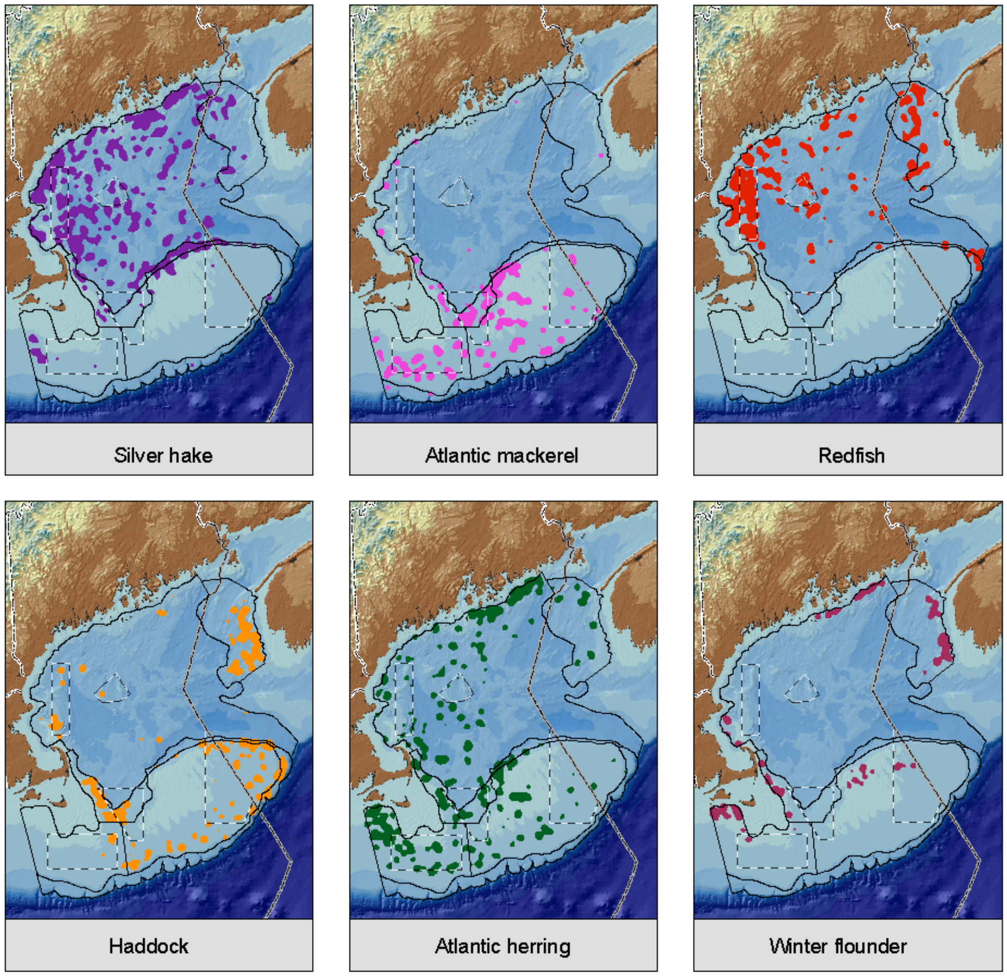



Figure 29a. Top 20% of juvenile kernel densities for selected species reclassified into values of 1. Closed fishing areas and the U.S. EEZ are also shown.

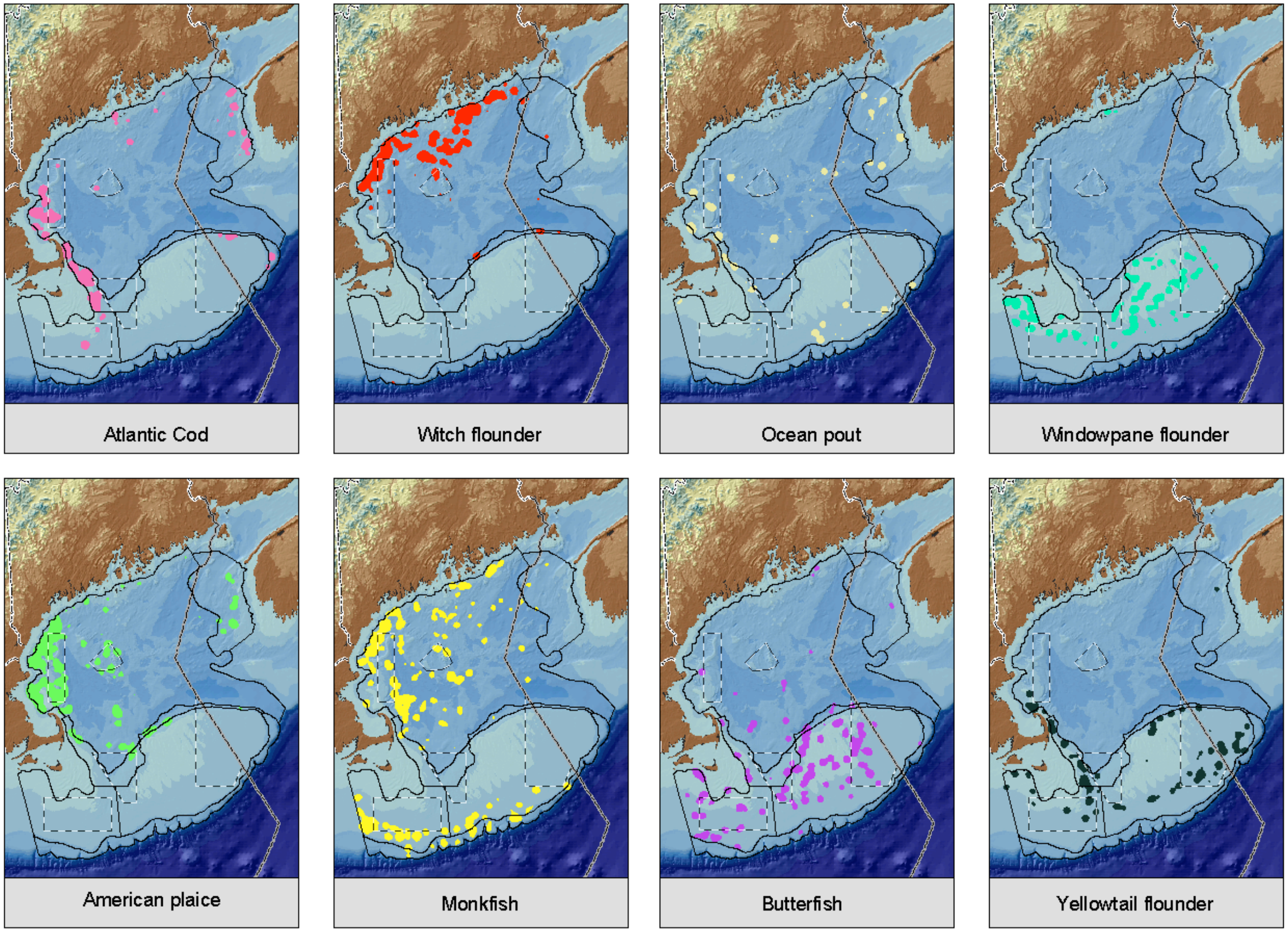



Figure 29b. Top 20% of juvenile kernel densities for selected species reclassified into values of 1. Closed fishing areas and the U.S. EEZ are also shown.

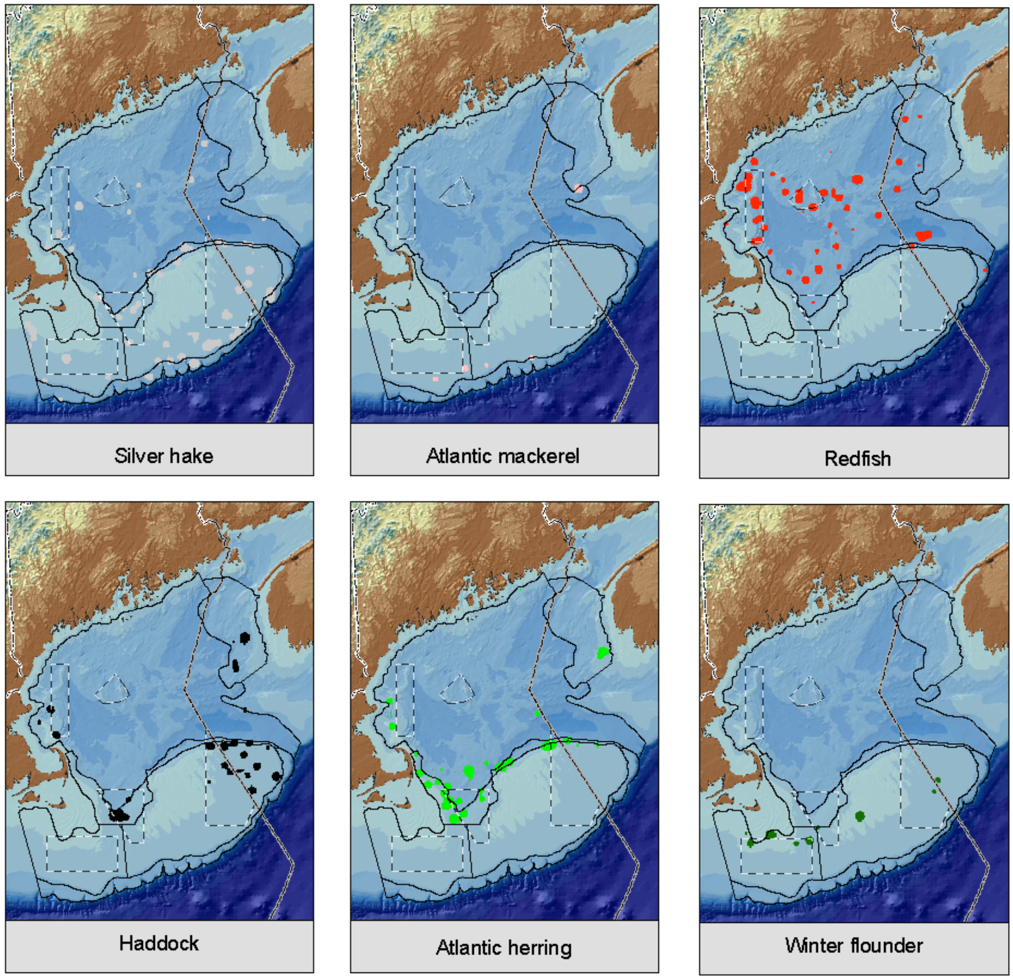



Figure 30a. Top 20% of spawning kernel densities for selected species reclassified into values of 1. Closed fishing areas and the U.S. EEZ are also shown.

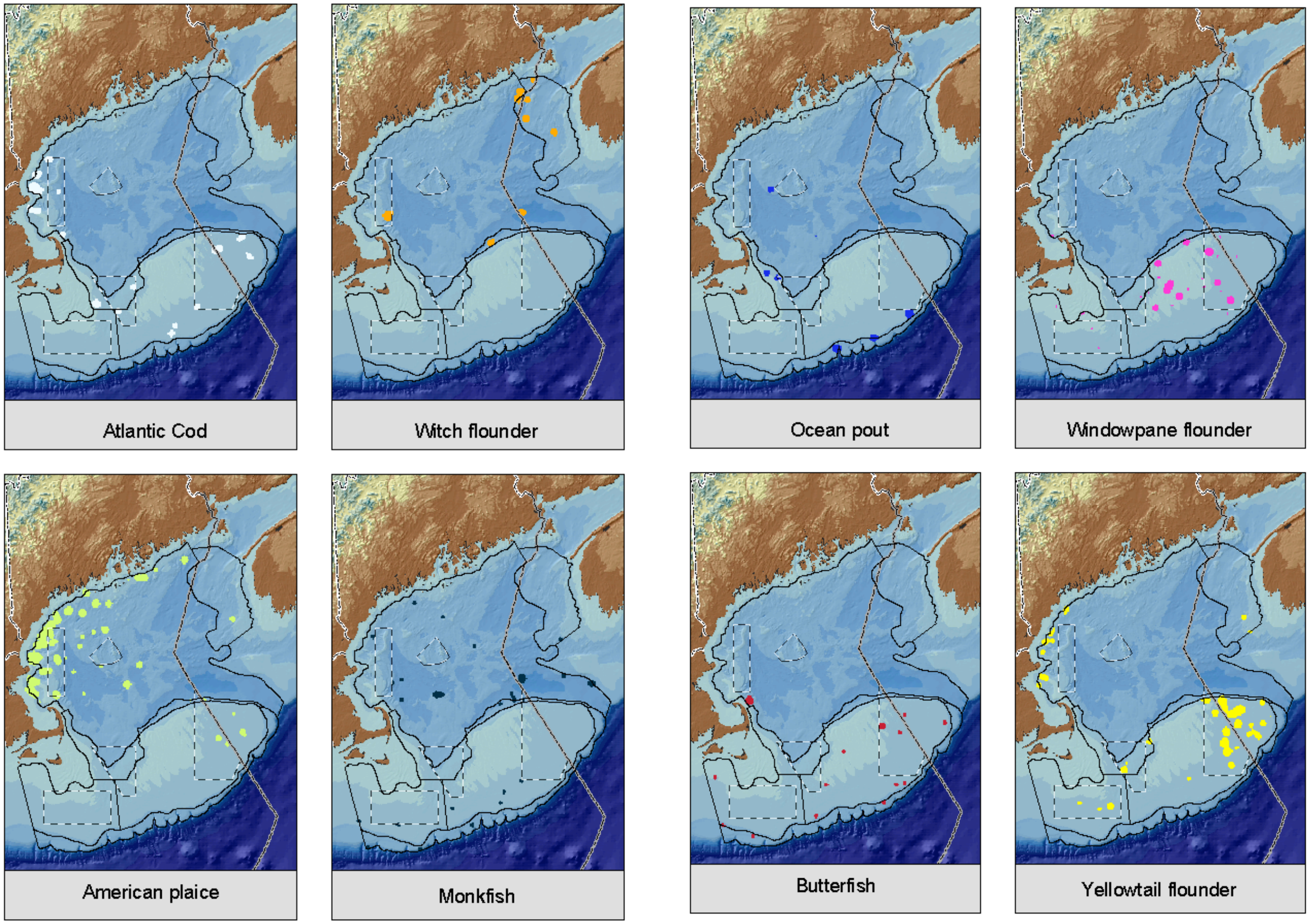



Figure 30b. Top 20% of spawning kernel densities for selected species reclassified into values of 1. Closed fishing areas and the U.S. EEZ are also shown.

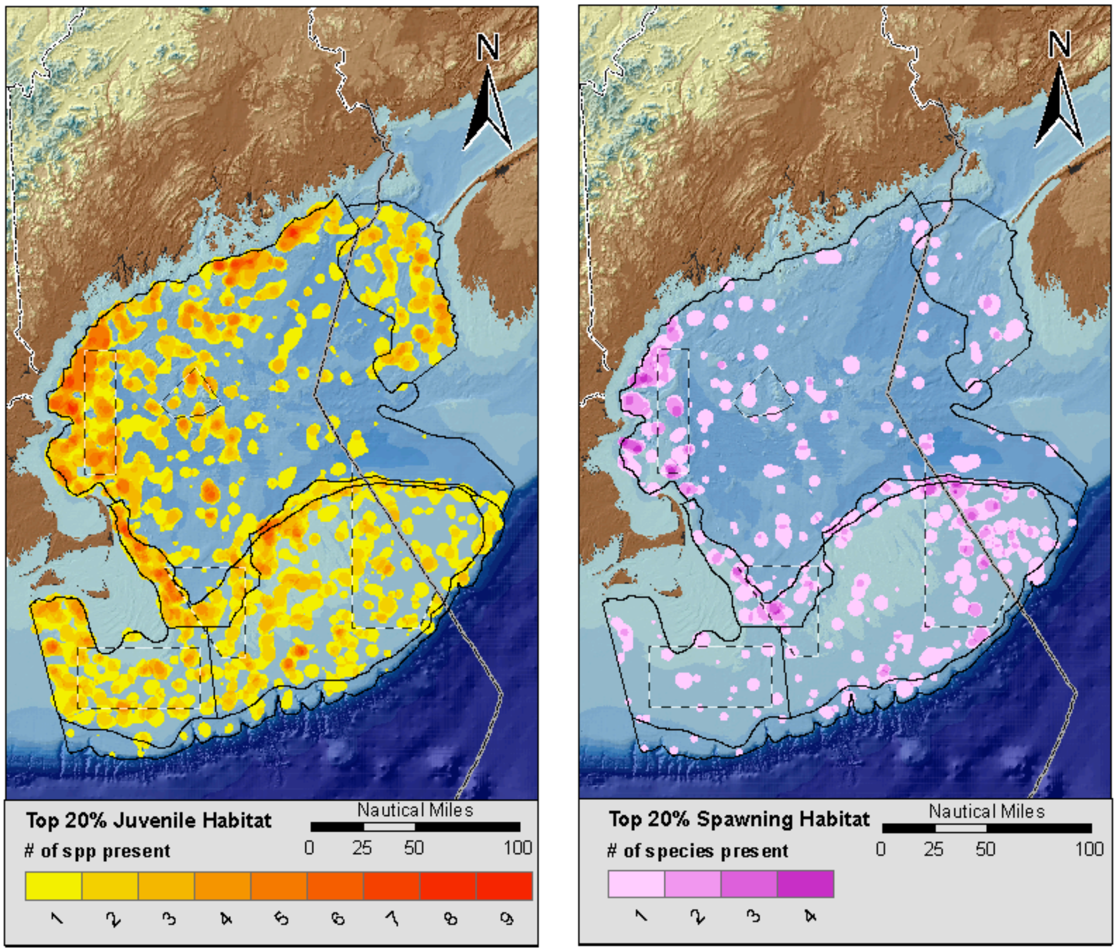



Figure 31. Cumulative juvenile and spawning habitat of the top 20% density maps for selected species. Values indicate the number of species present in each cell. Closed fishing areas and the U.S. EEZ are also shown.

**Essential Commercial Fishing Zones**

Essential commercial fishing zones showed a consistent pattern of landings on a regional scale. Each year of showed high landings concentrated along the near shore boundaries of the GOM and the transitional zone, i.e. the Great South channel, subregions, (Figure 32). The transitional zone subregion bordering the northern portion of the GBK subregion also showed high landings in most years. Landings data within the closed areas or falling on the Canadian side of the EEZ should be disregarded because commercial fishing by US fishers was not permitted in those regions for all or most of the time period studied. High landings were also seen along the SW corner of closed area II on Georges Bank.

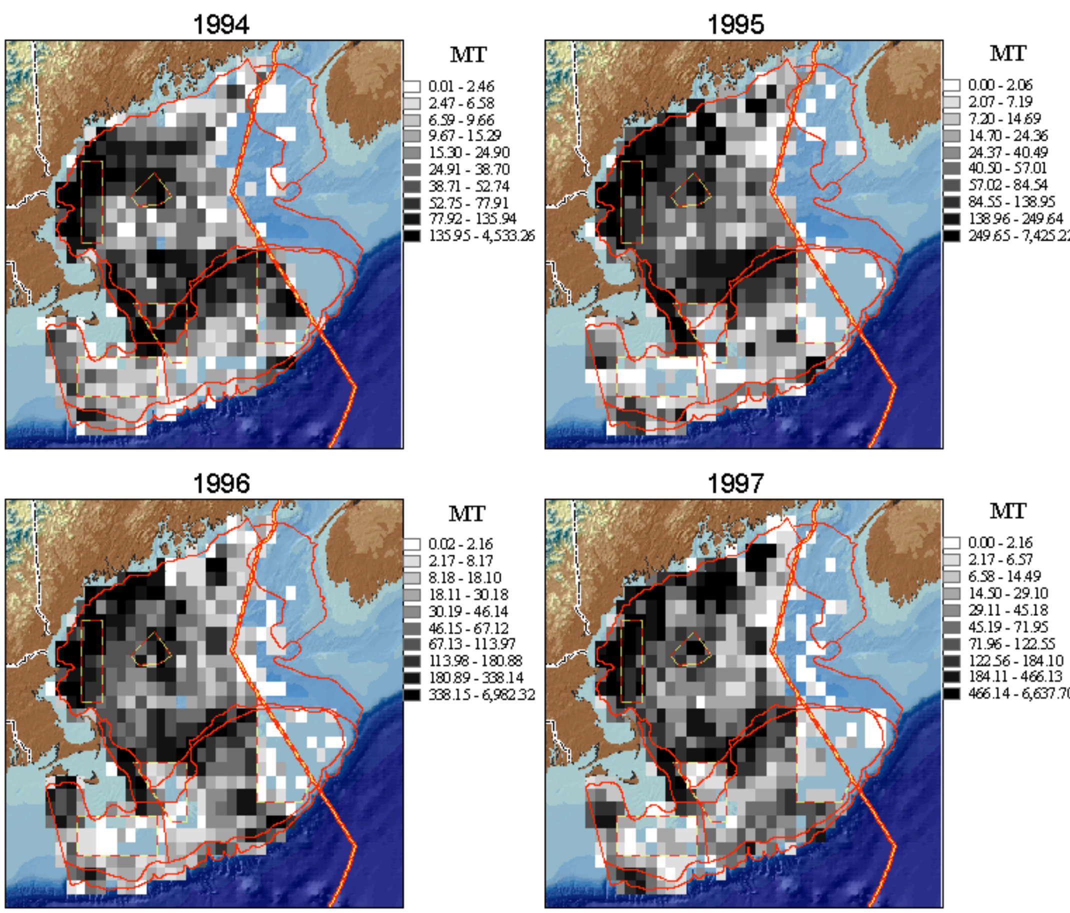



Figure 32. Commercial landings data in metric tons for selected species by year. Closed fishing areas and the U.S. EEZ are also shown.

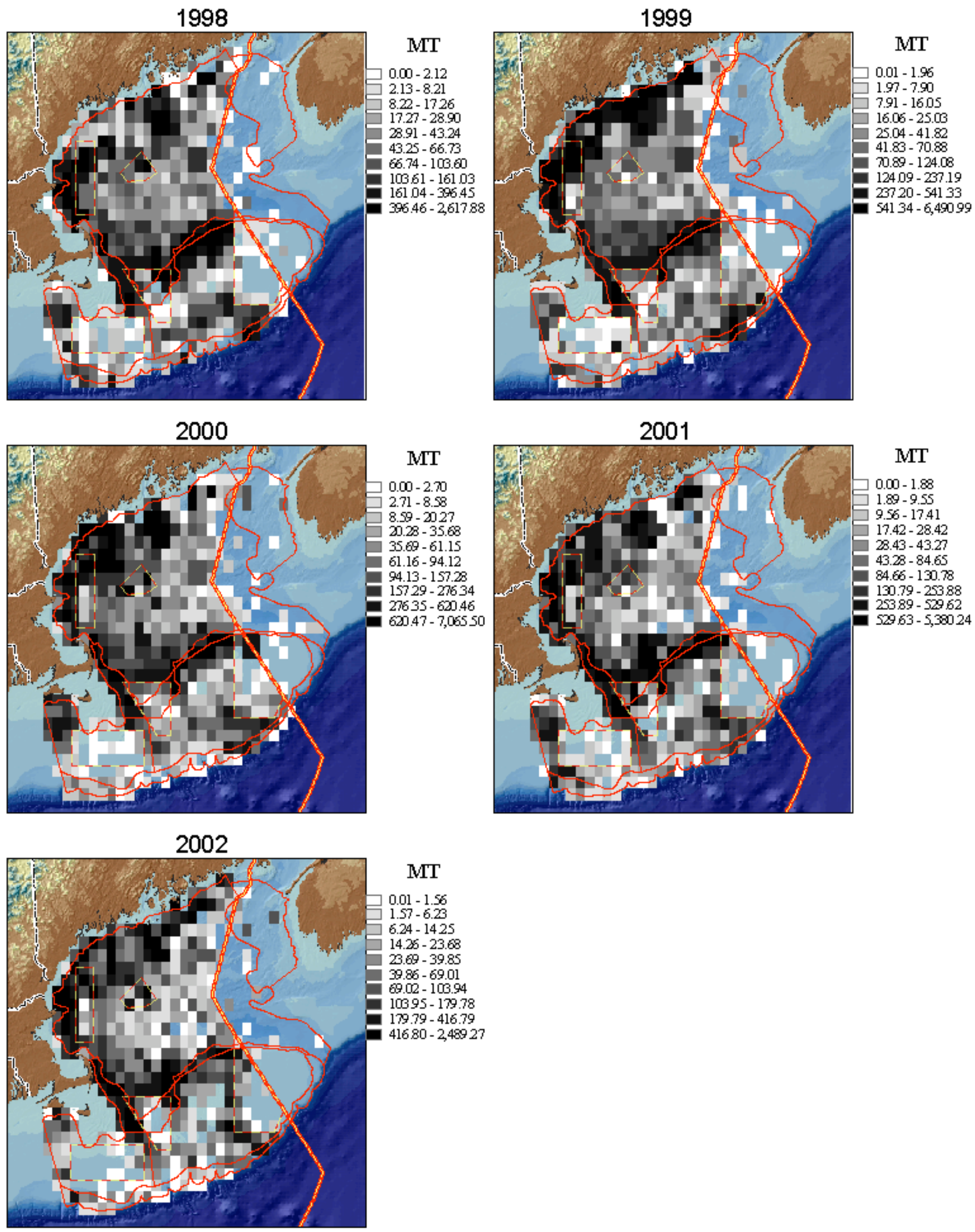



Figure 32 continued. Commercial landings data in metric tons for selected species by year. Closed fishing areas and the U.S. EEZ are also shown.

Average VTR landings maps punctuate the spatial trend of landings for the entire study area, (Figure 33). The best areas for fishing are can be found as stated earlier along the near shore portions of the GOM, in the transitional zone, south of the island of Martha's Vineyard, and near the SW corner of closed area II on GBK.

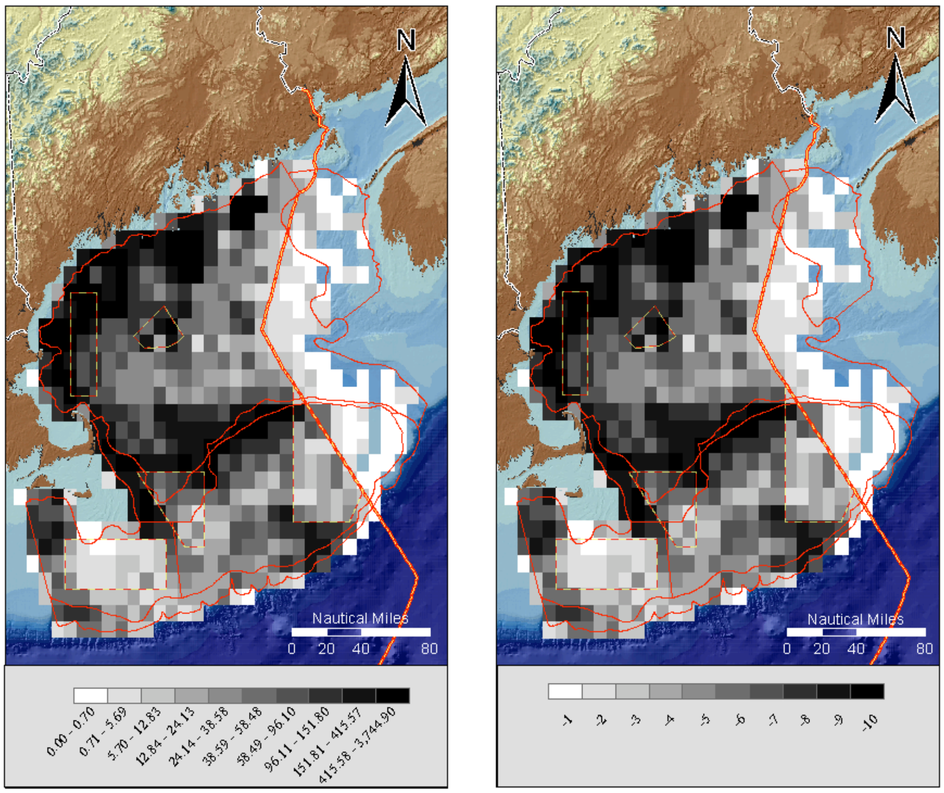



Figure 33. Average VTR landings of selected species for 1994-2002 in decile categories, (right) and reclassified average VTR landings into weighted values for the optimization model. Closed fishing areas and the U.S. EEZ are also shown.

**Weighted Optimization Model**

Two models were run to show that variable weights could be used in order to achieve specific management goals. Regardless of the management scenario implied in the model the combination of the data sets resulted in a spectrum of values ranging from negative values to positive values, such as the example shown in Figure 34. Weighted optimization results are interpreted as the more negative the number the more suitable the cell is for fishing and the more positive the number the more suitable the cell would be for MPA consideration. Due to data limitations analyses of Canadian waters and permanently closed areas were removed. Values within these areas are incomparable to those outside because commercial fishing is restricted for a majority of the time series investigated here.


Figure 34. Suitability index for management goals based on the optimization weighted model.

The results of the weighted optimization model 1, where equal weights were given resource use and conservation, (Figure 35, Table 15), illustrated that 21% of the study area was suitable for MPA designation, 63% should remain open to fishing and 14% of the region was neutral, i.e. showed no preference for MPA designation or continued fishing. The map on the left shows the spectrum of suitability values found within the study area. Area suitability as indicated by the model ranged from –9 to +8, these values were displayed from dark red to dark blue. The map to the right displays the values more simply as whether the region is suitable for fishing (-), suitable for a MPA (+), or neither (0). The color palette for these values was red, blue and light tan respectively.

Areas indicated as better for MPA designation were located in three main regions, see map to the right Figure 35. In the north along the EEZ, in a large swath across the central portion of the study area, and in the south on Georges Bank between the three closure areas. Highest priority areas for MPA designation can be seen in the left hand map on the US side of the Scotian shelf. Areas designated as essential commercial fishing zones can be found throughout Figure 35 right. The highest priority regions to remain open for fishing can be found above Caches Ledge and the Western Gulf of Maine closed areas, east of the NE corner of GBK closed area 1, in the deep subregion south of Closed area 2, south of Martha's Vineyard, and finally south of the SW corner of the Nantucket Lightship closed area.

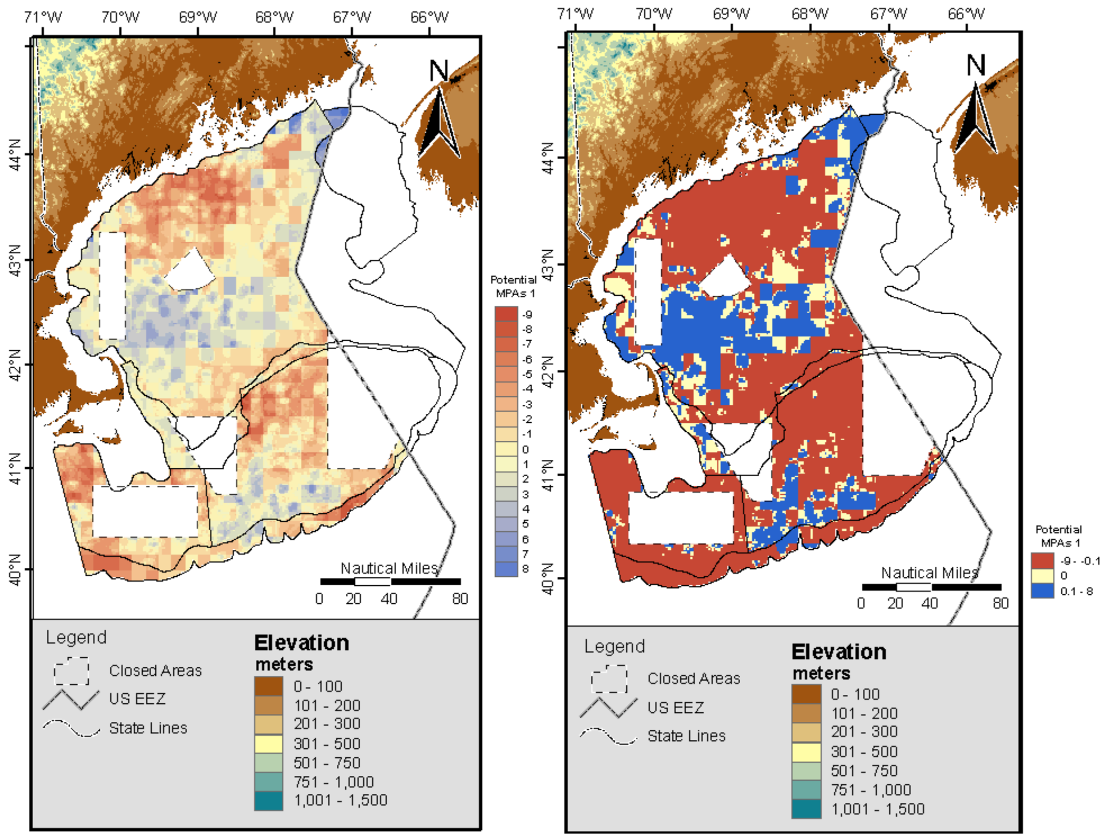



Figure 35. Results from the weighted optimization model, model 1, where weights were equal between resource conservation and resource use. Map on the left shows the results by the level of suitability, dark reds are best for fishing and dark blues are best for MPA consideration. Map on the rights shows results as either good for fishing, suitable for MPA designation, or neutral.

Table 15. Weighted optimization model results using two scenarios, equal weighting and conservation weighting.

**MPA priority**

area of a cell= 3.43 km^2

**Model 1 - Equal Weighting**

| Value | Count | Area | % Protected | |
|---|---|---|---|---|
| -1 | 16171 | 55,465 | 63.19 | % more suitable for Fishing |
| 0 | 3539 | 12,138 | 13.83 | % neutral |
| 1 | 5883 | 20,178 | 22.99 | % more suitable for MPA |
| sum | | 87,782 | | |

**Model 2 - Conservation Weighting**

| Value | Count | Area | % Protected | |
|---|---|---|---|---|
| -1 | 11186 | 38,367 | 43.71 | % more suitable for Fishing |
| 0 | 3129 | 10,732 | 12.23 | % neutral |
| 1 | 11278 | 38,682 | 44.07 | % more suitable for MPA |
| sum | | 87,782 | | |

Results from model 2, the conservation orientated model, showed that 44% of the region was suitable for MPA designation, 44% was more suitable for fishing, and 12% was neutral, (Figure 36, Table 15). The conservation model actually resulted in a balanced outcome protecting fishing and fishery resources. Values from model 2 ranged from –9 to +12 and were displayed using the same color palettes.

The area suitable for MPAs doubled from model 1 to model 2. The areas highlighted in model 1 expanded in the north along the EEZ, in the central region, as well as on GBK plus new areas were recruited including the areas west and north of the WGOM closed area and the great south channel region. New highest priority areas can be found west of the WGOM closure and in the great south channel west of closed area 1.

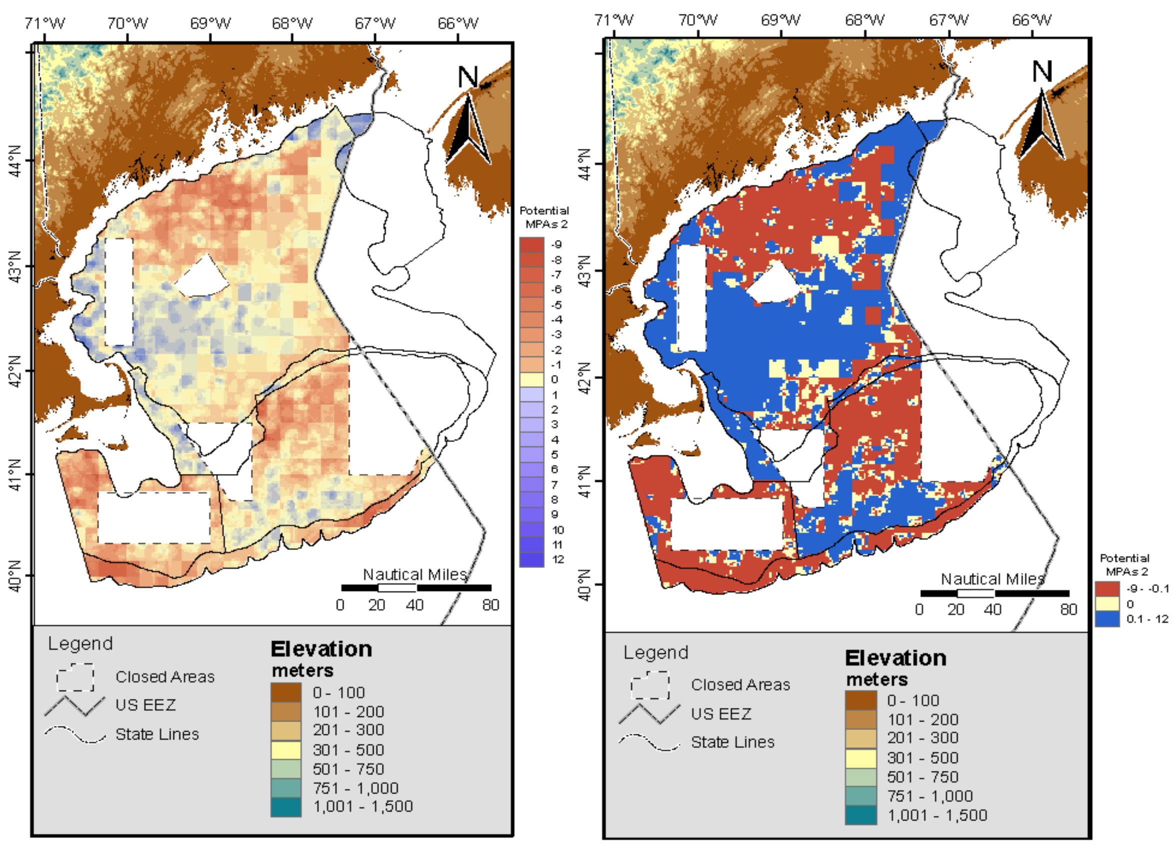



Figure 36. Results from the weighted optimization model, model 2, where conservation of biological resources was given higher weight. Map on the left shows the results by the level of suitability, dark reds are best for fishing and dark blues are best for MPA consideration. Map on the rights shows results as either good for fishing, suitable for MPA designation, or neutral.

The models were compared to look at differences between the amounts of area being considered for MPA designation by the level of suitability for model inputs, i.e. biodiversity, juvenile habitat, spawning habitat, and essential commercial fishing zones. These analyses were conducted to examine the effectiveness of the model on the biological and socioeconomic parameters. The model results were broken into two main categories, those not suitable for MPA designation, (i.e. essential fishing zones) and those suitable for MPA status. Input values, i.e. biodiversity, that fell within the not suitable for MPA raster data set became negative values, those in the suitable for MPA region became positive, and values in the neutral regions became zeros.

Table 16. Summarization of model results for each input (biodiversity, juvenile habitat, spawning habitat, and commercial fishing zones) in the weighted optimization model as indicated by area protected and input weight. * Commercial fishing zones' "% Protected" column indicates area to remain open to fishers.

**Biodiversity**

area of a cell= 3.43 km^2

**Model 1 - Equal Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| **Value** | **Count** | **Area** | **Value** | **Count** | **Area** | **Sum Area** | **% Protected** |
| -10 | 119 | 408 | 10 | 641 | 2,199 | 2,607 | **84.34** |
| -9 | 666 | 2,284 | 9 | 1522 | 5,220 | 7,505 | **69.56** |
| -8 | 1641 | 5,628 | 8 | 808 | 2,771 | 8,400 | **32.99** |
| -7 | 1369 | 4,696 | 7 | 1084 | 3,718 | 8,414 | **44.19** |
| -6 | 1664 | 5,707 | 6 | 899 | 3,083 | 8,791 | **35.08** |
| -5 | 2473 | 8,482 | 5 | 467 | 1,602 | 10,084 | **15.88** |
| -4 | 2875 | 9,861 | 4 | 290 | 995 | 10,856 | **9.16** |
| -3 | 1733 | 5,944 | 3 | 104 | 357 | 6,301 | **5.66** |
| -2 | 1875 | 6,431 | 2 | 33 | 113 | 6,544 | **1.73** |
| -1 | 1747 | 5,992 | 1 | 33 | 113 | 6,105 | **1.85** |
| 0 | 3539 | 12,138 | | | | **Cumulative** | **% Protected** |
| | | | | | 20,171 | 87,744 | **22.99** |

**Model 2 - Conservation Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| **Value** | **Count** | **Area** | **Value** | **Count** | **Area** | **Sum Area** | **% Protected** |
| -10 | 0 | 0 | 10 | 876 | 3,005 | 3,005 | **100.00** |
| -9 | 55 | 189 | 9 | 2,622 | 8,993 | 9,182 | **97.95** |
| -8 | 545 | 1,869 | 8 | 1,740 | 5,968 | 7,837 | **76.15** |
| -7 | 637 | 2,185 | 7 | 2,042 | 7,004 | 9,189 | **76.22** |
| -6 | 937 | 3,214 | 6 | 1,731 | 5,937 | 9,151 | **64.88** |
| -5 | 1,821 | 6,246 | 5 | 1,096 | 3,759 | 10,005 | **37.57** |
| -4 | 2,472 | 8,479 | 4 | 684 | 2,346 | 10,825 | **21.67** |
| -3 | 1,454 | 4,987 | 3 | 261 | 895 | 5,882 | **15.22** |
| -2 | 1,639 | 5,622 | 2 | 125 | 429 | 6,050 | **7.09** |
| -1 | 1,620 | 5,556 | 1 | 98 | 336 | 5,893 | **5.70** |
| 0 | 3,129 | 10,732 | | | | **Cumulative** | **% Protected** |
| | | | | | 38,672 | 87,751 | **44.07** |

Table 16. continued

## Juvenile Habitat

area of a cell= 3.43 km^2

**Model 1 - Equal Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -8 | 0 | 0 | 8 | 5 | 17 | 17 | **100.00** |
| -7 | 1 | 3 | 7 | 15 | 51 | 55 | **93.75** |
| -6 | 38 | 130 | 6 | 78 | 268 | 398 | **67.24** |
| -5 | 135 | 463 | 5 | 272 | 933 | 1,396 | **66.83** |
| -4 | 460 | 1,578 | 4 | 337 | 1,156 | 2,734 | **42.28** |
| -3 | 934 | 3,204 | 3 | 640 | 2,195 | 5,399 | **40.66** |
| -2 | 1,717 | 5,889 | 2 | 1,060 | 3,636 | 9,525 | **38.17** |
| -1 | 3,516 | 12,060 | 1 | 1,276 | 4,377 | 16,436 | **26.63** |
| 0 | 1,976 | 6,777 | | | | **Cumulative** | **% Protected** |
| | | | | | 12,632 | 42,737 | **29.56** |

**Model 2 - Conservation Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -8 | 0 | 0 | 8 | 13 | 45 | 45 | **100.00** |
| -7 | 0 | 0 | 7 | 59 | 202 | 202 | **100.00** |
| -6 | 10 | 34 | 6 | 203 | 696 | 731 | **95.31** |
| -5 | 51 | 175 | 5 | 553 | 1,897 | 2,072 | **91.56** |
| -4 | 217 | 744 | 4 | 647 | 2,219 | 2,963 | **74.88** |
| -3 | 516 | 1,770 | 3 | 1,150 | 3,944 | 5,714 | **69.03** |
| -2 | 1,120 | 3,841 | 2 | 1,800 | 6,174 | 10,015 | **61.64** |
| -1 | 2,248 | 7,710 | 1 | 2,346 | 8,047 | 15,757 | **51.07** |
| 0 | 1,527 | 5,237 | | | | **Cumulative** | **% Protected** |
| | | | | | 23,224 | 42,737 | **54.34** |

## Spawning Habitat

area of a cell= 3.43 km^2

**Model 1 - Equal Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -4 | 0 | 0 | 4 | 15 | 51 | 51 | **100.00** |
| -3 | 1 | 3 | 3 | 65 | 223 | 226 | **98.48** |
| -2 | 154 | 528 | 2 | 223 | 765 | 1,293 | **59.15** |
| -1 | 1,688 | 5,790 | 1 | 1,215 | 4,167 | 9,957 | **41.85** |
| 0 | 877 | 3,008 | | | | **Cumulative** | **% Protected** |
| | | | | | 5,207 | 14,536 | **35.82** |

**Model 2 - Conservation Weighting**

| Areas not suitable for MPAs | | | Areas suitable for MPAs | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -4 | 0 | 0 | 4 | 27 | 93 | 93 | **100.00** |
| -3 | 0 | 0 | 3 | 113 | 388 | 388 | **100.00** |
| -2 | 58 | 199 | 2 | 502 | 1,722 | 1,921 | **89.64** |
| -1 | 772 | 2,648 | 1 | 2,289 | 7,851 | 10,499 | **74.78** |
| 0 | 477 | 1,636 | | | | **Cumulative** | **% Protected** |
| | | | | | 10,053 | 14,536 | **69.16** |

Table 16. continued

**Commercial Fishing Zones***

| area of a cell= |
|---|
| 3.43 km^2 |

**Model 1 - Equal Weighting**

| Areas not suitable for Fishing | | | Areas suitable for Fishing | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -10 | 0 | 0 | 10 | 2,892 | 9,919 | 9,919 | **100.00** |
| -9 | 442 | 1,516 | 9 | 2,447 | 8,393 | 9,909 | **84.70** |
| -8 | 451 | 1,547 | 8 | 2,819 | 9,669 | 11,216 | **86.21** |
| -7 | 560 | 1,921 | 7 | 2,462 | 8,444 | 10,365 | **81.47** |
| -6 | 709 | 2,432 | 6 | 2,088 | 7,162 | 9,593 | **74.65** |
| -5 | 1,159 | 3,975 | 5 | 1,607 | 5,512 | 9,487 | **58.10** |
| -4 | 1,584 | 5,433 | 4 | 872 | 2,991 | 8,424 | **35.50** |
| -3 | 653 | 2,240 | 3 | 844 | 2,895 | 5,135 | **56.38** |
| -2 | 282 | 967 | 2 | 140 | 480 | 1,447 | **33.18** |
| -1 | 41 | 141 | 1 | 0 | 0 | 141 | **0.00** |
| 0 | 3,541 | 12,145 | | | | **Cumulative** | **% Protected** |
| | | | | | 55,465 | 87,782 | **63.19** |

**Model 2 - Conservation Weighting**

| Areas not suitable for Fishing | | | Areas suitable for Fishing | | | | |
|---|---|---|---|---|---|---|---|
| Value | Count | Area | Value | Count | Area | Sum Area | % Protected |
| -10 | 1,017 | 3,488 | 10 | 2,128 | 7,299 | 10,787 | **67.66** |
| -9 | 1,073 | 3,680 | 9 | 1,623 | 5,567 | 9,247 | **60.20** |
| -8 | 1,073 | 3,680 | 8 | 1,983 | 6,801 | 10,482 | **64.89** |
| -7 | 1,325 | 4,545 | 7 | 1,836 | 6,297 | 10,842 | **58.08** |
| -6 | 1,363 | 4,675 | 6 | 1,325 | 4,545 | 9,220 | **49.29** |
| -5 | 2,003 | 6,870 | 5 | 1,020 | 3,499 | 10,369 | **33.74** |
| -4 | 1,975 | 6,774 | 4 | 665 | 2,281 | 9,055 | **25.19** |
| -3 | 1,079 | 3,701 | 3 | 523 | 1,794 | 5,495 | **32.65** |
| -2 | 323 | 1,108 | 2 | 83 | 285 | 1,393 | **20.44** |
| -1 | 45 | 154 | 1 | 0 | 0 | 154 | **0.00** |
| 0 | 3,131 | 10,739 | | | | **Cumulative** | **% Protected** |
| | | | | | 38,367 | 87,782 | **43.71** |

Cumulative results of the models indicated the conservation model protected more overall area than the equal weight model in all cases except for the commercial fishing zones (Table 16). If management were implemented exactly as model results indicated then 44% of the biodiversity in the study area would be afforded protection through model 2 and 23% with model 1. Juvenile habitat would receive 54% and 30% protection, spawning habitat 69% and 36% by the respective models. The commercial fishing zones analysis determined if the cells were suitable for fishing not MPA designation. The equal weight model, (model 1), preserved more area for commercial fishing at 63% compared to 44% by the conservation model, (model 2). Table 14 also shows 84% of the cells ranked as having level-10 of biodiversity were protected in model 1, where as model 2 protected 100% of the level-10 biodiversity cells. Model 1's results for the juvenile habitat ranged from 100-27% and model 2 ranged from 100-50%. Spawning habitat protected in model 1 ranged from 100-42% and model 2 from 100-75%. Commercial fishing zones ranged from 100-0% and model 2 from 68-0%. Again model 2's "% Protected" values for each individual weight were always greater than model 1 except in the commercial fishing zone analysis. Zeros indicate areas where biodiversity values occurred in an area with a neutral designation for suitability status.

Effectiveness of the five existing closures was examined for the three biologically important input parameters, biodiversity, juvenile habitat, and spawning habitat. This was done by calculating the percent area of each weighting level from the total area that the parameter of interest occupies inside the closure, (Table 16). Weighting values for the input parameters were identified as being in or out of the closed areas, those outside the areas remained identical as before ranging from 1-10 and values inside the closures ranged from 100-1000, 100 equivalent to 1 and 1000 to 10.

Table 15 indicates that the current closures do offer some protection for each of the parameters identified as important to this analysis but they are not protecting the highest priority areas. This is apparent by examining the % Protected field in table 15. The column shows the percent of area protected for each parameter is higher for the less critical weights, (closer to 1) and lower for the more critical areas.

Table 17. Effectiveness of permanent spatial closures on biodiversity, juvenile and spawning habitats within the Gulf of Maine.

## Biodiversity Protected by Closed Areas

cell area = 0.25 km^2

| Outside Current Closed Areas | | | Inside Current Closed Areas | | | |
|---|---|---|---|---|---|---|
| **Value** | **Count** | **Area** | **Value** | **Count** | **Area** | **% Protected** |
| 1 | 25,393 | 6348.25 | 100 | 15,945 | 3986.25 | **19.32** |
| 2 | 27,624 | 6906 | 200 | 8,553 | 2138.25 | **10.36** |
| 3 | 27,157 | 6789.25 | 300 | 6,227 | 1556.75 | **7.54** |
| 4 | 48,277 | 12069.25 | 400 | 3,555 | 888.75 | **4.31** |
| 5 | 47,342 | 11835.5 | 500 | 5,530 | 1382.5 | **6.70** |
| 6 | 42,633 | 10658.25 | 600 | 6,009 | 1502.25 | **7.28** |
| 7 | 41,537 | 10384.25 | 700 | 11,381 | 2845.25 | **13.79** |
| 8 | 39,798 | 9949.5 | 800 | 13,510 | 3377.5 | **16.37** |
| 9 | 39,143 | 9785.75 | 900 | 7,873 | 1968.25 | **9.54** |
| 10 | 12,552 | 3138 | 1000 | 3,955 | 988.75 | **4.79** |
| | | | | sum | 20634.5 | |

## Juvenile Habitat Protected by Closed Areas

cell area = 0.25 km^2

| Outside Current Closed Areas | | | Inside Current Closed Areas | | | |
|---|---|---|---|---|---|---|
| **Value** | **Count** | **Area** | **Value** | **Count** | **Area** | **% Protected** |
| 1 | 74,409 | 18602.25 | 100 | 22,196 | 5549 | **45.78** |
| 2 | 44,671 | 11167.75 | 200 | 13,230 | 3307.5 | **27.29** |
| 3 | 25,899 | 6474.75 | 300 | 6,486 | 1621.5 | **13.38** |
| 4 | 13,595 | 3398.75 | 400 | 4,292 | 1073 | **8.85** |
| 5 | 8,721 | 2180.25 | 500 | 2,049 | 512.25 | **4.23** |
| 6 | 3,077 | 769.25 | 600 | 229 | 57.25 | **0.47** |
| 7 | 805 | 201.25 | 700 | 0 | 0 | **0.00** |
| 8 | 165 | 41.25 | 800 | 0 | 0 | **0.00** |
| 9 | 20 | 5 | 900 | 0 | 0 | **0.00** |
| | | | | sum | 12120.5 | |

## Spawning Habitat Protected by Closed Areas

cell area = 0.25 km^2

| Outside Current Closed Areas | | | Inside Current Closed Areas | | | |
|---|---|---|---|---|---|---|
| **Value** | **Count** | **Area** | **Value** | **Count** | **Area** | **% Protected** |
| 1 | 48,621 | 12155.25 | 100 | 16,722 | 4180.5 | **73.00** |
| 2 | 8,155 | 2038.75 | 200 | 4,748 | 1187 | **20.73** |
| 3 | 1,589 | 397.25 | 300 | 1,273 | 318.25 | **5.56** |
| 4 | 361 | 90.25 | 400 | 165 | 41.25 | **0.72** |
| | | | | sum | 5727 | |

## Discussion

### Weighted Optimization Model

The optimization model shows promise in predicting where MPAs might be most beneficial and even where the fishing community may concentrate efforts to stay productive. Balancing these parameters is the overall goal of the optimization model giving managers options on how to design a network of MPAs to fit the optimization model results. Including important parameters such as biodiversity, essential fish habitat and important fishing areas is critical to find a balance in meeting fisheries management goals. The model may be adjusted to fit many scenarios to meet management objectives whether it is to protect biodiversity, spawning/juvenile habitats or areas critical to fishing communities by adjusting the weights of the various input parameters. Strengths of the GIS optimization model also include the ability to calculate the areas that could be set aside for resource protection/enhancement or to estimate those areas that should remain open for fishing.

Including other analyses would improve the utility of this process. Incorporating remotely sensed data such as primary production information, sea surface temperatures, sea floor rugosity and ocean circulation models would benefit managers and MPA design. Other socioeconomic analyses like fleet capacity for major ports would help ensure that ports dominated by vessels with a limited fishing capacity would be able to persist into the future. This model can be adjusted to work in any region of the world to delineate potential MPAs as long as data are available.

The results from the optimization models suggest that 23 and 44% of the regions would be suitable for MPA designation according to model 1 and 2 respectively. This does not imply that all of the area should be closed to fishing. Priority may be given to the areas with the highest suitability levels for MPAs. These areas are afforded the greatest amount of protection and would provide the most benefits to the marine resources. Marginal areas may be left open to fishing because it is less likely that fishers will concentrate efforts in regions with lower average landings. MPA network design may follow any scenario ranging from many small closures to several large. Managers may also take enforcement of closures into consideration as large areas with a regular shape are more easily enforced.

According to the models potential MPAs are most suitable in the northern portion of the Gulf of Maine mostly within the Scotian shelf subregion just west of the EEZ. These cells contained the highest values in the weighted optimization analysis, ranging from +6 to +8 (model 1) and +10-+12 (model 2). Small patches east of Mount Desert Island off the Maine coast and west of the NW corner of the Western GOM closure are also most suitable for MPA designation. The areas within the Scotian shelf subregion had high biodiversity values, between 9-10, and some juvenile and spawning habitat weighting, approximately 1-2. This combined with low fishing effort allowed the model to highlight this region. The small patch east of Mt. Desert Island had moderate biodiversity values, high juvenile habitat scores, low spawning habitat weighting and low fishing effort. The optimal MPA cells west of the Western GOM were influenced by moderate biodiversity, moderate, juvenile habitat, high spawning habitat scores, and moderate to heavy fishing effort. These examples show there are many ways to find an optimal site for a potential MPA site.

The most important commercial fishing zones were found where conflict between competing biological resources was minimized. According to the commercial fishing zone analysis all of the highest level, (–10), areas would be available for continued commercial fishing, an area encompassing approximately 9,900 $km^2$. Areas suggested as optimal for fishing are concentrated in the inshore regions of the Gulf of Maine, offshore on Georges Bank, in most of the N. Mid-Atlantic Bight subregion, and in the deepwater subregions. Some areas designated as highly significant for commercial fishing occur along the boundaries of closed areas. These high landings may be due to the proximity of the fishing grounds to the closed region and are likely affected by the higher abundances of marine species spilling over from the closed region.

The five current closures in the study area, Closed Area I, Closed Area II, Nantucket Lightship, Caches Ledge, and the Western Gulf of Maine Closed Area, all protect portions of the valuable resources and hotspots found within. Analyses show the resources afforded protection by the closed areas are not the highest priority areas found in the study area. Additional closures would be able to protect areas with higher biodiversity levels, and more dense concentrations of juvenile and spawning fish.

**Biodiversity Hotspots**

The model resulting from stepwise linear regression is overly simplistic as the inputs can only explain 5% of the variation in the model, (Table 11). Many parameters not included in the model are needed to better describe the variation in biodiversity. Factors likely to influence the model and the spatial locations of biodiversity are sea surface and bottom temperature. Many marine species have temperature affinities and will migrate according to environmental triggers like temperature. Temperature variations from year to year may result in the bottom trawl surveys missing the presence of some species and may impact species abundance. This simple example would affect the Shannon index, which is based on proportional abundance and species richness, and therefore the interpolated kriging surfaces and the semivariograms resulting from these point data.

Unadjusted abundance estimates may also affect the biodiversity analyses. Catchability varies from species to species with the bottom trawl gear used in the NEFSC BTS. Groundfish and other species that tend to the bottom are more readily available to the gear than pelagic species. Catchability coefficients should be used to adjust the abundance estimates before the Shannon index is calculated. Diel or day night catchability differences occur among the species in the biodiversity hotspot analysis. Some species are more active during the day or night, which affects their associated catchability and adjustments should be made to reflect these differences.

Large nugget values from the semivariograms suggest that a large amount of sampling error occurs in the Shannon index data sets, (Table 14). Some correlation exists between the Moran's index and the semivariograms in suggesting that biodiversity is randomly distributed throughout much of the study area, (Figures 16-22). This breaks the first law of geography, that everything is related and that close features should be more similar than distant ones. Poor autocorrelation may be due to the different shapes, orientations, and area of the subregions. Directional semivariograms may give further insight into the spatial dynamics of biodiversity in the study area. Lag size used in computing the semivariograms may also be the cause of lack of spatial autocorrelation and should be further investigated.

**Spawning and Juvenile Habitats**

Results from these analyses show the concentrations of spawning and juvenile populations. The critical spawning and juvenile areas were designated as the top 20% densest regions. The density metric was set at 20% to afford for the inclusion of the most important areas of juvenile and spawning habitat by the selected species but not the marginal regions where individuals may be captured. Juvenile and spawning individuals shared some of the same high priority habitats in the areas west of the Western GOM closure and in the Great South Channel. This indicates that the habitats in these regions are particularly important for the selected species. Apparent linkages between juvenile and spawning habitat and biodiversity values can be seen when examining the respective maps, (Figures 24 & 29). Since the Shannon index (biodiversity) is influenced by species richness and evenness it is not surprising that high overlap among species occurs in the juvenile and spawning habitat maps where high densities are found.

These analyses included selected demersal and pelagic species within the study area. More demersal species, those found on or near the sea floor, were included in the analysis than pelagics, which may have influenced the analyses. Important regions in deep waters found on the edge of the Continental shelf or within the GOM may have been unnoticed.

Spawning habitat was more spatially restricted than the juvenile habitat analysis, (Figure 29). Spawning density limited to 20% may have been too limited and not reflect all of the critical areas needed by theses important commercial species. The limited spatial extent may also be due to fishers targeting larger individuals and thereby removing these animals from the population. It is also important to note that spawning individuals may use regions outside the study area or prefer mid-water or estuarine habitat instead of demersal areas.

**Essential Commercial Fishing Zones**

The essential commercial fishing zone analysis was the limiting parameter, from a spatial resolution viewpoint, in the optimization model due to the accuracy of reported landings by commercial fishers. If VTR data were more reliable than a fine resolution grid could have been used to allocate fishing effort. This analysis was based on the commercial landings of a select set of species. The fishing community may believe that other species are more important to them as a whole than the ones selected here. Revenue derived from the species is also an important variable and would likely influence the zones that commercial fishers would like to keep open. If the species analyzed here are not the most monetarily valuable then others may need to be included.

Discards of species are also an important variable in protecting and enhancing fisheries. Discards are individuals caught but not retained due to management restrictions or because the species are not valuable to the fishers. A penalty coverage could be created that would evaluate the amount of species discarded per 10-minute quadrilateral. This could be implemented into the model to decrease the likelihood of a cell remaining open to fishing if the discards are too high.

Confounding factors are likely to have influenced the outcome of the essential commercial fishing zone analysis. Currently three permanent closed areas on Georges Bank and two in the Gulf of Maine have restricted fishing activities since 1994. These closure areas coincide with historical fishing grounds for cod haddock and yellowtail flounder (Fogarty and Murawski, 1998). Areas inside the closed areas maybe more valuable for commercial fishing than a permanent closure but since effort is restricted from occurring inside the area this type of analysis is unavailable.

## Conclusion

Fishery managers are required to protect our national marine resources, which includes a cultural way of life for our coastal communities. They face many problems in accomplishing this daunting goal but they have many tools in which to achieve this. In order to accomplish this goal managers must rely on traditional fisheries management practices, i.e. reducing fishing effort and gear restrictions, and also on spatial fisheries management, i.e. MPAs. Marine protected areas offer many benefits such as protecting biodiversity, enhancing fisheries, and protecting against poor fishery management decisions. These benefits occur with certain tradeoffs such as losing critical fishing grounds relied on by today's commercial fishers. Managers and commercial fishers must simultaneously educate each other on the costs and benefits of various management scenarios. An optimization model using GIS can be used effectively to balance tradeoffs between MPAs and areas critical for the fishing community. GIS brings geographic tools and science into the field of fisheries management.

The optimization model requires quality fishery independent and fishery dependent data. Fishery independent data are necessary to define the spatial extent of biodiversity and important juvenile and spawning habitats. Fishery dependent data are critical in the analysis because they define the critical fishing zones required by the fishing community but due to the nature of the data collected it also limits the spatial resolution of the optimization model. However decision-making on the placement of MPAs must include the social concerns of fishers (Malakoff, 2002). MPAs selection based on both biological and socioeconomic parameters will show the fishing community that managers are working with them and not against them (Jennings et al, 2001).

In order to effectively implement any optimization model results fishery scientists, geographers, regional managers, enforcement agents, and most importantly commercial fishers must be involved in designing the various biological and socioeconomic parameters required within the model. Each stakeholder groups must be involved throughout the design and implementation processes.  Team effort and cooperation would lead to other possible model input parameters, such as fleet capacity analysis and rugosity studies, to improve the model results and possibly limit potential conflicts.

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