

**Estimating the Maine green sea urchin stock biomass
using a spatial statistics approach^a**

**A report submitted to the Maine Department of Marine Resources
and Maine Sea Urchin Zone Council**

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by

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Executive summary

The first formal stock assessment for the Maine green sea urchin fishery was conducted in 2001 using fisheries-dependent and biological data. The annual fishery-independent survey program was established in 2001 to provide spatially referenced fisheries-independent information. The objective of this study was to investigate the large-scale spatial patterns in sea urchin abundance to estimate the fishery's exploitable biomass. Triangulated irregular networks (TINs) were used to linearly interpolate urchin densities, characterizing large-scale patterns. The resulting density surfaces were modified to only include areas of the appropriate substrate type and depth zone and were used to calculate total biomass. Exploitable biomass was calculated as the total weight of legal-sized urchins that are at a density (10 urchins m^{-2}) high enough to be attractive to fishermen. Exploitable biomass was estimated at 5878 and 7101 metric tons for management zones 1 and 2, respectively. These estimates are almost identical to estimates calculated using a length-structured fisheries population dynamics model on fisheries-dependent data. We conclude that TINs are useful for stock biomass estimation in the green sea urchin fishery.

Introduction

The green sea urchin, *Strongylocentrotus droebachiensis*, is a benthic echinoderm with a wide arctic-boreal distribution (Scheibling and Hatcher 2001). It is most commonly found on rocky substrate in the shallow subtidal, but can be found down to 300m in depth. The green sea urchin is generally associated with laminarian kelps, but destructive grazing can reduce the kelp beds to “barrens” dominated by crustose coralline algae. Urchin densities vary considerably by habitat; low densities of cryptic adults occur within kelp beds but high densities occur within barrens and feeding fronts.

The green sea urchin is omnivorous, however, most of its diet consists of macroalgae (Scheibling and Hatcher 2001). Laminarian kelps are the primary component of the diet and can be in the form of attached fronds, drifting fronds or detritus. Urchin aggregations occur primarily because of food availability, leading to the formation of feeding fronts (Vadas et al. 1986). Individual growth rates vary considerably due to food quality and availability, as well as sea urchin density; therefore, growth is much greatest for individuals in kelp beds and lowest in urchin barrens.

The green sea urchin stores nutrients in its gonads year-round prior to the production of gametes (Scheibling and Hatcher 2001). This rich gonadal tissue is the target for the commercial fishing industry. The urchin populations in Maine reproduce and spawn once a year, between February and May (Vadas et al. 1997). There are spatial and temporal differences in spawning within the Gulf of Maine. Western populations spawn 4 to 6 weeks earlier than eastern ones, whereas, eastern populations spawn for 4 to 6 weeks longer than western ones. Fertilization is external and the planktotrophic larvae can remain in the water column for 4 to 21 weeks (Scheibling and Hatcher 2001). There are large-scale recruitment

patterns within the Gulf of Maine that correspond to coastal circulation patterns and depth. At smaller scales, recruitment is spatially and temporally variable and appears to be lower in kelp beds than in barrens. Post-settlement mortality rates are higher in fleshy macroalgal habitats, possibly due to higher densities of micropredators (McNaught and Steneck 1998)

The green sea urchin can profoundly alter the rocky subtidal habitat. Destructive grazing can transform lush, diverse kelp beds into urchin barrens (Scheibling and Hatcher 2001). High levels of sea urchin recruitment and low mortality rates, along with high levels of algal predation, help to maintain the urchin barren state. Conversely, high levels of algal recruitment, along with low levels of sea urchin recruitment and high urchin mortality rates, help to maintain the kelp bed state. For these reasons, kelp beds and urchin barrens have been considered alternate stable states, and may be locally stable for decades (Vavrinec and McNaught 2001).

Urchin barrens are currently targeted for the sea urchin fishery; however, these barrens may be an artifact of the historic fishing industry in Maine. Research has suggested that an anthropogenic release in predation on sea urchins, due to intensive fishing on lobster and predatory fishery, may have allowed the development of high-density feeding fronts and barrens (Vadas and Steneck 1995). The large-scale removal of urchins through the commercial fishing industry could feasibly shift urchin barrens back to kelp beds (Vavrinec and McNaught 2001). In fact, researchers have documented this type of habitat switch in eastern portions of the Gulf of Maine, which historically received the earliest and heaviest fishing pressure.

The green sea urchin is an important component of the fishing industry in the state of Maine, currently ranking fourth by value. Commercial landings began in the late 1980's,

quickly reaching a peak of more than 22,000 metric tons in 1993 (Figure 1). It has since experienced a continuous declining trend in yield, with landings of less than 5000 metric tons in 2001. This decline has been attributed to decreasing stock abundance over the last decade (Chen and Hunter 2003).

The sea urchin fishery is managed by the Maine Department of Marine Resources (DMR) using a number of management tools, including limited entry, opportunity days and minimum (52mm) and maximum (76mm) size limits. The fishing grounds are divided into two management zones based on spatial/temporal variations in spawning, in which management differs only by fishing seasons (Vadas et al. 2002) (Figure 2). Fishery-dependent data, including landings and catch size compositions, have been collected by the DMR since the commercial fishery started. This information has formed the basis of subsequent management decisions. A fisheries-independent survey program commenced in 2001 and provides annual estimates of abundance, spatial distribution and population structure for the green sea urchin stock along the coast of Maine.

The first formal stock assessment for the Maine green sea urchin fishery was conducted in 2001 (Chen and Hunter 2003). Fishery-dependent data and urchin life history parameters were used to assess the population dynamics of the Maine sea urchin stock. A length-based stock assessment model was used with a Bayesian approach to determine current stock biomass and exploitation rate. The study estimated that the current stock biomass was extremely low, about 10% of the virgin biomass.

Data sampling technique has a large impact on the quality of the stock assessment. The quality of fishery-dependent data is more questionable than fishery-independent data and its sole use in stock assessments may lead to large uncertainty or even bias (Hilborn and

Walters 1992). Only fishery-dependent data were available for the first stock assessment (Chen and Hunter 2003), however in 2001 the DMR began an extensive fishery-independent survey program. This large, spatially referenced, scientific data set can be used in both traditional stock assessments and in those incorporating spatial analysis techniques.

Scientists have realized the importance of incorporating spatial variability into stock assessments and have adapted a number of spatial analysis techniques to explore spatial trends and to estimate or predict stock abundances. Moving averages, kernel estimation, spline methods, and tessellation are all spatial analysis techniques that can be used to estimate spatial patterns of population abundance (Ripley 1981; Bailey and Gatrell 1995).

Spatial statistics or spatial analyses are employed to model first and second order, or large and small-scale, spatial variability of a variable in order to estimate the value at unobserved locations (Bailey and Gatrell 1995; Petitgas 2001). Intrinsic second-order methods, along with kriging, have become the most popular geostatistical tools and are now commonly used to estimate exploited fish stock biomass (e.g., Simard et al 1992; Pelletier and Parma 1994; Maravelias 1996; Lembo et al. 1998; Maynou et al. 1998; Rivoirard et al. 2000; Petitgas 2001). First, the spatial distribution of the stock cannot be affected by the geometry of the region, *i.e.* the spatial distribution cannot differ near the borders of the zone (Petitgas 1993; Bailey and Gatrell 1995; Warren 1998; Rivoirard et al. 2000). Second, the process must exhibit some degree of second-order stationarity, or spatial dependence, which means that small-scale deviations in variables are similar in neighboring sites. If these assumptions are violated, we must use other spatial analysis techniques to estimate the spatial patterns.

Tessellation investigates first-order, or large-scale, spatial variability in a variable, meaning it estimates how the mean values vary over a study area (Peucker et al. 1976; Ripley

1981; Bailey and Gatrell 1995). The triangulated irregular network (TIN), or Delauney triangulation, is the simplest and most common tessellation technique for the creation of surfaces. The TIN surface consists of contiguous, non-overlapping triangles created by linear interpolation of the variable. TINs are most commonly used for visualization purposes but have been used to estimate stock biomasses (Simard et al. 1992; Guan et al. 1999).

The objective of this study is to investigate the large-scale spatial trends in green sea urchin abundance using spatial analysis techniques in order to estimate biomass of the stock. This paper addresses how suitable TINs are for biomass estimation, specifically for the green sea urchin fishery. This study can provide the DMR with critical information on the sea urchin stock that can aid in the development of future management plans and help ensure a sustainable fishery.

Materials and Methods

Urchin density and size frequency information were obtained from the 2001 pilot study for the State's annual fishery independent survey. The Department of Marine Resources sampled 144 sites along the Maine coast using SCUBA. At each site, they randomly sampled 90 quadrats (1m^2) along a linear transect set perpendicular to shore. Sampling intensity was equally divided amongst three depth zones: 0-5m, 5-10m, and 10-15m. At each site, size frequency data were obtained by subsampling one quadrat per depth zone, in which test diameters were measured for all individuals in the quadrat. In the 15-40 m depth zone, an additional 148 sites were sampled using a video camera that recorded 10 quadrats (0.5m^2) at each site. Due to the low urchin densities, test diameters were measured

for all recorded urchins. Mean urchin density values were calculated for each site (n=292), and by depth zone within each site (n=580).

Five test diameter categories were created to more accurately represent the wide range of individual urchin weights. The categories were based on the State's minimum and maximum size restrictions, allowing us to separately estimate the biomass of urchins that have not yet recruited to the fishery, urchins within the fishery, and urchins that have escaped the fishery. Urchin density values were scaled by the size frequency data, to generate urchin density values for each size category. Weight per urchin was calculated based on the mean length of the category using a length-weight relationship (Scheibling et al. 1999).

Representations of the large-scale trends in sea urchin density were created using the TIN method (ArcView 3.2a, 3D and Spatial Analyst Extensions). TIN surfaces were generated for 40 different scenarios, according to the size category, depth zone and management zone (Figure 3). The surface was then modified to only include areas of the appropriate depth and substrate type, using a customized C++ program. A map of surficial geology was used to identify areas of urchin habitats predominately including gravel or rock substrate (Kelley et al. 1999) (Figure 4). Digital gridded bathymetry data with 15 arc second resolution were used to create a plot of 5m isoline contours (Figure 5). This data source consists of digital bathymetry datasets from sources such as NOAA and the Naval Oceanographic Office (Roworth and Signell 2002). Modified urchin density plots were created for each scenario (Figure 6). The volume beneath the modified TIN surface was calculated, based on Riemann sums, and multiplied by the mean weight to determine total urchin biomass for each scenario. This estimation process is described in a cartoon in Figure 7.

Fishable biomass is defined as the biomass of all legal sized urchins, and is simply the subset of the total biomass corresponding to legal sized urchins. Exploitable biomass was calculated by incorporating a threshold, or cut-off, density value for legal sized urchins, so volume was calculated only for areas with more than 10 urchins m^{-2} . This value was considered as the minimum density that could attract fishermen to fish in the urchin fishery. Estimation uncertainty was estimated using cross validation ($n=60$), which involves randomly removing sites and then modeling the process to calculate residuals. Urchin biomass values for depth zones and management zones were calculated based on the arithmetic mean to provide comparisons to the spatially derived estimates. Exploitation rates, or the ratio of commercial landings for the 2000-2001 fishing season to the exploitable biomass estimates, were calculated to facilitate comparison to the results generated from a traditional stock assessment (Chen and Hunter 2003).

Results

Sea urchin densities per m^2 and standard deviations varied by survey strata, being lowest in the western strata and highest in the eastern one (Table 1). Average site densities had a mean number of 4.93 and were highly skewed to the right, with a skewness coefficient of 7.21 (Figure 8). Mean density was similar for the three shallow depth zones with approximately 9.50 urchins m^{-2} , however the 15-40m zone was substantially less with 0.32 urchins m^{-2} . Urchin diameters varied from 8 mm to 114 mm with a mean at 35.90 mm (Figure 9).

Total sea urchin biomass was estimated at approximately 250,000 metric tons, in which over 80% was found in management zone 2 (Table 2). Half of the total biomass was

found in the 0-5m depth zone in management zone 2 (Figure 10). The majority of the estimated total biomass was comprised of 50-80 mm and 39-64 mm urchins for management zones 1 and 2, respectively (Figure 11). Fishable biomass was estimated at approximately 165,000 metric tons (Table 2). The majority of the fishable biomass in each zone was within the 0-5m depth zone, with approximately 75% of the total fishable biomass within zone 2 (Figure 12). There was no fishable biomass estimated for the 15-40 m depth zone for either management zone.

Patterns in exploitable biomass by depth differed from the patterns seen in total and fishable biomass (Figures 10, 12 and 13). Over 95% of the fishable biomass in management zone 1 was found in the 0-5 m depth zone, which exceeded the corresponding estimate for management zone 2. However, the exploitable biomass estimate for management zone 2 was higher than zone 1 due to higher biomass estimates in the 5-10 m and 10-15 m depth zones.

The exploitable biomass estimates closely approximated the landings for the 2000-2001 fishing season (Table 2). Exploitation rates calculated from the exploitable biomass estimates were 0.37 and 0.45 for management zones 1 and 2, respectively. Cross validation of sea urchin density surfaces estimated a mean residual of 0.50 (median=0, standard deviation=1.86, skewness=2.80, n=60).

Discussion

The objective of this study was to investigate the large-scale spatial patterns in sea urchin abundance to estimate the stock biomass. There are a number of spatial analysis techniques available that can generate this type of information. The most widely employed

spatial analysis technique in fisheries is intrinsic geostatistics, which along with kriging can generate precise estimates of biomass based on the small-scale variations.

Intrinsic geostatistics are applicable to spatially auto-correlated processes based on two assumptions (Petitgas 1993; Bailey and Gatrell 1995; Warren 1998; Riviorard et al. 2000). First, the variable and the region's geometry are independent of one another. This cannot be assumed for sea urchin abundance data, which are not independent of the study area, but are dependent on the depth and substrate type. Second, there must be some degree of stationarity, either strict stationarity or stationarity of increments. The sea urchin data are highly skewed and spatially variable; stationarity does not exist so the variogram is an unreliable representation of the spatial continuity (Rossi et al. 1992). For example, an empirical variogram of site density means shows no spatial correlation (Figure 14). There are ways to modify the data to make them more appropriate for variogram analysis, such as trend removal, lognormal transformation of data and stratification of the region based on variances (Rossi et al. 1992; Simard et al. 1992; Maravelias 1996; Riviorard et al. 2000). However, these techniques are labor-intensive and provide marginal improvements in the variogram analysis for the sea urchin data. Since we cannot assume that the data is appropriate for intrinsic geostatistics, we used another spatial analysis technique, triangulated irregular networks, to characterize the large-scale spatial patterns in sea urchin abundance.

TINs are a simple spatial analysis technique for exploring the spatial variability of a process. They have received limited uses in fisheries stock assessment; however, because most stocks exhibit some degree of stationarity so intrinsic geostatistics provide more precise biomass estimates (Simard et al. 1992; Guan et al. 1999; Bailey and Gatrell 1995). When sampling locations are relatively evenly spaced, as in the sea urchin abundances by depth

zones, TINs are a good estimator of the large-scale spatial patterns for spatially uncorrelated processes (ESRI 1998; Guan et al. 1999). The technique requires no complex statistical decisions, making it an accessible tool for fisheries managers (Bailey and Gatrell 1995). However, this technique does not incorporate a variance structure into the estimation process, so uncertainty cannot be directly quantified. In this study, cross-validation showed that mean residuals of the modified density surfaces were greater than zero. This result suggests that there is a global bias in the TIN surfaces and that the biomass estimates were likely overestimated (Simard et al. 1992). However, exploitable biomass estimates were probably less affected than total biomass estimates because the subdivision of abundance estimates by management zones, depth zones and size categories minimizes the spatial variability and the impact of outliers.

Exploitable biomass, not fishable biomass, was used as an estimation of the stock biomass (Table 2 and Figure 13). This distinction was necessary because some areas incorporated in the estimation technique were not subjected to fishing pressure due to geographic isolation or low urchin densities. The exploitable biomass estimates accounted for this difference because a threshold density value of 10 urchins m^{-2} was incorporated into the analysis, upon recommendation by fishermen, ecologists and DMR fisheries biologists. Areas with densities below the threshold receive negligible commercial fishing pressure, and are not incorporated in the biomass estimations. Their impacts on the fishery, in particular in their contributions to the recruitment of the fishery, need to be assessed in future studies.

Biomass estimates generated using spatial analysis approaches were similar to ones generated using different assessment techniques. Total biomass estimated based on arithmetic means, stratified by zone and depth, was comparable to the TIN estimate for total biomass

(Table 2). Even more significant, the exploitable biomass estimates based on TINs were almost identical to ones calculated using traditional stock assessment techniques (Table 2). This similarity is evident in the calculated exploitation rates, for which spatial analysis estimates (2001) were 0.37 and 0.45 for management zones 1 and 2, respectively, and the traditional techniques estimates were 0.38 (2001) and 0.57 (2000) for the management zones, respectively. These techniques are based on fundamentally different theories and the analyses used entirely different data sources; fishery-independent data for the spatial analysis assessment but fishery-dependent and biological data for the traditional fisheries stock assessment. Despite these differences, the biomass estimates and exploitation rates were almost identical. The implications of this lie in the status and management of the sea urchin fishery. Stock biomasses and exploitation rates can be used to gauge the stock status. The work on biological reference points suggests that current exploitation rates far exceed target reference points, signifying that the Maine sea urchin stock is over-fished. The confirmation of the two independent assessments not only validates the techniques, but also indicates that we are generating good biomass estimates and providing quality information to the stock managers.

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Table 1. Descriptive statistics for quadrat density counts (m^{-2}) by management zone and survey strata

Zone	Stratum	Density	St Dev	Density	Density	N
		Mean		Min	Max	
1	1	0.17	1.62	0	36	1706
1	2	2.57	10.63	0	130	1600
1	3	3.20	11.29	0	141	1580
2	4	4.20	14.13	0	180	1490
2	5	4.24	12.52	0	127	1580
2	6	10.06	17.59	0	147	1530
2	7	7.90	13.85	0	113	1498
2	8	13.50	20.38	0	113	1570
2	9	34.45	44.03	0	280	1540

Table 2. Summary of biomass estimates derived using the TIN method, the arithmetic mean, and a fishery population dynamics approach for 2001, in comparison to the 2000-2001 commercial landings.

	Zone 1	Zone 2	Total
TIN Method			
Total Biomass	45868	204304	250172
Fishable Biomass	39060	126725	165786
Exploitable Biomass	5878	7101	12979
Arithmetic Mean			
By Zone	74168	381809	455977
By Zone and depth	24409	242017	266426
Fish. Pop. Dynamics	6550	8452*	15002
2000-2001 Landings	2148	3213	5361

* 2000 value

Figure 1. Commercial landings in metric tons for the Maine sea urchin fishery.

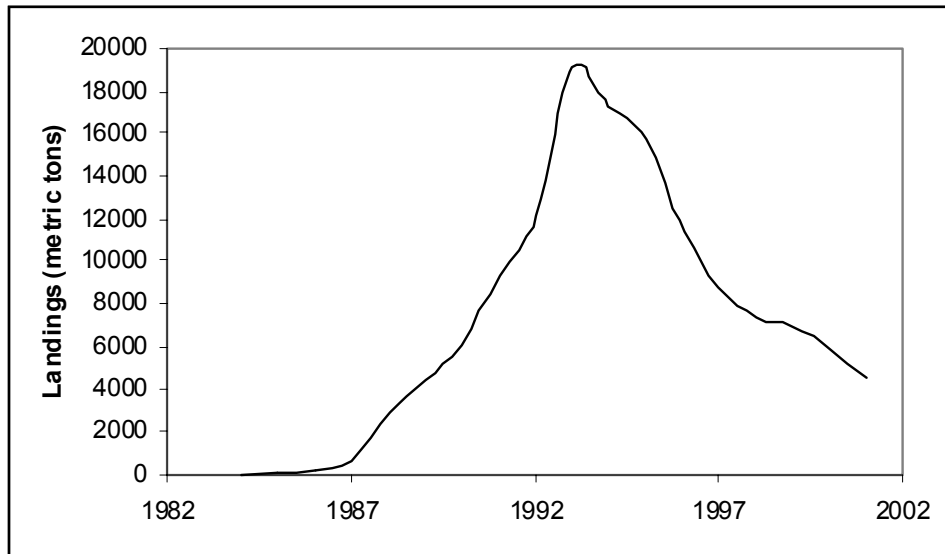
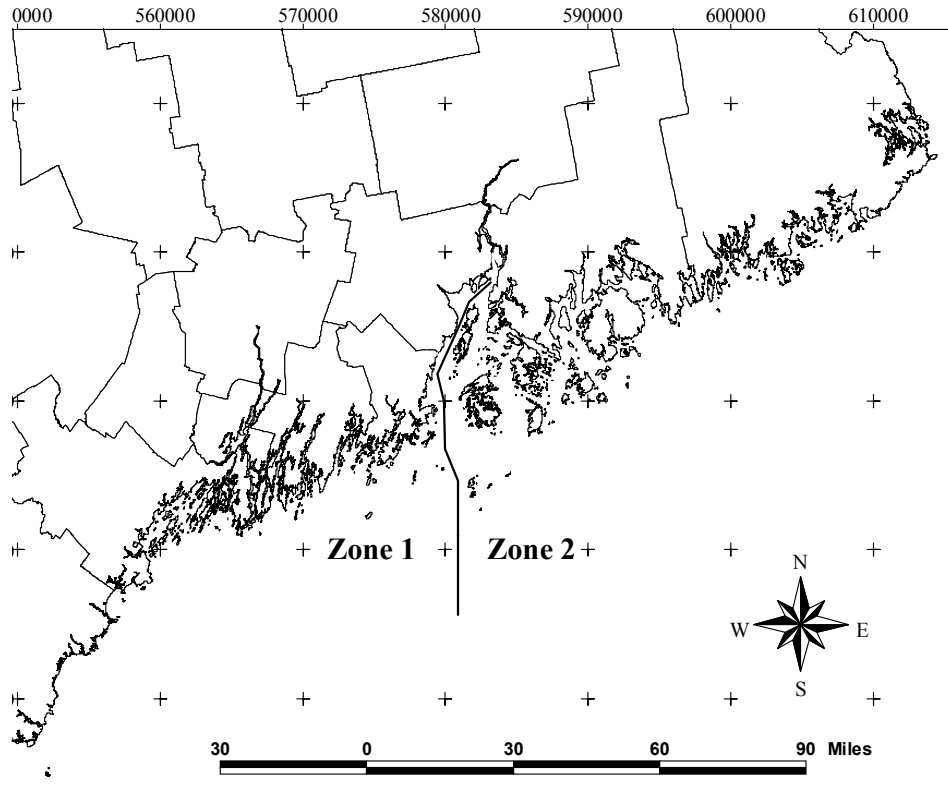


Figure 2. Management zones for the Maine sea urchin fishery.



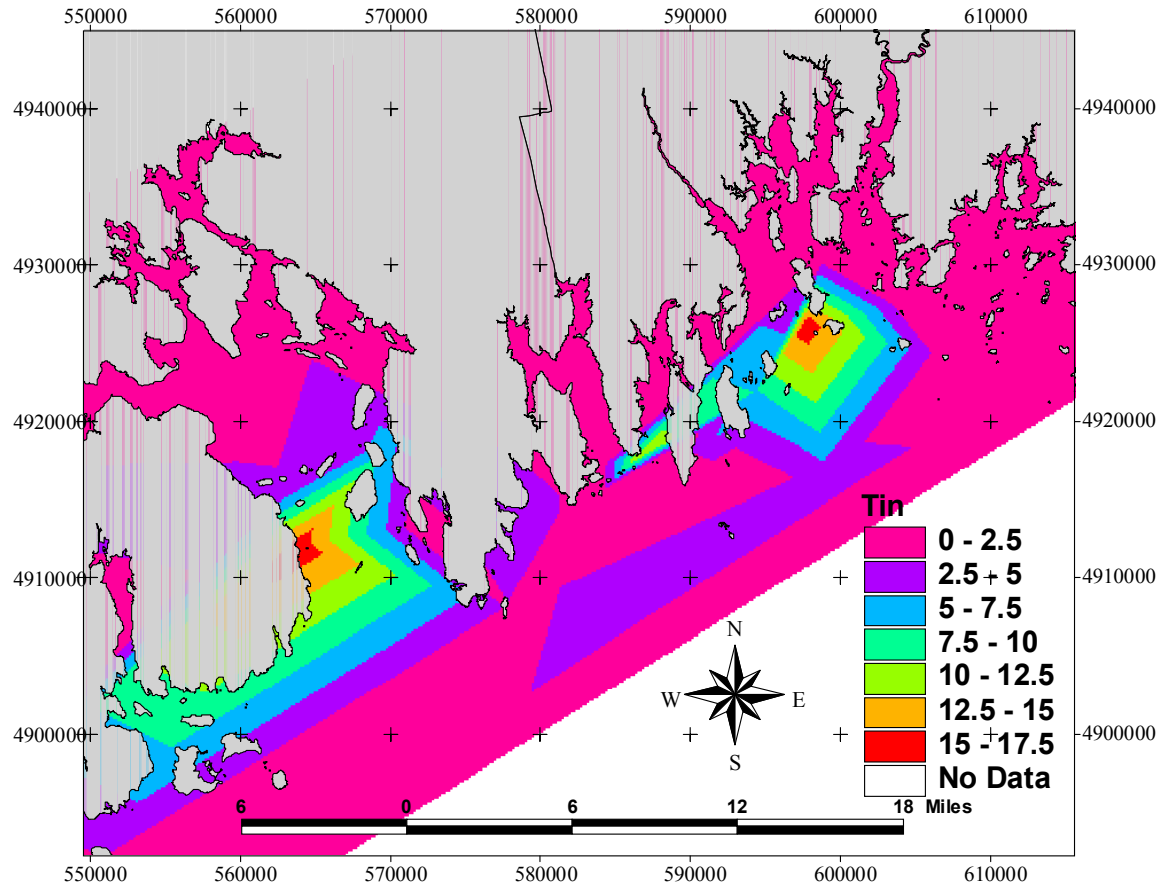


Figure 3. Plot of the urchin density surface for 50-65 mm urchins within the 0-5 m depth zone for the Mt. Desert Island area, in management zone 2, created using a triangulated irregular network (TIN).

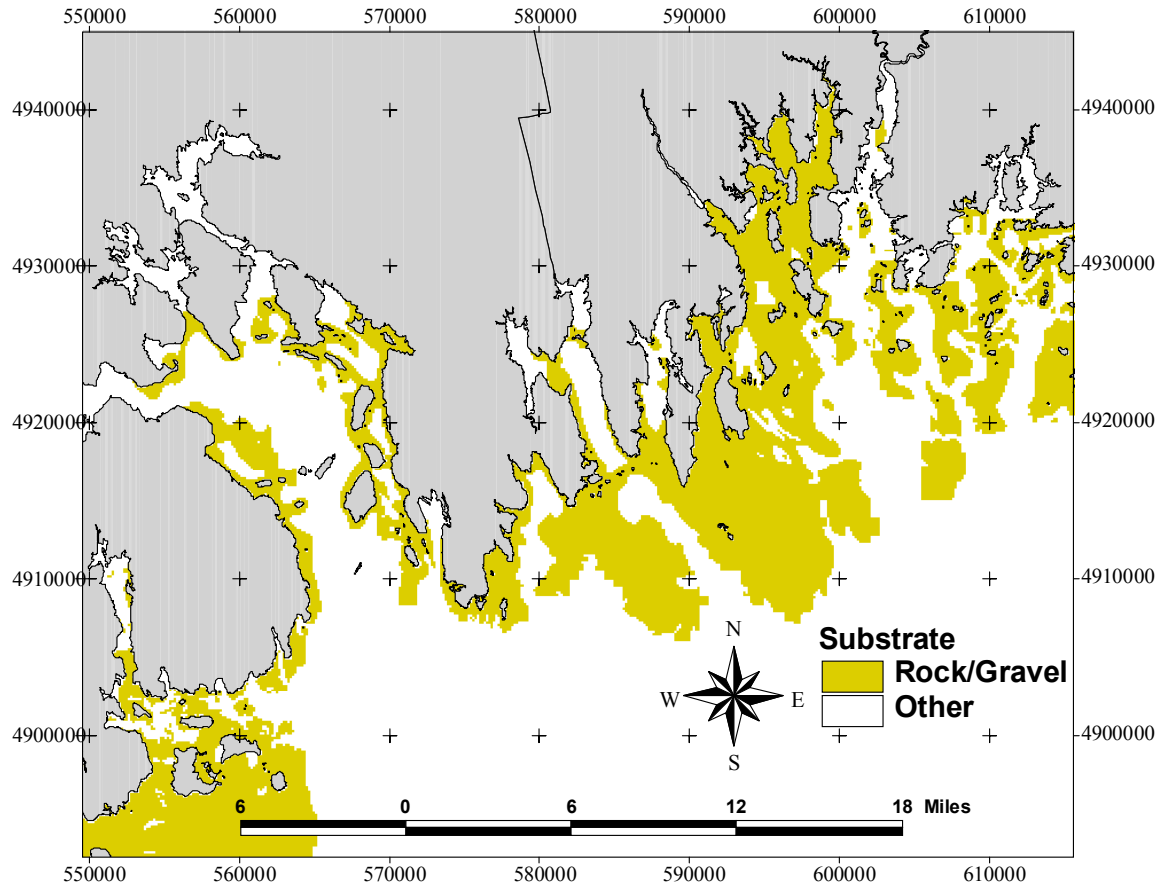


Figure 4. Plot of rock and gravel substrate within 40 m depth for the Mt. Desert Island area, in management zone 2.

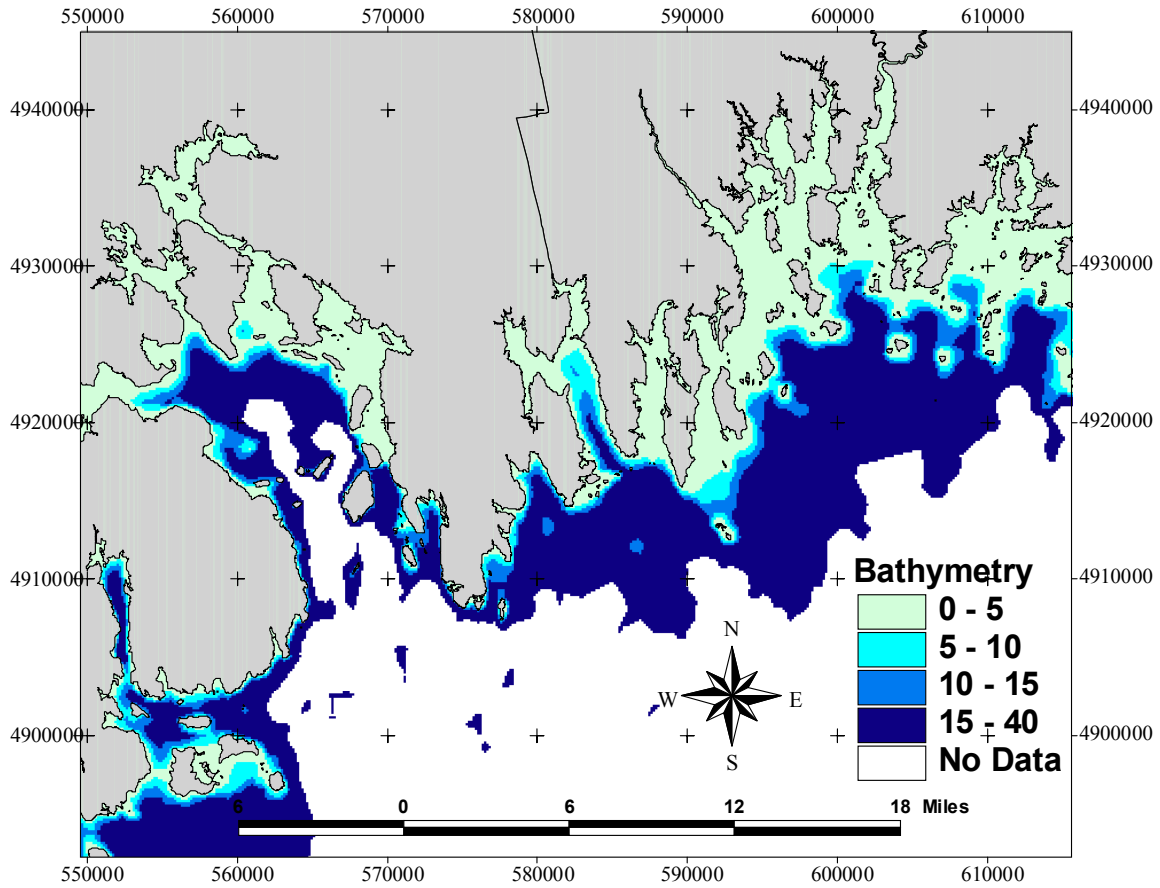


Figure 5. Plot of bathymetry (in meters) for the Mt. Desert Island area, in management zone 2, showing the 4 depth zones used in this study.

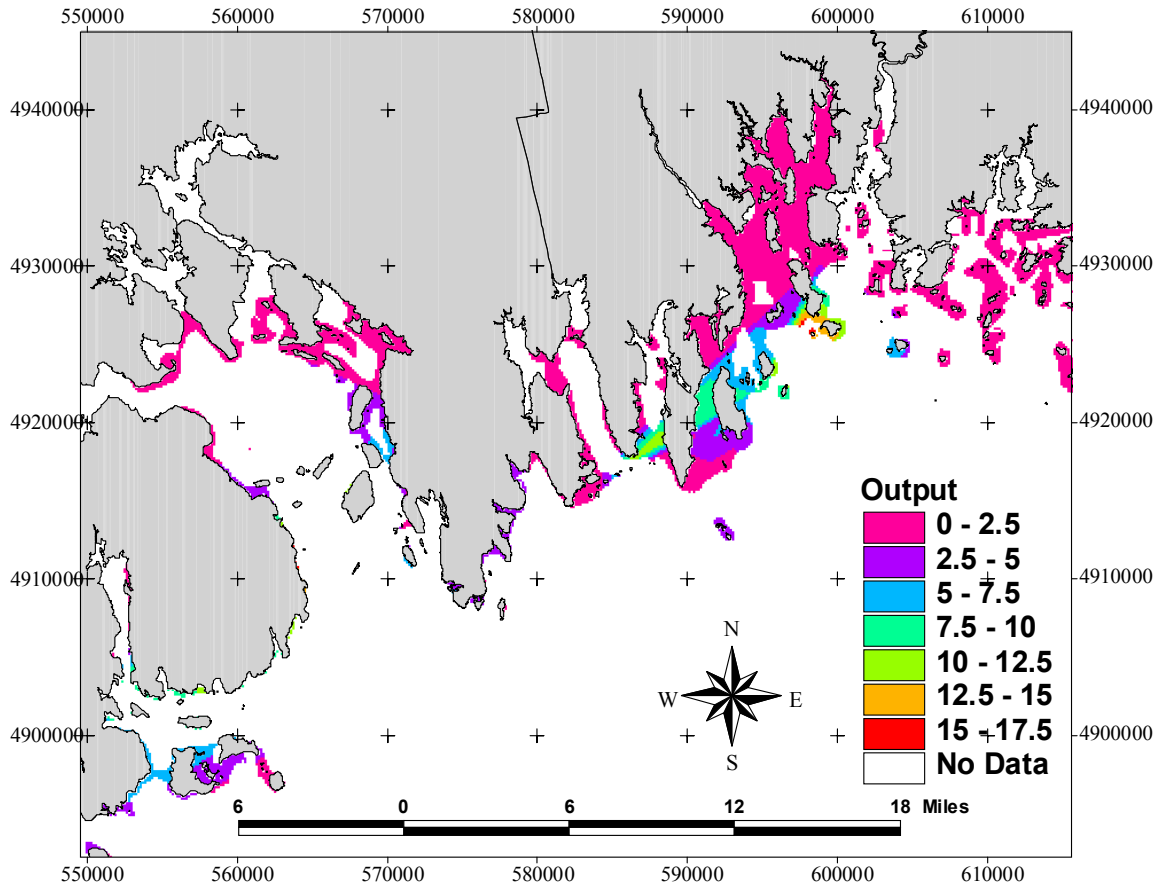
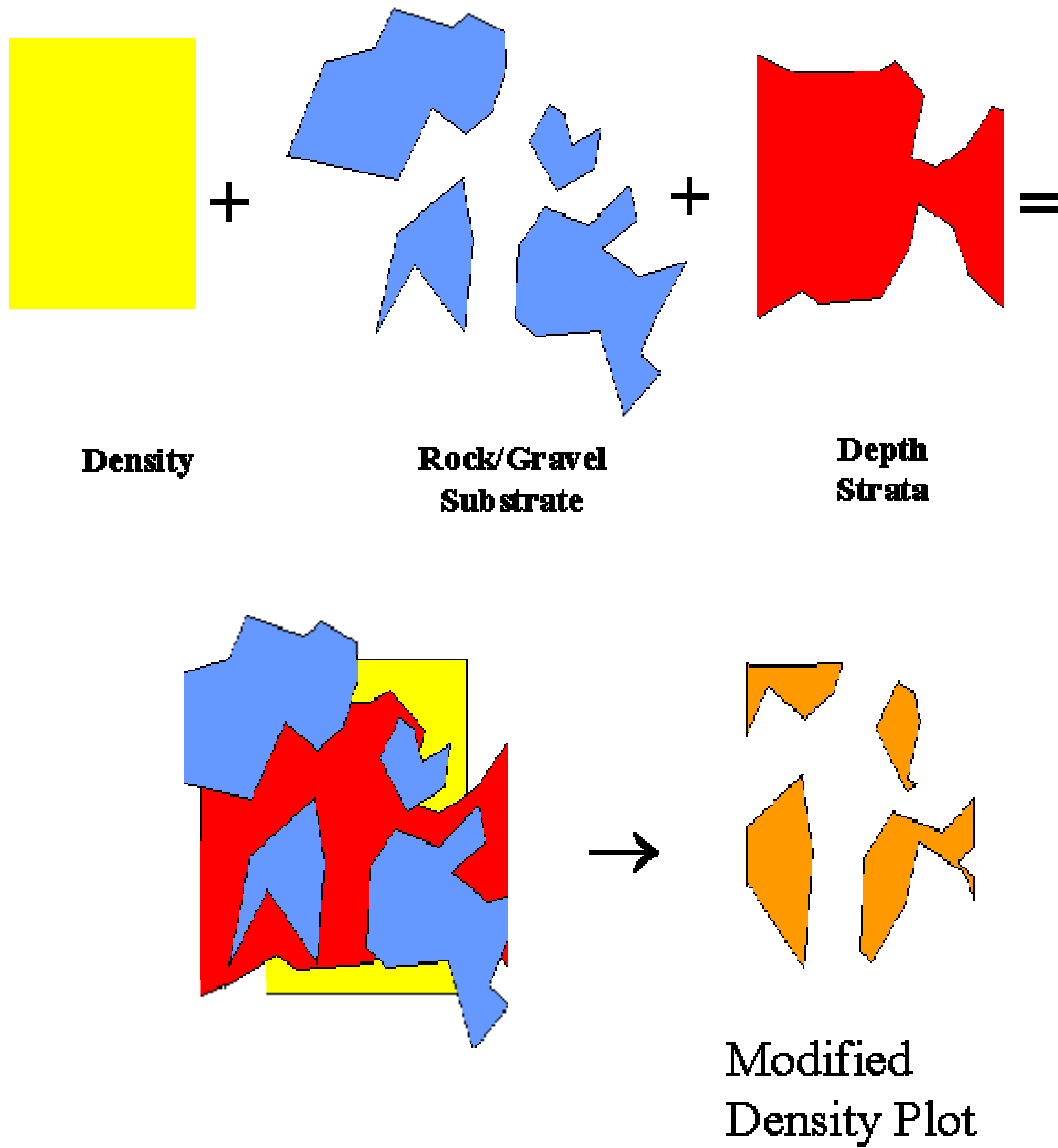


Figure 6. Plot of urchin densities for 50-65 mm urchins within the 0-5 m depth zone for the Mt. Desert Island area, in management zone 2. This plot was created by limiting the original triangulated irregular network (TIN) (Figure 3) to areas of rock/gravel substrate (Figure 4) within the 0-5 m depth zone (Figure 5)

Figure 7. A cartoon showing the process of estimating the sea urchin biomass used in this study.



$$\text{Biomass} = \text{Volume of Density Plot} * \text{Urchin Weight}$$

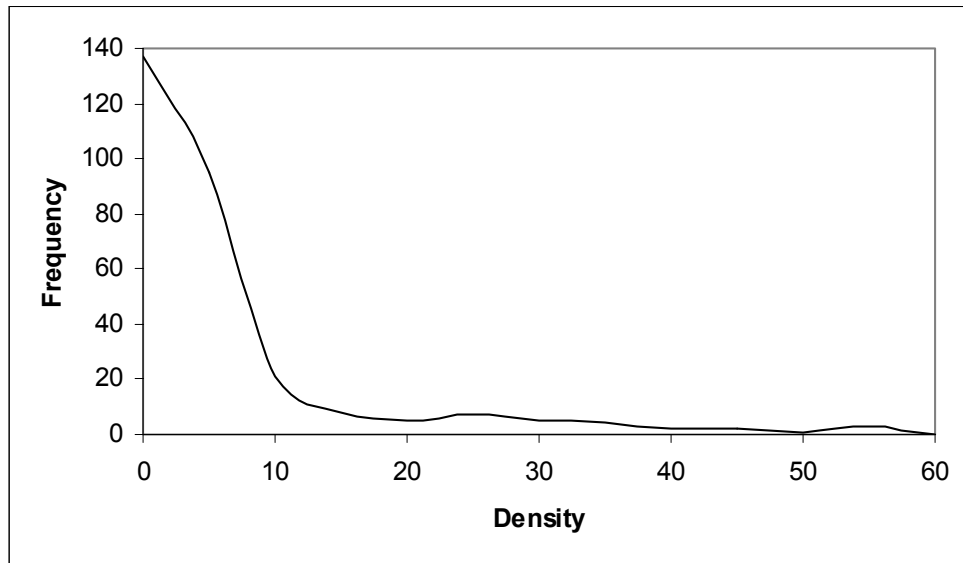


Figure 8. Histogram of urchin density values per m² for all sites, excluding one outlier with 174 urchins m⁻².

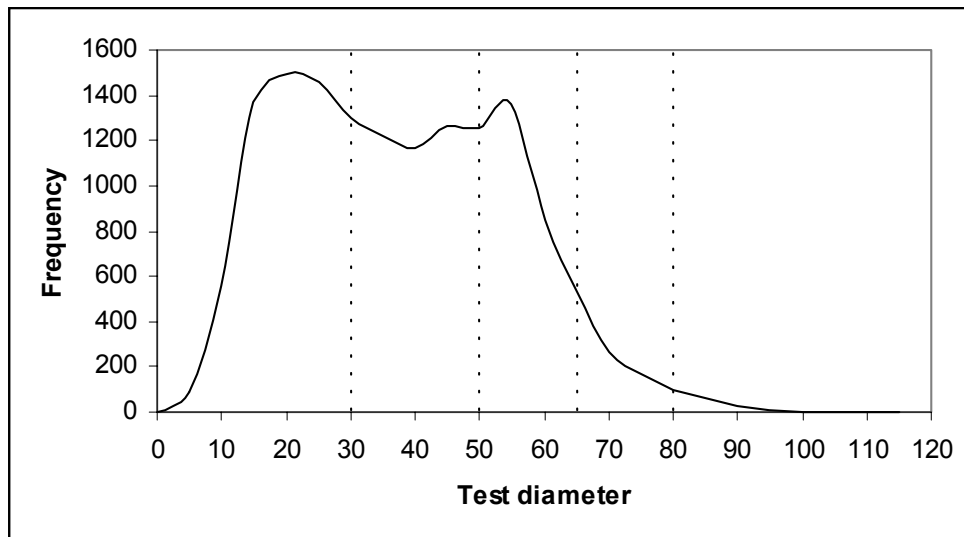


Figure 9. Histogram of urchin test diameters for all sampled quadrats. Dashed lines delineate the 5 size categories. Mean density is 35.90mm, with category mean densities of 18.5, 39.25, 55.35, 70.59, and 86.30mm.

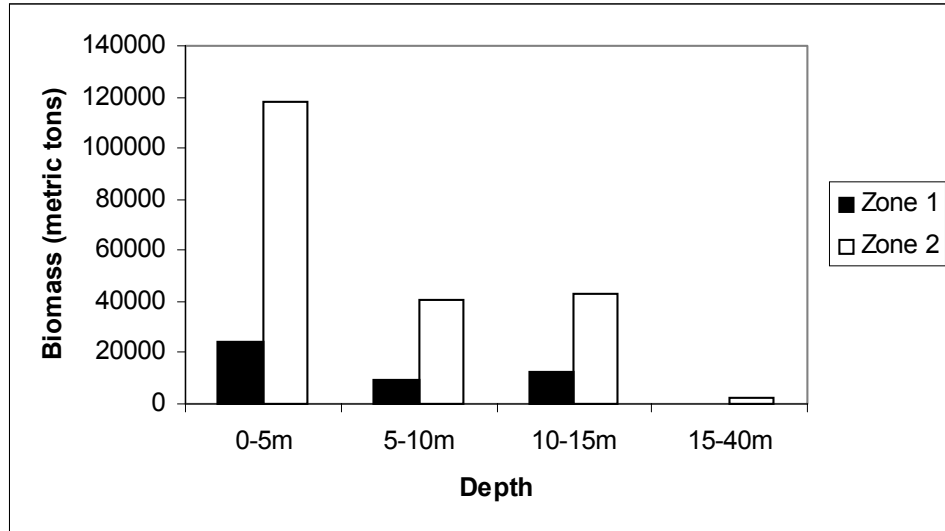


Figure 10. Total biomass estimates by depth zone according to management zone.

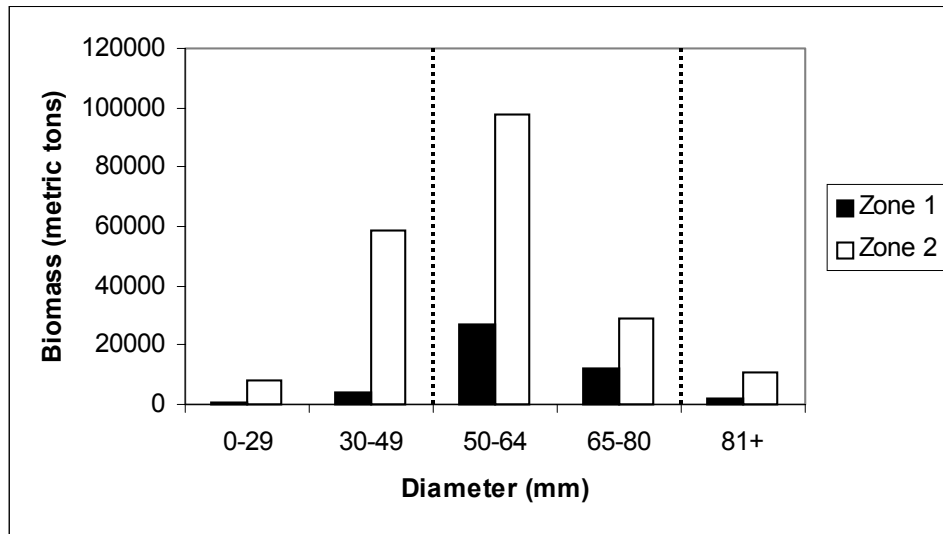


Figure 11. Total biomass estimates by sea urchin test diameter according to management zone. Urchins between 50 and 80 mm are legal sized urchins and constitute the fishable biomass.

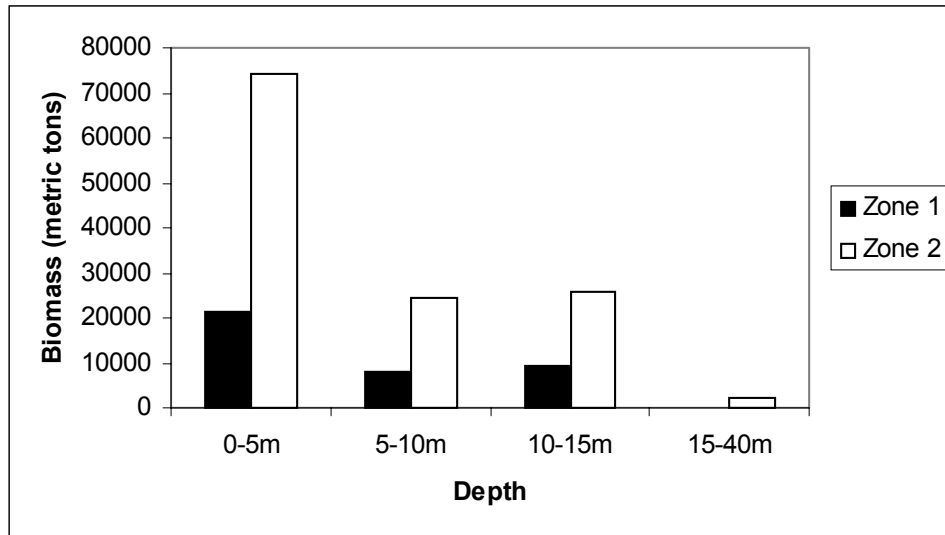


Figure 12. Fishable biomass estimates by depth zone according to management zone.

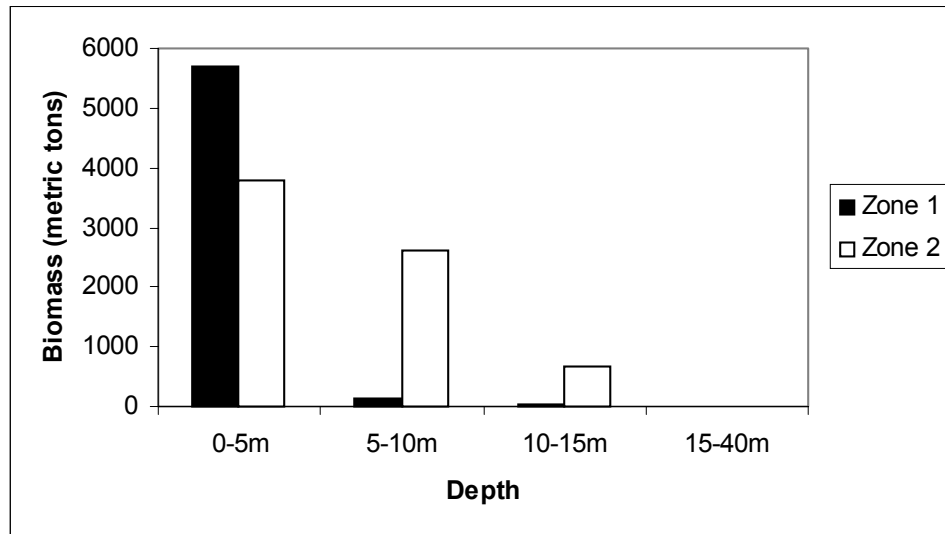


Figure 13. Exploitable biomass estimates (densities >10 urchins m^{-2}) by depth zone for the entire Maine coast.

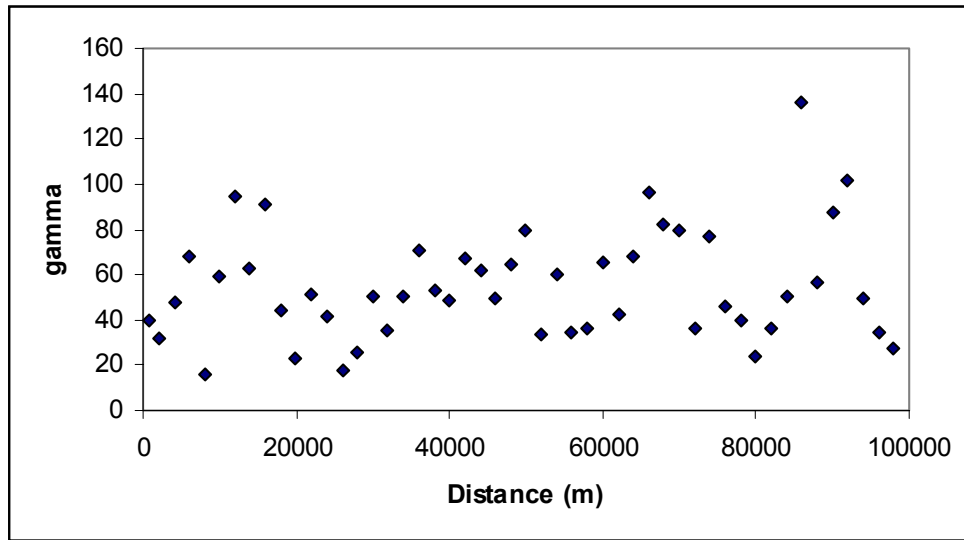


Figure 14. Sample empirical variogram representing the spatial covariance of average urchin density values per site, excluding one outlier with 174 urchins m^{-2} .

Appendix

Procedure for estimating exploitable biomass using TINs

1. Create size (length) categories for the fish species. If the fishery has size restrictions, they should be considered when creating the size categories.
2. Calculate mean size for each category based on the size frequency information. Use a length-weight relationship to estimate the mean weight per urchin for each size category.
3. Using the size frequency information, calculate the proportion of fish at each site that belong to each size category.
4. Calculate mean densities by depth zone for each site
5. Scale each site's mean density value based on the size category proportions. So if you have 3 depth zones and 8 size categories, each site should have 24 different density values, which should sum to the total site average. Also, you will now have 24 different scenarios to run in order to estimate biomass.
6. Create text files with site locations and densities for each scenario.
7. Import each text file as a table into ArcView GIS 3.2a. ("Add table" command).
8. Add as an event theme to the view.
9. If the locations are not in the correct coordinate system, the data must be projected before you can continue. The following is one way to project data.
 - a. Convert the text file to a shapefile
 - b. Open the ArcToolbox Program in ArcINFO 7.1
 - c. Define the coordinate system used in the density information

- d. Project the data to the correct coordinate system
 - e. Add the projected shapefile back into ArcView GIS.
10. Choose the Extensions command under the File heading. Select 3D Analyst.
 11. Activate the themes and select “Create TIN from features” under the Surface heading.
Choose the following settings:
 - a. Class=Point
 - b. Height Source=Density
 - c. Input as=Mass Points
 - d. Value Field=<none>
 12. Create Tins for all of the scenarios.
 13. Convert TINs to Grids (“Convert to Grid” command under Theme heading)
 14. Convert Grids to an ArcASCII format, using ArcToolbox
 15. Repeat steps 9-14 to create ArcASCIIs for bathymetry and habitat. I recommend converting all of the files to Grids (step 11) at the same time, to ensure they all have the same resolution and orientation.
 16. Once all ASCIIs are created, rename the urchin density ASCII to “gridA.asc,” the habitat ASCII to “gridB.asc,” and the bathymetry ASCII to “gridC.asc.” Place these files in the same folder as the C++ biomass estimation program.
 17. Run the C++ biomass estimation program. Follow the directions on the program.
Note: Threshold values are density values used for estimating exploitable biomass. To estimate total or fishable biomass, enter a threshold value of 0.
 18. The program will output the total number of urchins and the urchin biomass. An ASCII raster image will also be created for each scenario.

C++ Computer code for estimating biomass using ASCII files

biomass.cpp : calculates biomass of an arc ascii grid A based on constraints defined by arc ascii grids B and C.

```

#include "stdafx.h"
#include "biomass.h"
#include <fstream.h>
#include "math.h"
#include "Matrix.h"

#ifdef _DEBUG
#define new DEBUG_NEW
#undef THIS_FILE
static char THIS_FILE[] = __FILE__;
#endif

////////////////////////////////////
// The one and only application object

CWinApp theApp;

//using namespace std;

int _tmain(int argc, TCHAR* argv[], TCHAR* envp[])
{
    int nRetCode = 0;

    // initialize MFC and print and error on failure
    if (!AfxWinInit(::GetModuleHandle(NULL), NULL, ::GetCommandLine(), 0))
    {
        // TODO: change error code to suit your needs
        cerr << _T("Fatal Error: MFC initialization failed") << endl;
        return nRetCode = 1;
    }

    //////////////////////////////////////

    ifstream inFile; // Input data file.
    ofstream outFile; // Output data file.
    CMatrix gridA, gridB, gridC;
    char chardummy;

```

```

int gridAx, gridAy, gridBx, gridBy, gridCx, gridCy;
int intdummy = 0, i, j, nodata, zone;
double gridAres, gridBres, gridCres, doubledummy, biomass, count, weight, minx,
miny, coor, limit;

cout << "Enter 1 to load gridA, gridB, and gridC\n";
cin >> intdummy;

gridA.Empty(); // open and read grids
gridB.Empty();
gridC.Empty();

inFile.open("gridA.asc");
if(!inFile)
{
    cout << "Error opening file\n";
    return nRetCode;
}

// Prime gridA with data
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridAx;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridAy;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> minx;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> miny;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy;
inFile >> gridAres;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy >> chardummy >>
chardummy >> chardummy;
inFile >> nodata;

gridA.SetMatrixSize(CSize (gridAx, gridAy));

```

```

for (i=0;i<gridAy;i++)
    {
        for (j=0;j<gridAx;j++)
            {
                inFile >> doubledummy;
                gridA.SetAt(CPoint (j,i), doubledummy);
            }
    }

inFile.close();

inFile.open("gridB.asc");
if(!inFile)

{
    cout << "Error opening file\n";
    return nRetCode;
}

// Prime gridB with data
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridBx;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridBy;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> coor;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> coor;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy;
inFile >> gridBres;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy >> chardummy >>
chardummy >> chardummy;
inFile >> nodata;

gridB.SetMatrixSize(CSize (gridBx, gridBy));

for (i=0;i<gridBy;i++)
    {
        for (j=0;j<gridBx;j++)

```

```

        {
            inFile >> doubledummy;
            gridB.SetAt(CPoint (j,i), doubledummy);
        }
    }

inFile.close();

inFile.open("gridC.asc");
if(!inFile)

{
    cout << "Error opening file\n";
    return nRetCode;
}

// Prime gridC with data
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridCx;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> gridCy;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> minx;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy;
inFile >> miny;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy;
inFile >> gridCres;
inFile >> chardummy >> chardummy >> chardummy >> chardummy >> chardummy
>> chardummy >> chardummy >> chardummy >> chardummy >> chardummy >>
chardummy >> chardummy;
inFile >> nodata;

gridC.SetMatrixSize(CSize (gridCx, gridCy));

for (i=0;i<gridCy;i++)
    {
        for (j=0;j<gridCx;j++)
            {
                inFile >> doubledummy;
            }
    }

```

```

        gridC.SetAt(CPoint(j,i), doubledummy);
    }
}

inFile.close();

intdummy = 1;

if((gridAx != gridBx) || (gridAy != gridBy) || (gridAres != gridBres) || (gridAx !=
gridCx) || (gridAy != gridCy) || (gridAres != gridCres))
{
    cout << "\n" << "gridA, gridB, and gridC are not congruent!!!!\n" <<
"\n";
}

    cout << "gridAx: " << gridAx << "  gridBx: " << gridBx << "  gridCx: " << gridCx
<< "\n";
    cout << "gridAy: " << gridAy << "  gridBy: " << gridBy << "  gridCy: " << gridCy
<< "\n";
    cout << "gridAres: " << gridAres << "  gridBres: " << gridBres << "  gridCres: " <<
gridCres << "\n";
    cout << "\n";
    cout << "Enter 1 to continue\n";
    cout << "Enter 2 to abort\n";
    cout << "Your choice: ";
    cin >> intdummy;
    cout << "\n";

    biomass = 0;
    count = 0;

    cout << "Please enter a threshold density: ";
    cin >> limit;
    cout << "\n";

    outFile.open("output.asc");
    if(!outFile)
    {
        cout << "Error opening file\n";
    }
}

```



```

        return nRetCode;
    }

    outFile << "NCOLS " << gridAx << "\n";
    outFile << "NROWS " << gridAy << "\n";
    outFile << "XLLCORNER " << minx << "\n";
    outFile << "YLLCORNER " << miny << "\n";
    outFile << "CELLSIZE " << gridAres << "\n";
    outFile << "NODATA_VALUE " << nodata << "\n";

    if (intdummy == 1)
    {
        cout << "\n" << "Plese enter the weight of 1 urchin: ";
        cin >> weight;
        cout << "\n";
        cout << "Please make your depth choice:\n";
        zone = 0;
        cout << "1 ... 0 >= zone >= -5\n";
        cout << "2 ... -5 > zone >= -10\n";
        cout << "3 ... -10 > zone >= -15\n";
        cout << "4 ... -15 > zone >= -40\n";
        cin >> zone;
        cout << "\n";

        for (i=0;i<gridAy;i++)
        {
            for (j=0;j<gridAx;j++)
            {
                if ((gridB.GetAt(CPoint (j,i)) != nodata)
                {
                    if ((gridA.GetAt(CPoint (j,i)) != nodata)
                    {
                        switch(zone)
                        {
                            case 1: if ((gridC.GetAt(CPoint
(j,i)) <= 0) && (gridC.GetAt(CPoint (j,i)) >= -5))
                                {
                                    if
                                    {

```

```

count += gridA.GetAt(CPoint (j,i));
outFile << gridA.GetAt(CPoint (j,i));
}
else
{
outFile << nodata;
}
}
else outFile <<
break;
case 2: if ((gridC.GetAt(CPoint
(j,i)) < -5) && (gridC.GetAt(CPoint (j,i)) >= -10))
{
if
{
count += gridA.GetAt(CPoint (j,i));
outFile << gridA.GetAt(CPoint (j,i));
}
else
{
outFile << nodata;
}
}
else outFile <<
break;
case 3: if ((gridC.GetAt(CPoint
(j,i)) < -10) && (gridC.GetAt(CPoint (j,i)) >= -15))

```

```

(gridA.GetAt(CPoint (j,i)) >= limit)
    count += gridA.GetAt(CPoint (j,i));
    outFile << gridA.GetAt(CPoint (j,i));
}
else
{
    outFile << nodata;
}
}
else outFile <<
break;
case 4: if ((gridC.GetAt(CPoint
(j,i)) < -15) && (gridC.GetAt(CPoint (j,i)) >= -40))
{
    if
    {
        count += gridA.GetAt(CPoint (j,i));
        outFile << gridA.GetAt(CPoint (j,i));
    }
    else
    {
        outFile << nodata;
    }
}
else outFile <<
break;
nodata;

```

```

(j,i) <= 0) && (gridC.GetAt(CPoint (j,i)) >= -15))
(gridA.GetAt(CPoint (j,i)) >= limit)

count += gridA.GetAt(CPoint (j,i));
outFile << gridA.GetAt(CPoint (j,i));

outFile << nodata;

nodata;

select one of the zones 1 to 5, try again!!!!!!\n";

case 5: if ((gridC.GetAt(CPoint
{
    if
    {
        }
    else
    {
        }
    }
else outFile <<
break;

default: cout << "You can only
}
}
else outFile << nodata;
}
else
{
    outFile << nodata;
}
outFile << " ";
}
outFile << "\n";

```

```
    }  
  
    count = count * gridAres * gridAres;  
  
    biomass = count * weight;  
  
}  
  
cout << "biomass: " << biomass << "\n";  
cout << "total # of urchins: " << count << "\n";  
cout << "resolution: " << gridAres << "\n";  
cout << "the raster overlay is stored in the file output.asc\n";  
cout << "enter 1 to finish\n";  
cin >> intdummy;  
  
return nRetCode;  
}
```