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Geospatial Analysis of Eastern Oyster Habitat and Disease in the Chesapeake Bay

An Honors College Project Presented to
the Faculty of the Undergraduate
College of Science and Math
James Madison University

by Hannah Louise Bradley

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Accepted by the faculty of the Department of Biology, James Madison University, in partial fulfillment of the requirements for the Honors College.

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Introduction

Ecosystem and Economic services of Oysters

Even though the eastern oyster, *Crassostrea virginica* is considered to be a resilient species, their population size in the Chesapeake Bay is currently at 1% of historic levels (Frankenberg, 1995; Rothschild, B.J.; Ault, J.S.; Gouletquer, P.; Heral, 1994). This major decline has changed the ecosystem of the bay because the eastern oyster is an “ecologically important ecosystem engineer” (Grabowski & Peterson, 2011).

Oysters provide numerous ecosystem services in the Bay. One of the most crucial services is filtration and removal of nutrients carbon, nitrogen, and phosphorus from the water column. Individual oysters are carbon sinks that ultimately lead to a decrease in atmospheric concentrations of this greenhouse gas via their calcium carbonate shells (Grabowski & Peterson, 2011; Peterson, , and Lipcius, 2003). Oysters also remove excess nutrients from the water column through feeding and depositing feces and pseudofeces on the Bay floor that become food for other organisms (Newell, 2004). From an economic perspective, nitrogen removal by oyster reefs had an estimated value average of $4050 per hectare per year in 2011 (Grabowski et al., 2012). Overall, this filtration of excess nutrients results in decreased turbidity of the water column and reduces the effects of eutrophication, such as hypoxia resulting from overgrowth of algal blooms, (Grabowski & Peterson, 2011), which enhances growth of submerged aquatic vegetation (SAV) such as seagrasses (Newell, 2004).
The creation of oyster reefs as individuals settle and secrete their shells on top of one another provides areas for larval recruitment, shelter, and protection for a variety of fish and crabs species (Coen, L. D., 1999). These reefs also stabilize shorelines by providing a solid structure in otherwise soft sediment, which leads to an increased growth of SAV (Barnes, T. K.; Volety, A. K.; Chartier, K.; Mazzotti, F. J.; Pearlstine, 2007). Overall, the presence of oyster reefs increases biodiversity of the ecosystem, and thus restoration of these reefs has become a major aquatic conservation focus.

Life History of Oysters

The two distinct stages of eastern oysters are the free-swimming larval stages and the sessile adult stages. Free-swimming larvae in the veliger stage live in the water column and feed on phytoplankton. Once they reach approximately 2 weeks of age, they descend to attach to a hard substrate on the bay floor (EOBRT, 2007). Once settled, they metamorphose into the first life stage of their adult forms, called spat. (EOBRT, 2007). Shell materials are filtered from the water column and calcium carbonate shells are secreted at a rate of approximately one inch per year (EOBRT, 2007). As oysters settle on top of one another, they accumulate and grow into reefs, and eventually into larger reefs called oyster bars.

Adult eastern oysters most commonly occur at depths between 0.6 meters and 8 meters in water bodies classified as bays, estuaries, and streams (EOBRT, 2007). They can tolerate extreme temperatures from -2°C to 36°C, with the optimal temperature range occurring between 20°C and 32.5°C for both larvae and adults; spawning
occurring at 20°C (EOBRT, 2007). Larvae have a salinity tolerance of 10 ppt to 27.5 ppt, while adults have broader salinity tolerance from 5 ppt to 40 ppt (EOBRT, 2007). Both larvae and adults can survive at a pH range between 6.75 and 8.75, and with dissolved oxygen levels above 1.51 mg/L (EOBRT, 2007).

Oyster decline in the Chesapeake Bay

One cause for the drastic decline in the Chesapeake Bay population of the eastern oyster is overharvesting. Aside from the obvious negative impact of removing oysters from reefs, overharvesting has an additional implication for the severity of the decline, changing the sex ratio. The eastern oyster exhibits low levels of protandric hermaphrodite tendencies (Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994) in which older male individuals in the population tend to transition into females. This phenomenon results in a higher production of eggs per adult biomass. Thus, overharvesting of large size classes by commercial fishermen leads to a decrease in the proportion of females disrupting the natural female to male ratio in the species (Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). This disruption accelerates the decrease in birth rate of the population more than in a non-hermaphroditic species.

A more recently discovered cause of the decline in the eastern oyster population in the Bay are the epizootics of *Haplosporidium nelsoni* (MSX) and *Perkinsus marinus* (*Dermo*). *H. nelsoni* is a plasmodium parasite originally discovered in the Chesapeake Bay populations of the eastern oyster in 1959 (Ewart & Ford, 1993). The intensity of *H. nelsoni* infections has been determined to be dependent on salinity, becoming most
intense at salinities above 15 ppt. *P. marinus* is a protozoan parasite identified in the Chesapeake Bay around the late 1950s. The presence of this parasite is correlated with temperatures above 25˚ C and above salinities of 12 ppt (Ewart & Ford, 1993). Both diseases have their greatest impact during the summer and fall.

The previously mentioned reasons for the decline in the oyster population in the Chesapeake Bay are important, but the most the most disruptive cause of the decline of the oyster population in the Bay is habitat loss from anthropogenic destruction of oyster reefs. A conservative estimate for loss of oyster bar acreage loss in Maryland between the years of 1907 and 1982 is 50% (Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). The destruction increased with the introduction of more efficient mechanical harvesting gear compared to than the original method of hand tongs. Prior to 1887, oyster landings in Maryland exhibited an almost exclusively exponential growth, until the production peaked in 1884 (Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). This peak followed the legalization of dredging in 1865, but a subsequent decline in landings began soon after because dredging resulted in substantive damage to the established oyster reefs that had been growing for centuries (Goulletquer, Héral, & Rothschild, 1994; Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). The steepest decline in oyster landings occurred in Maryland between 1887 and 1950 (Goulletquer et al., 1994; Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). Despite the knowledge that the oyster landings were decreasing, reflecting an overall decrease in the abundance of oysters, attempts at regulating harvesting were ineffective and harvesting companies instead responded by adding another harvesting mechanism to
their repertoire in 1950: hydraulic-powered patent tongs. These tongs efficiently break off large areas of oyster reefs repeatedly making tongs the most destructive technology to date, (Rothschild, B.J.; Ault, J.S.; Goulletquer, P.; Heral, 1994). This destruction of oyster reduces the oyster bar acreage suitable for the settling of new oyster recruits, slowing down the recovery of oyster populations in the Bay.

Figure 1. Timeseries of oysters landings and harvesting machinery/techniques in Maryland between the years of 1820 and 1995 (Rothschild, 1994).
Effect of temperature rise on oyster habitat

The prediction by the Intergovernmental Panel on Climate Change is a maximum of an average increase of 2°C by the end of the century (IPCC, 2013). A study of the Pacific oyster predicted that rising water temperatures will create more suitable habitat in the northern waters because areas with temperatures outside of the species range will warm into temperatures within the species range (Jones, Dye, Pinnegar, Warren, & Cheung, 2013). Another study with a climate science approach to eastern oysters in the Chesapeake Bay also predicts that there will be higher juvenile abundance in many areas (Kimmel, Tarnowski, & Newell, 2014). A third study, however, found that increasing temperatures correlated with increased infections of Dermo in oysters (Beseres Pollack, Cleveland, Palmer, Reisinger, & Montagna, 2012). Thus, it is difficult to make sweeping predictions on the effect of a 2 degree change in temperature for global oyster populations. Overall, this uncertainty is an important factor affecting sustainability of restoration efforts.

Current restoration efforts

There has not been substantial success in addressing all of the causes of the decline of the eastern oyster populations in the Bay. State organizations such as the Virginia Marine Resources Commission (VMRC) and the Maryland Department of Natural Resources (MDNR), have enacted limitations for commercial harvesting of oysters but limiting harvest is likely not sufficient to allow the population to become
reestablished (Rothschild et al., 1994). Efforts must also be made to restore and preserve quality habitat. A major obstacle to these efforts seems to be the difficulty coordinating efforts among the six states in the watershed of the Bay: Virginia, Maryland, West Virginia, Delaware, Pennsylvania, and New York, as well as Washington, D.C. Additional obstacles include a general lack of consideration of oyster population dynamics and ecology when analyzing potential solutions for the decline (Mann et al., 2007).

The first step for addressing these obstacles is identifying suitable habitat for oyster restoration. Areas of suitable habitat are often identified by spatial data analysis programs, such as ArcGIS, through creation of a habitat model (Pollack, 2012). One benefit of using ArcGIS for habitat modeling is the breadth of analyses possible with a large number of data layers. This breadth helps to identify the environmental parameters used to determine the physical location of the most suitable habitat. Another benefit is the ability to weight environmental parameters by their impact on species survivorship, since some parameters may be more influential than others. Once environmental parameters are weighted, ArcGIS can be used to identify the physical areas that would be most the suitable habitat for that species. Identification of these areas provides target locations that consider the focal species population dynamics and ecology.

In an effort to contribute to the conservation and restoration efforts of the eastern oyster in the Chesapeake Bay, I performed GIS analysis of five water quality parameters. The water quality parameters consisted of: temperature in degrees Celsius,
salinity in parts per thousand, pH, dissolved oxygen in milligrams per liters, and bathymetry in meters. These parameters were chosen because they have been determined to be influential in determining the spatial distribution of eastern oysters (EOBRT, 2007). This analysis aims to identify areas of suitable habitat recommended to be targeted for restoration for both larval and adult oysters. I also investigated the potential effects of climate change on suitable habitat for the eastern oyster with simulations of increasing water temperature conditions modeled for an increase of 2°C. I hypothesized that areas best suited for larval and adult oyster survival will be different, but that some areas will exist that are suitable for both life stages, and those areas will be the best targets for restoration efforts. I also hypothesized that a 2°C water temperature increase, based on the IPCC projections, will reduce the amount of suitable habitat area.

**Methods**

The purpose of this project is to develop evidence-based restoration methods using geospatial information system (GIS) mapping of eastern oyster habitat in current and future temperature conditions. GIS mapping involves data that is associated with geospatial location. GIS data can be collected and subsequently displayed in a variety of forms, including points, polygons, and rasters. Points and polygons are classified as vector data, which consists of information associated with specific spatial locations, generally defined by X and Y coordinates. Points are spatially dimensionless while polygons are larger, defined areas of data. Vector data contain an attribute table where
all of the data are displayed in a tabulated format. Fields within the table are the columns that separate and contain different types of data organizationally. For example, a polygon of Virginia would be visually the shape of the state of Virginia and the information associated with this polygon in the attribute table could have fields of state name, state population, and state area in meters squared.

Data layers

The following data layers came from the Chesapeake Bay program (Chesapeake Bay Program, 2006):

1. The polygons for the six states in the Chesapeake Bay watershed combined into "watershed" layer (Figure 2) that were restricted to the appropriate water bodies and created the “watershed_selected” layer (Figure 3) (Appendix I, II).

2. Monthly measurements of temperature, salinity, pH, and dissolved oxygen for from every monitoring station from 2013-2017 (Figure 4, Figure 5). Data points outside of the polygon layer for the selected bay area were removed (Figure 6) and the layers consisting of the seasonal average for each parameter were created (Appendix III, IV).

The Bathymetry as a Digital elevation model raster was obtained from the Special Projects Office within NOAA. The polygons, environmental seasonal average layers of each parameter (Figure 7), and the bathymetry layer were projected to the Universal Transverse Mercator zone 18N to avoid distorting calculations involving area.
Figure 2. The six states and Washington, D.C. polygons were drawn in ArcMap using the geographic coordinate system of NAD83. Using the “project” tool these polygons were projected into the projected coordinate system of UTM zone 18N. This projected coordinate system conserves area in the time zone of this study so that calculations of area would not be distorted. Once these polygons were projected, the “merge” tool was used to combine them into a single polygon layer containing the entire watershed of the Chesapeake Bay.

Figure 3. The polygon for the Bay contained areas within the watershed classified as bays, estuaries, streams, marshes, lakes/ponds, submerged streams, and channels. The “select by attributes” tool was used to select for only the areas classified as “bay/estuaries” and “stream”. The “create layer from selection” tool was then used to create a permanent polygon layer only containing the bay, estuaries, and streams.
Figure 4. Locations of the water quality monitoring stations within the Chesapeake Bay and its estuaries and streams following projection (Chesapeake Bay Program, 2006).
Figure 5. Creation of water quality layers. Water quality parameter data were all obtained from the Chesapeake Bay program data hub. These files consisted of all sampling data from water quality monitoring stations throughout the Bay from the years of 2013 through 2017. These files were input into ArcMap in csv format containing longitude and latitudinal coordinate attributes with the geographic coordinate system of NAD83. The “display XY data in ArcMap” tool was used to assign the geographic coordinate system of NAD83 to the values and draw them as points. Once drawn in ArcMap, the “export as data layer” tool was used to create a permanent points layer of the water quality parameters.
Figure 6. To isolate the analysis area to only the selected watershed areas the “clip” tool was used to remove points in the water quality parameter layers that lie outside of the desired area of study. Once clipped, the “select by attributes” tool was then used to select for water quality measurements that were taken at a depth of 1 meter in order to condense the quantity of the data being analyzed and standardize the measurements used for the analysis.
Figure 7. The four water quality parameter points layer and the and the bathymetry raster were all projected into the UTM zone 18N projected coordinate system using the “project” tool and “project raster” tool, respectively. Within the “project raster” tool the original geographic coordinate system of the bathymetry layer of NAD1927 was transformed into NAD83 in addition to the projection that occurred.
Habitat Models

For the purpose of analyzing the entire Bay for the most suitable areas for eastern oyster habitat, continuous rasters were created by interpolating the water quality parameter point data across the area contained within the bay polygon. The interpolation technique used was inverse distance weighting and output rasters contained cells sized 600 meters by 600 meters (Figure 8a-8d). The interpolation occurred only within the specified barrier of the bay polygon so that the calculations would not use points that were separated by land masses, avoiding inaccurate interpolations.
(c)

**Diagrams showing spatial interpolation processes**

1. **pH_win_avg** → **IDW** → **pH_win**
   - Extent, snap, mask, barrier: watershed_30
   - Cell size: 600m
   - Power: 2
   - Search radius: variable, 12 points minimum

2. **pH_sp_avg** → **IDW** → **pH_sp**
   - Extent, snap, mask, barrier: watershed_30
   - Cell size: 600m
   - Power: 2
   - Search radius: variable, 12 points minimum

3. **pH_sum_avg** → **IDW** → **pH_sum**
   - Extent, snap, mask, barrier: watershed_30
   - Cell size: 600m
   - Power: 2
   - Search radius: variable, 12 points minimum

4. **pH_fal_avg** → **IDW** → **pH_fal**
   - Extent, snap, mask, barrier: watershed_30
   - Cell size: 600m
   - Power: 2
   - Search radius: variable, 12 points minimum
Figures 8a-8d. The averaged seasonal water quality parameter layers of (a) temperature, (b) salinity, (c) pH, and (d) dissolved oxygen, were converted into continuous rasters using the “IDW” tool. The “IDW” tool uses inverse weighted distances to calculate all of the cells within a specified area to create a raster layer from the interpolation. The processing extent, snap raster, mask, and barrier feature for the interpolation was limited to the extent of the watershed_30 raster that was created using the tool “polygon to raster”. The snap raster setting ensure that the input and output rasters are aligned, while the mask setting ensures that cells containing no data in the input raster also are classified as “no data” in the output raster. The barrier setting limits the location of the points used to create the interpolated cells with the purpose of not allowing interpolation to occur using points physically separated by terrestrial peninsulas jutting into the bay area. This barrier setting allows for a more realistic interpolation output.
**Boolean Raster Creation**

Rasters are different from vector data and consist of a continuous surface of pixels, also called cells, with each cell corresponding to a specific associated value. Boolean rasters assign 1’s to cells in which the conditions of the optimal range of the parameter are met and 0’s to cells in which they are not. Boolean rasters were created for:

1. The optimum range for all the water quality parameters based on the interpolation of their seasonal averages (Figure 10a-10e) (Table 1). Separate seasonal average salinity rasters were created for larval and adult oyster environmental conditions since the physiological tolerance for salinity for the two life stages are different (Figure 10b, 10c).

2. The Bathymetry based on depth tolerance (Figure 9) (Table 1)

Following the creation of the boolean rasters of the environmental conditions, the layers were combined to identify the areas where the majority of the conditions were met. To identify the larval oyster habitat the boolean rasters for larval conditions of each season for temperature, salinity, dissolved oxygen, pH boolean rasters, and the bathymetry boolean raster were added together (Figure 11a) (Appendix V). This process was repeated to identify the adult oyster habitat, using the boolean rasters for adult conditions (Figure 11b).
Table 1. Environmental tolerances of habitat parameters for the Eastern Oyster (EOBRT, 2007).

<table>
<thead>
<tr>
<th>Life stage</th>
<th>Parameter</th>
<th>Tolerance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Both</td>
<td>Temperature</td>
<td>20-32.5°C</td>
</tr>
<tr>
<td>Larvae</td>
<td>Salinity</td>
<td>10-27.5 ppt</td>
</tr>
<tr>
<td>Adults</td>
<td>Salinity</td>
<td>5-40 ppt</td>
</tr>
<tr>
<td>Both</td>
<td>Bathymetry</td>
<td>0.6-8 m</td>
</tr>
<tr>
<td>Both</td>
<td>Dissolved Oxygen</td>
<td>≥ 1.51 mg/L</td>
</tr>
<tr>
<td>Both</td>
<td>pH</td>
<td>6.75-8.75</td>
</tr>
</tbody>
</table>

Figure 9. The “raster calculator” tool was used to create the boolean raster for the bathymetry raster with the required conditions being from - 8 meters to - 0.6 meters for suitable eastern oyster habitat.
(a)

Temp_win — Raster calculator — Temp_winter_b

("temp_win" >= 20.0) &
("temp_win" <= 32.5)

Temp_sp — Raster calculator — Temp_spring_b

("temp_sp" >= 20.0) &
("temp_sp" <= 32.5)

Temp_sum — Raster calculator — Temp_summer_b

("temp_sum" >= 20.0) &
("temp_sum" <= 32.5)

Temp_fal — Raster calculator — Temp_fall_b

("temp_fal" >= 20.0) &
("temp_fal" <= 32.5)
(b)

```
sal_win -> Raster calculator -> sal_winter_b
("sal_win" >= 10.0) &
("sal_win" <= 27.5)

sal_sp -> Raster calculator -> sal_spring_b
("sal_sp" >= 10.0) &
("sal_sp" <= 27.5)

sal_sum -> Raster calculator -> sal_summer_b
("sal_sum" >= 10.0) &
("sal_sum" <= 27.5)

sal_fal -> Raster calculator -> sal_fall_b
("sal_fal" >= 10.0) &
("sal_fal" <= 27.5)
```
(c)

- **sal_win**
  - **Raster calculator**
  - **sal_winter_a**
  - Condition: "sal_win" >= 5.0) & ("sal_win" <= 40.0)

- **sal_sp**
  - **Raster calculator**
  - **sal_spring_a**
  - Condition: "sal_sp" >= 5.0) & ("sal_sp" <= 40.0)

- **sal_sum**
  - **Raster calculator**
  - **sal_summer_a**
  - Condition: "sal_sum" >= 5.0) & ("sal_sum" <= 40.0)

- **sal_fal**
  - **Raster calculator**
  - **sal_fall_a**
  - Condition: "sal_fal" >= 5.0) & ("sal_fal" <= 40.0)
Environmental tolerances of eastern oysters were used in the queries of the “raster calculator” tool to create boolean rasters for each of the seasonal averages for each water quality parameter. The boolean raster for all seasonal temperature rasters (a) used values from 20.0°C to 32.5°C. The boolean raster for all seasonal salinity rasters used values from 10 ppt to 27.5 ppt for the larval tolerances (b) and from 5 ppt to 40 ppt for the adult tolerances (c). The boolean raster for all seasonal dissolved oxygen rasters (d) used values greater than or equal to 1.51 mg/L. The boolean raster for all seasonal pH rasters (e) used values from 6.75 to 8.75 units.
Figures 11a-11b. All appropriate boolean raster parameters were added together using the “raster calculator” tool for both the (a) larval habitat and (b) adult habitat conditions. For each model the bathymetry layer was weighted by multiplying the raster by 100.

Climate Change Model Conditions

Models of a 2°C average increase of water temperature were created the using the same methods as the habitat model, however all the temperature rasters were increased by 2°C (Figure 12a, 12b, Appendix VI).
All appropriate environmental parameters were added together using the “raster calculator” tool to create the models for both the (a) larval habitat and (b) adult habitat with the temperature rasters with a 2°C increase.

**MSX and Dermo Conditions**

The epizootic diseases, Dermo and MSX, have decimated oyster populations in the Bay. I aimed to determine the effect of temperature changes on the potential distribution of the disease Dermo during the summer and fall. Similar to the creation of the habitat models, the seasonal average temperature and salinity rasters and the environmental tolerances for each disease were used to create Boolean rasters, but only for the summer and fall seasons (Table 2) (Figure 13a-13b) (Appendix VII, VIII). This process was also repeated using the salinity rasters and MSX salinity tolerance for the summer and fall (Table 2) (Figure 14) (Appendix IX).
Table 2. Environmental conditions necessary for the proliferation of oyster diseases MSX and Dermo.

<table>
<thead>
<tr>
<th>Disease</th>
<th>Parameter</th>
<th>Tolerance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dermo</td>
<td>Temperature</td>
<td>$\geq 25^\circ$C</td>
</tr>
<tr>
<td>Dermo</td>
<td>Salinity</td>
<td>$\geq 12$ ppt</td>
</tr>
<tr>
<td>MSX</td>
<td>Salinity</td>
<td>$\geq 15$ ppt</td>
</tr>
</tbody>
</table>

(a)
Figure 13a-13b. Rasters consisting of (a) summer and fall average temperatures as well as (a & b) summer and fall average salinity were converted into boolean rasters for the conditions for proliferation of Dermo using the “raster calculator” tool. Conditions used in the query were (a) temperatures greater than or equal to 25°C and salinities greater than or equal to 12 ppt. These conditions were also used to create boolean rasters using the (b) temperature rasters with a 2°C increase. (a) The summer boolean temperature raster and the summer salinity boolean raster were then added together to create the model for the summer Dermo proliferation conditions. (a) The fall temperature boolean raster was added to the fall salinity boolean raster to create the model for the fall Dermo proliferation conditions. (b) The same additions were executed for the boolean temperature rasters of a 2°C increase.
Figure 14. Summer and fall average salinity rasters were converted into boolean rasters for salinities greater than or equal to 15 ppt, the condition at which MSX proliferates. These boolean rasters were then added together in the “raster calculator” tool to obtain the model for the MSX proliferation in the Bay.

For the purpose of this study, the resulting habitat models were classified using a relative ranking system from “optimal” to “poor” areas of habitat (Table 3). Areas where the most limiting condition, bathymetry, were not met were identified and assigned the classification of “Depth condition not met”. This ranking system was based on the number of the seasonal environmental conditions of bathymetry, water temperature, salinity, pH, and dissolved oxygen that were met, with a maximum of 17 conditions (Table 3). This ranking system is comparable across the different habitat models resulting from this study by using the classification terms, although the total number of environmental conditions met may vary. This variation in the number of environmental
conditions met at a specific classification is distinctly related to the extreme fluctuation in water temperatures between seasons. When water temperature reaches its lower ranges, such as in the spring and winter, eastern oysters hibernate. Because of this hibernation, all classified habitat areas did not meet temperature conditions in the winter season, and only some habitat areas met temperature conditions in the spring season. These models did not account for hibernation and for this reason, no habitat models had areas that met all 17 conditions.

Table 3. Definition of habitat quality classifications.

<table>
<thead>
<tr>
<th>Classification</th>
<th># of Environmental Conditions Met</th>
</tr>
</thead>
<tbody>
<tr>
<td>Optimal</td>
<td>16-15</td>
</tr>
<tr>
<td>Very Good</td>
<td>15-14</td>
</tr>
<tr>
<td>Good</td>
<td>14-13</td>
</tr>
<tr>
<td>Fair</td>
<td>13-12</td>
</tr>
<tr>
<td>Poor</td>
<td>12-11</td>
</tr>
<tr>
<td>Depth condition not met</td>
<td>N/A, limiting factor of depth not met</td>
</tr>
</tbody>
</table>

The resulting disease models were also classified using a relative ranking system from “minimal” to “high” risk of infection (Table 4). This ranking system was based on the number of the seasonal environmental conditions of water temperature and salinity that were met, with a maximum of 2 conditions for the Dermo fall and summer models (Table 4). This ranking system is comparable across the different Dermo models resulting from this study by using the classification terms. The MSX model uses a similar ranking system (Table 5).
Table 4. Definition of Dermo risk of infection classifications.

<table>
<thead>
<tr>
<th>Classification</th>
<th># of Environmental Conditions Met</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td>2</td>
</tr>
<tr>
<td>Moderate</td>
<td>1, temperature condition</td>
</tr>
<tr>
<td>Low</td>
<td>1, salinity condition</td>
</tr>
<tr>
<td>Minimal</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 5. Definition of MSX risk of infection classifications.

<table>
<thead>
<tr>
<th>Classification</th>
<th># of Environmental Conditions Met</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td>2</td>
</tr>
<tr>
<td>Moderate</td>
<td>1</td>
</tr>
<tr>
<td>Low</td>
<td>0</td>
</tr>
</tbody>
</table>

Results

The larval and adult oyster habitat models had a similar spatial distribution of high-ranking habitat classifications, with a few differences in the total area of each classification (Figure 15a, 15b). Specifically, the larval habitat classified as “optimal” covered 7.47% more area than the adult habitat with the same classification (Table 6). Similarly, the habitat classified as “poor” increased by 6.89% in the adult habitat model when compared to the larval habitat model (Table 6).
Figure 15a-15b. (a) Habitat model using current water quality conditions of larval eastern oysters and (b) habitat model of adult easter oysters with habitat quality classifications.
Table 6. Calculated area for both larval and adult oyster habitat for each level of habitat classification for the current seasonal water temperature conditions. “Cell count” pertains to the number of 600 meter by 600 meter pixels in the raster that were classified for each rank.

<table>
<thead>
<tr>
<th>Current Conditions</th>
<th>Larval</th>
<th></th>
<th>Adult</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cell count</td>
<td>Area km²</td>
<td>% of Total Bay area</td>
<td>Cell count</td>
</tr>
<tr>
<td>Optimal, summer and fall spawning</td>
<td>1741</td>
<td>626.76</td>
<td>6.73</td>
<td>1327</td>
</tr>
<tr>
<td>Optimal, summer spawning</td>
<td>10270</td>
<td>3697.2</td>
<td>39.69</td>
<td>8749</td>
</tr>
<tr>
<td>Very Good</td>
<td>819</td>
<td>294.84</td>
<td>3.17</td>
<td>858</td>
</tr>
<tr>
<td>Good</td>
<td>479</td>
<td>172.44</td>
<td>1.85</td>
<td>547</td>
</tr>
<tr>
<td>Fair</td>
<td>499</td>
<td>179.64</td>
<td>1.93</td>
<td>1313</td>
</tr>
<tr>
<td>Poor</td>
<td>863</td>
<td>310.68</td>
<td>3.34</td>
<td>1877</td>
</tr>
<tr>
<td>Depth condition not met</td>
<td>11202</td>
<td>4032.72</td>
<td>43.30</td>
<td>11202</td>
</tr>
</tbody>
</table>

The larval and adult habitat models for the simulated 2°C increase in water temperature also had similar spatial distributions of high-ranking habitats (Figure 16a, 16b). The habitat area classified as “optimal” for adults was 6.47% greater relative to the area designated as “optimal” for larvae (Table 7). Similarly, the quantity of the habitat area classified as “poor” was 6.0% lower for adults than for larvae (Table 7). Overall, the habitat models for larvae had relatively higher proportions of “fair” or “poor” quality relative to the habitat models for the adults (Table 6, Table 7).
Figure 16a-16b. (a) Habitat model using water quality conditions with temperature conditions increased by 2°C of larval eastern oysters and (b) habitat model of adult eastern oysters with habitat quality classifications. Inset maps are displaying the area where cells classified as “optimal, summer, fall, and spring spawning” occur.
Table 7. Calculated area for both larval and adult oyster habitat for each level of habitat classification for the projected average of 2°C increase in water temperature.

<table>
<thead>
<tr>
<th>Classifications</th>
<th>Larval</th>
<th></th>
<th>Adult</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell count</td>
<td>Area km²</td>
<td>% of Total Bay area</td>
<td>Cell count</td>
<td>Area km²</td>
</tr>
<tr>
<td>Optimal, summer, fall, and spring spawning</td>
<td>2</td>
<td>0.72</td>
<td>0.01</td>
<td>2</td>
</tr>
<tr>
<td>Optimal, summer and fall spawning</td>
<td>8610</td>
<td>3099.6</td>
<td>33.36</td>
<td>10280</td>
</tr>
<tr>
<td>Very Good</td>
<td>2129</td>
<td>766.44</td>
<td>8.25</td>
<td>2315</td>
</tr>
<tr>
<td>Good</td>
<td>499</td>
<td>179.64</td>
<td>1.93</td>
<td>530</td>
</tr>
<tr>
<td>Fair</td>
<td>717</td>
<td>258.12</td>
<td>2.78</td>
<td>442</td>
</tr>
<tr>
<td>Poor</td>
<td>2153</td>
<td>775.08</td>
<td>8.34</td>
<td>603</td>
</tr>
<tr>
<td>Depth condition not met</td>
<td>11701</td>
<td>4212.36</td>
<td>45.33</td>
<td>11701</td>
</tr>
</tbody>
</table>

In the MSX infection conditions model the highest risk areas were located closer to the mouth of the Bay, closest to the Atlantic Ocean, while the level of infection risk decreased moving north and out of the main stem (Figure 17). The largest area is classified as “high” risk of infection, at 4003.92 km² (Table 8). The area classified as “moderate” risk had the next highest area at 3164.04 km², and the area classified as “low” risk had the smallest area at 2435.04 km² (Table 8).
Suitable conditions for *Haplosprodidium nelsoni* proliferation within the Chesapeake Bay

**Figure 17.** Geospatial distribution of MSX conditions throughout the Bay from “high” levels of risk for infection to “low” levels of risk of infection.
Table 8. Calculated area for each level of risk of MSX infection in oysters for the current summer and fall conditions combined.

<table>
<thead>
<tr>
<th>MSX conditions</th>
<th>Risk of Infection</th>
<th>Cell count</th>
<th>Area km²</th>
<th>% of Total Bay area</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>High</td>
<td>11122</td>
<td>4003.92</td>
<td>41.69</td>
</tr>
<tr>
<td></td>
<td>Moderate</td>
<td>8789</td>
<td>3164.04</td>
<td>32.95</td>
</tr>
<tr>
<td></td>
<td>Low</td>
<td>6764</td>
<td>2435.04</td>
<td>25.36</td>
</tr>
</tbody>
</table>

The Dermo infection model for fall and the fall climate change temperatures resulted in similar distributions of the areas classified as "low" and "minimal" risk of infection (Figure 18a, 18b). The major difference between these two models is the appearance of areas of "moderate" and "high" risk of Dermo infection in the fall climate change model, although in only small percentages of the total area of the Bay (Table 9). The Dermo infection models for the summer and summer climate change temperatures also resulted in a similarity of spatial distribution of certain level risk areas, specifically those classified as "high" and "moderate" risk (Figure 19a, 19b). The major difference in these summer and summer climate change models is the disappearance of the area classified as "low" risk with the temperature increase, subtly increasing the percentage of "high" risk areas from 62.49% to 65.19% (Table 10).
Suitable conditions for *Perkinsus marinus* proliferation within the Chesapeake Bay during the fall

The map illustrates the risk of infection with *Perkinsus marinus* within the Chesapeake Bay. The risk is categorized into three levels:

- **Minimal**
- **Low**
- **Insufficient Data**

The coastline and the Atlantic Ocean are clearly marked, indicating the area affected by these conditions.
Suitable conditions for *Perkinsus marinus* proliferation within the Chesapeake Bay in the fall with climate change conditions

(b) **Figure 18a-18b.** Geospatial analysis model of the level of risk of infection of Dermo in the Chesapeake Bay in the (a) fall current temperature conditions and (b) fall temperature after a 2°C increase. Inset map for the fall map with a 2°C increase (b) displays area where areas of “high” risk are occurring.
Table 9. Calculated area for each level of risk of Dermo infection in oysters for the current fall conditions and the projected fall conditions after a 2°C increase in water temperature.

<table>
<thead>
<tr>
<th>Risk of Infection</th>
<th>Cell count</th>
<th>Area km²</th>
<th>% of Total Bay area</th>
<th>Cell count</th>
<th>Area km²</th>
<th>% of Total Bay area</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
<td>9</td>
<td>3.24</td>
<td>0.03</td>
</tr>
<tr>
<td>Moderate</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
<td>114</td>
<td>41.04</td>
<td>0.43</td>
</tr>
<tr>
<td>Low</td>
<td>22571</td>
<td>8161.56</td>
<td>84.95</td>
<td>22662</td>
<td>8158.32</td>
<td>84.91</td>
</tr>
<tr>
<td>Minimal</td>
<td>4017</td>
<td>1446.12</td>
<td>15.05</td>
<td>3903</td>
<td>1405.08</td>
<td>14.62</td>
</tr>
</tbody>
</table>
Suitable conditions for *Perkinsus marinus* proliferation within the Chesapeake Bay during the summer.
Figure 19a-19b. Geospatial analysis model of the level of risk of infection of Dermo in the Chesapeake Bay in the (a) summer current temperature conditions and (a) summer temperature after a 2°C increase.
Table 10. Calculated area for each level of risk of oyster Dermo infection for the current summer conditions and the projected summer conditions after a 2°C increase in water temperature.

<table>
<thead>
<tr>
<th>Risk of Infection</th>
<th>Cell count</th>
<th>Area km²</th>
<th>% of Total Bay area</th>
<th>Cell count</th>
<th>Area km²</th>
<th>% of Total Bay area</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td>16669</td>
<td>6000.84</td>
<td>62.49</td>
<td>17389</td>
<td>6260.04</td>
<td>65.19</td>
</tr>
<tr>
<td>Moderate</td>
<td>9287</td>
<td>3343.32</td>
<td>34.81</td>
<td>9287</td>
<td>3343.32</td>
<td>34.81</td>
</tr>
<tr>
<td>Low</td>
<td>720</td>
<td>259.2</td>
<td>2.70</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
</tr>
</tbody>
</table>

Discussion

Both the adult and larval habitat models for the 2°C water temperature increase exhibited an overall reduction in the quantity of habitat area classified as “optimal” when compared to the larval and adult models for current temperature conditions. This reduction demonstrates the trend that increasing water temperatures resulting from climate change may negatively impact aquatic populations. Other aquatic species, such as the microbenthic marine ciliate *Euplotes crassus* and the green alga *Dunaliella tertiolecta*, have shown a similar response to modelled climate change temperature conditions (Gomiero, Bellerby, Manca Zeichen, Babbini, & Viarengo, 2018).

Another phenomena that appears in the climate change habitat models is the occurrence of suitable habitat where the minimum temperature of 20°C, which cues spawning in the eastern oyster populations of the Bay, is present in the spring season. This occurrence is alarming because it alludes to a future trend of potential premature spawning of oyster populations. This early spawning could ultimately result in large portions of larvae die-off because of other water quality conditions (such as salinity) not
being suitable for survival. This die-off would reduce the overall survivorship of the eastern oyster population, exacerbating the already low population numbers. An alternative result, however, could be increased population growth. Some studies have shown that survivability of oyster larvae are dependent on the salinity that the source population was acclimated to during growth (Eierman & Hare, 2013). This means that larvae may survive following premature spawning in the spring and result in population regeneration.

Another consequence of the projected 2°C increase that emerges from these geospatial models is the increased proliferation of Dermo. High levels of Dermo infection in oysters are correlated with higher water temperatures, specifically above 25°C. The models of the risk of Dermo infection exhibit the overall trend of higher infection rates in current water quality conditions in the summer as compared to the fall. When modelled with a 2°C increase in water temperature, however, areas classified as high risk begin to appear in the fall in some areas and more areas in the summer are classified as high risk. This finding is supported by other oyster habitat models that have shown that Dermo infections will proliferate at increased temperatures (Beseres Pollack, Cleveland, Palmer, Reisinger, & Montagna, 2012). This occurrence again exhibits that increasing water temperature will have an overall negative impact on eastern oyster population survivability, due to increased Dermo infections.

When comparing the larval and adult eastern oyster habitat models based on current conditions, the main difference in the input water quality conditions was the salinity ranges, with larvae having a more limited range than the adults. Additionally, the
limiting factor in the habitat models was the bathymetry because the topography of the bay floor is the least variable parameter, only changing over a long geological timespan or with sudden, but rare, tectonic events. Noting these observations, the spatial distribution of the larval and adult habitat models exhibit differences in only the distribution of the quality of the habitat, and these differences can be attributed to variations in the seasonal salinity.

The largest variation in quality of the habitats is between the main stem and the streams of the Bay. The main stem and the portion of the streams closest to the stem contain more habitat classified as “optimal” and “very good” than the more inland streams. This distribution is supported by studies that have analyzed the dissolved oxygen to be lowest in the upstream areas due to lack of replenishment from gravitational circulation (Shen, Hong, & Kuo, 2013). Additionally, the greatest amount of overlap of similar habitat of larvae and adults overlap occurs in the areas classified as “optimal”; on the edges of the main stem. These results indicate that restoration efforts involving implantation of adult reef structures in these areas would be sustainable and suitable for reproduction and future generations.

One of the major obstacles for assessing the accuracy of these models in this study was the lack of accessibility to eastern oyster GIS survey data. Upon contacting a habitat ecologist and GIS analyst at NOAA, he disclosed that there is no central repository for oyster survey data because it is largely collected by state governmental agencies that neglect to make this information easily accessible to others. This lack of accessibility follows a similar trend of coordination issues among the states of the
Chesapeake Bay watershed. Restoration efforts in the Bay for the eastern oyster population, including precautionary measures necessary to tackling the imminent issue of climate change, must include cooperation and coordination of all states in the watershed in order to be successful. Of equal importance is the need to implement geospatial information system habitat modelling into common practice when locations are being chosen for targeting restoration efforts to ensure that the locations chosen will be sustainable in the long-term in a changing climate.

Based on these findings, more studies on the issue of climate change impacts on the eastern oyster population in the Chesapeake Bay are a necessity. An interstate database for uploading and consolidating oyster survey data must be created to allow researchers to analyze current locations of oyster reefs in the Bay. In addition to locating these reefs, assessments should be made to determine the health of these subpopulations and their reproductive status. Furthermore, oyster survey data for the entire Bay should be compared to the findings of these models to determine the validity of these models and adjustments should be made where applicable.

Other additional GIS studies would be beneficial to assessing the true distribution of suitable and sustainable eastern oyster habitat in the Chesapeake Bay. This study did not include the analysis of the overlap of the habitat models with information about water use in the Bay. There is potential that many of the “optimal” habitat areas coincide with areas that are leased to private owners for aquaculture, harvesting, or public recreational sites, making them unsuitable for oyster reef restoration. These areas need to be excluded when choosing areas to target for restoration efforts.
Another additional study should be the comparison of the interaction between the habitat models and the disease proliferation models. Areas where the disease conditions are most likely to be prevalent should be crossanalyzed with the modelled habitat areas to assess the sustainability of these areas further. Finally, other projected changes to water quality parameters should be analyzed in addition to temperature. Interactive effects of all water quality parameters should be assessed for the purpose of creating the most accurate habitat models with climate change conditions. Overall, more factors, such as water flow, turbidity, and point and nonpoint source pollution, that impact eastern oyster survivability and population growth should be included and studied in both current and projected climate change conditions to increase the ability to make the best decisions concerning restoration efforts in the future.
Literature Cited


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Appendix

I. Creation of watershed polygon layer

This GIS analysis is intended to create a habitat model for the eastern oyster in the Chesapeake Bay watershed. In order to confine the area of analysis to the Bay and its estuaries, a polygon for each of the six states in the watershed and Washington, D.C. was obtained from the Chesapeake Bay Program data hub (Chesapeake Bay Program, 2006). Once these polygons were added to ArcMap they were projected using the “project” tool into the UTM zone 18N projection to conserve area in the specified time zone (18N) that the Chesapeake Bay exists in (Figure 2). Once projected, the polygons of each individual states and Washington, D.C. were combined into the “Watershed” layer together using the “merge” tool.

II. Projections of water quality and environmental parameter layers and data selection

The exported point layers were then re-added into ArcMap and projected into UTM zone 18N (Figure 7). A digital elevation model raster was obtained from the Special Projects Office within NOAA to analyze the bathymetry environmental parameter. This bathymetry layer was also projected into UTM zone 18N (Figure 7). Following the projection of the water quality and environmental parameter layers, excess data points outside of the polygon layer for the selected bay area were removed (Figure 6). The attribute tables created within ArcGIS from the CSV files for each layer
contained a field for the depth of the observation taken. Only measurements taken at a depth of 1 meter were used (Figure 6).

**III. Manipulation of water quality parameter layers to create seasonal averages**

Each attribute table contained a “sampledate” field where the month, day, and year of the sample was recorded in “dd/mm/yyyy” format. First, to reclassify each sampling by the number associated with the month (i.e. January = 1), the “convert time field” tool was used to create a new field with only the month number (Figure 20a-20d). The field was named “month” and set to contain short numeric entries. Second, the “Select by attributes” tool was used with the queries for the three numbers of the months for each season individually, followed by the “export selected features” tool to create new separate layers for each season (Figure 20a-20d).
(c)
Figures 20a-20d. Each attribute table of the water quality parameters contained a field called “SampleDate” that contained a time field with the numerical format of the date the parameter was sampled. In order to manipulate this information, the “convert time field” tool was used to create a new field called “month” containing the short integer value associated with the month the sample was taken. Next, the “select by attributes” tool was used to select for the months within each season. The winter months of December, January, and February were selected using the values of 12, 1, and 2. The spring months of March, April, and May were selected using the values of 3, 4, and 5. The summer months of June, July, and August were selected using the values of 6, 7, and 8. The fall months of September, October, and November were selected using the values of 9, 10, and 11. This entire process was repeated for each of the water quality parameters: (a) temperature, (b) salinity, (c) pH, and (d) dissolved oxygen.
IV. Calculation of average measurement fields in seasonal water quality parameter attribute tables

The “summarize” tool was then used to calculate the seasonal average of the “measured value” field, which was the field containing the measured parameter for that sampling, for each monitoring station. This “summarize” tool created a new table containing a field for the monitoring station identifier and a field for the calculated average measurement associated with that monitoring station identifier. Finally, the “table join” tool was used to connect the new average measurement field to the corresponding monitoring station using the latitude and longitude field. The “export data” tool was then used to permanently join the average measurement field to the original attribute table.

V. Creation of larval and adult habitat quality layers

A. Larval: The “raster calculator” tool was used to add appropriate boolean rasters together corresponding to larval oyster habitat using the query

\[ \text{('bathymetry1' * 100) + 'temp_winter_b' + 'temp_summer_b' + 'temp_spring_b' + 'temp_fall_b' + 'sal_winter_b' + 'sal_summer_b' + 'sal_spring_b' + 'sal_fall_b' + 'do_winter_all' + 'do_summer_all' + 'do_spring_all' + 'do_fall_all' + 'ph_winter_all' + 'ph_summer_all' + 'ph_spring_all')} \]

B. Adult: The “raster calculator” tool was used to add boolean rasters together corresponding to adult oyster habitat using the query
VI. Creation of larval and adult habitat quality layers in climate change conditions

A. Following the creation of the boolean rasters of the environmental conditions in the climate change model, the layers were combined to identify the areas where the conditions were met. To identify the larval oyster habitat in the climate change model, the boolean rasters for larval conditions of each seasonal temperature plus 2°C and salinity were added to the dissolved oxygen and pH boolean rasters, plus the bathymetry boolean raster (Figure 21). To identify the adult oyster habitat in the climate change model the boolean rasters for adult conditions of each seasonal temperature plus 2°C and salinity were added to the dissolved oxygen and pH boolean rasters for each season, plus the bathymetry boolean raster.
Figure 21. Values in each of the seasonal average temperature rasters were increased by 2°C by a query in the “raster calculator” tool. Boolean rasters were created using the same temperature range of 20°C to 32.5°C as were used for the current temperature rasters.

B. Larval: The “raster calculator” tool was used to add appropriate boolean rasters together corresponding to larval oyster habitat using the query

'("bathymetry1" * 100) +"t_winter_2" +"t_summer_2" +"t_spring_2" +
"t_fall_2" +"sal_winter_b" +"sal_summer_b" +"sal_spring_b" +
"sal_fall_b" +"do_winter_all" +"do_summer_all" +"do_spring_all" +
"do_fall_all" +"ph_winter_all" +"ph_summer_all" +"ph_fall_all" +
"ph_spring_all"'.

C. Adult The “raster calculator” tool was again used to add boolean rasters together corresponding to adult oyster habitat using the query
VII. Creation of Dermo risk of infection model for current water temperature conditions

To identify the areas where in the summer both the temperature and salinity conditions for Dermo proliferation occur simultaneously, the summer boolean rasters of temperature and salinity with the Dermo conditions were added together (Figure 13a). Similarly, to identify the areas where in the fall both the temperature and salinity conditions for Dermo proliferation occur simultaneously, the fall boolean rasters of temperature and salinity with the Dermo conditions were added together (Figure 13a). To analyze the changes to the distribution of the areas that have the conditions for the proliferation of Dermo with the modelled water temperature increase, this process was also repeated using the temperature rasters with 2°C increases (Figure 21).

VIII. Creation of Dermo risk of infection models for climate change conditions

The summer average temperature plus 2°C raster and the environmental tolerances (Table 2) were used to create the boolean raster of the summer average temperature plus 2°C conditions for Dermo, and this process was repeated for the fall
The average temperature plus 2°C raster. To identify the areas where in the summer both the temperature plus 2°C and salinity conditions for Dermo proliferation occur simultaneously, the summer boolean rasters of temperature 2°C and salinity with the Dermo conditions were added together (Figure 13b). Similarly, to identify the areas where in the fall both the temperature 2°C and salinity conditions for Dermo proliferation occur simultaneously, the fall boolean rasters of temperature 2°C and salinity with the Dermo conditions were added together (Figure 13b).

IX. Creation of MSX risk of infection model for current salinity conditions

The summer average salinity raster and the environmental condition for MSX (Table 2) were used to create the boolean raster of the summer average salinity conditions for MSX proliferation, and this process was repeated for the fall average salinity raster (Figure 14). To visualize the areas where both the fall and summer salinity conditions for the proliferation of MSX occur, the fall and the summer boolean salinity rasters with MSX conditions were added together (Figure 14).