A model for estimating the TMDL-related benefits of oyster reef restoration: Harris Creek, Maryland, USA

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A MODEL FOR ESTIMATING THE TMDL-RELATED BENEFITS OF OYSTER REEF RESTORATION

Harris Creek, Maryland, USA

A final report to:
Oyster Recovery Partnership
and
National Fish and Wildlife Foundation

Prepared by:
M. Lisa Kellogg, Mark J. Brush, Elizabeth W. North
and Younjoon Lee
A model for estimating the TMDL-related benefits of oyster reef restoration

HARRIS CREEK, MARYLAND, USA

Award Information

Project Title: A model for estimating the TMDL-related benefits of oyster reef restoration in Harris Creek, MD

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Abstract

A user-friendly, web-accessible model has been developed that allows restoration practitioners and resource managers to easily estimate the TMDL-related benefits of oyster reef restoration per unit area, run restoration scenarios in Harris Creek, MD to optimize restoration planning and implementation, and calculate the benefits of the chosen plan. The model is rooted in scientifically defensible data and is readily transferrable to systems throughout the Chesapeake Bay and Eastern Shore. The model operates in five vertically well-mixed boxes along the main axis of the creek. Exchanges among creeks are computed using a tidal prism approach and were compared to exchanges provided from a high resolution 3D hydrodynamic model. Watershed inputs for the model were obtained for the Harris Creek sub-watershed from the Phase V Chesapeake Bay Program Watershed Model. The base model simulates daily concentrations over an annual cycle of chlorophyll-a, dissolved inorganic nitrogen (N) and phosphorus (P), dissolved oxygen, total suspended solids, the biomass of benthic microalgae, and the water column and sediment pools of labile organic carbon (C) and associated N and P. Water quality data for model forcing and calibration were obtained from the Chesapeake Bay Program, the Choptank Riverkeeper, the University of Maryland Center for Environmental Science, and the Maryland Department of Natural Resources. An oyster sub-model has been coupled to this base model and computes the volume of water filtered, removal of phytoplankton, suspended solids, and associated nutrients via filtration, recycling of nutrients and consumption of oxygen by oyster respiration, production of feces, N and P accumulation in oyster tissues and shell, oyster-enhanced denitrification, and N and P burial associated with restored reefs. The completed model is served online and operates through a web browser, enabling users to conduct scenario analysis by entering box-specific values for acres restored, restored oyster density, and restored oyster size, as well as the economic value of associated N and P removal.

Rationale

Efforts to restore viable oyster reefs and expand oyster populations in Chesapeake Bay and elsewhere have been increasingly motivated by the desire to enhance ecological functions and attendant ecosystem services. Increasingly, interest has focused on the potential use of oyster reef restoration and oyster aquaculture as a means of mitigating the effects of eutrophication (Newell 1988, Newell 2004, Coen et al. 2007, Rose et al. 2014 and references therein). Most recently, the United States Environmental Protection Agency’s implementation of a nutrient reduction program for Chesapeake Bay (US EPA 2010) has further heightened interest in the potential water quality benefits of oyster reef restoration. US EPA is using a Total Maximum Daily Load (TMDL) approach toward setting nutrient reduction targets; however, relatively few quantitative tools exist to compute the TMDL- and ecosystem-level benefits of oyster restoration.
Focusing on the first of a planned series of tributary-scale oyster reef restoration efforts (US ACE 2012), our goal was to use scientifically defensible data to develop a user-friendly, web-accessible model that would allow restoration practitioners and resource managers to easily estimate the TMDL-related benefits of oyster reef restoration per unit area, run restoration scenarios to optimize restoration planning and implementation, and calculate the benefits of the chosen plan. Model outputs needed to include the: 1) amount of N removed via denitrification, 2) volume of water filtered, 3) amount of chlorophyll-a and suspended solids removed from the water column, 4) amounts of N and P buried in the sediments, and 5) amounts of N and P sequestered in animal tissue and shell. The model also needed to include an option for the user to input nutrient trading credits; if entered, the model would estimate the economic value of each restoration option. By implementing a reduced complexity, reduced spatial resolution model in Harris Creek, the model could readily incorporate new data collected as restoration proceeds. The reduced complexity approach also enables fast run times (seconds to minutes) on personal computers and enables the model to be served online for direct use by stakeholders through a web browser, eliminating the need for purchase and operation of modeling software or extensive modeling expertise.

**Model Approach**

**Spatial and Temporal Resolution:**

Given the desire to have a fast-running, online model that is easy to update with new data, Harris Creek was divided into five vertically well-mixed spatial elements or boxes (Fig. 1). The location of box boundaries were set according to key geomorphic constrictions within the estuary, to capture the main down-estuary gradients in salinity and water quality, and to contain a number of water monitoring stations.
quality monitoring stations within each box (as well as outside the system to set boundary conditions).

While a number of monitoring stations exist within Harris Creek (see Fig. 1 and discussion below), the data are somewhat limited in that different stations were sampled in different years (some only for 1-2 years), different parameters were sampled at different stations, and many of the data sets contain data only for the warmer months (e.g., May – October). Given the limited data available for calibration and the desire to have the model capture the long-term mean conditions in the estuary, the model was designed to simulate the average annual cycle of water quality and impacts of restored oyster reefs in the system.

**Estuarine Ecosystem Model:**

We applied a mechanistic, reduced complexity, management-relevant estuarine ecosystem model that simulates state variables and processes of first-order importance to estuarine eutrophication (Fig. 2; Brush 2002, 2012). The model simulates daily concentrations over an average annual cycle of chlorophyll-a (Chl), C, N, and P in both phytoplankton (PHYTO) and benthic microalgae (BMA); the water column pools of total suspended solids (TSS), dissolved oxygen (DO or O₂), dissolved inorganic nitrogen (DIN),

![Fig. 2. Schematic of the estuarine ecosystem model applied to Harris Creek. All terms are defined in the text.](image-url)
and dissolved inorganic phosphorus (DIP); and the pools of labile organic carbon ($C_{wc}$ and $C_{sed}$) and associated N and P in the water column and sediments, respectively. The model is forced with daily water temperature (TEMP or T), salinity (S), photosynthetically active radiation (PAR), inputs of freshwater (FLOW), TSS, DIN, DIP, and C from the watershed, atmospheric deposition of N, and mean wind speed. Exchanges between spatial elements and with the lower Choptank River are computed using a tidal prism approach; boundary conditions in the lower Choptank are forced from long-term monitoring data (see below). A core set of key rate processes (phytoplankton production, water column respiration or $R_{wc}$, carbon flux to the sediments, and denitrification or DNF in the absence of oysters) are formulated using robust, cross-system empirical relationships shown to apply across a wide range of temperate estuaries and rooted in actual measurements, thereby reducing the number of unconstrained parameters and uncertainty in model predictions (Brush 2002; Brush et al. 2002; Brush and Brawley 2009). This approach is in line with recent calls for management-relevant models of intermediate complexity as an alternative to more complex, highly parameterized models (e.g., NRC 2000; Duarte et al. 2003).

**Oyster Sub-Model:**

We coupled a model of restored oyster reefs (Fig. 3) to the estuarine ecosystem model above. The oyster model computes the daily growth of an individual oyster based on the balance between ingestion, production of feces, and respiration. Model formulations are based on Cerco and Noel (2005, 2007) and Fulford et al. (2007). Briefly, filtration is a function of individual weight, water temperature, salinity, TSS, and DO. Individual filtration is

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*Fig. 3. Oyster sub-model coupled to the estuarine ecosystem model in Harris Creek. Terms are defined in the text. Photo is from the New York State Department of Environmental Conservation.*
multiplied by total oyster abundance and used to draw down the pools of TSS, phytoplankton biomass, and associated N and P which are allocated to tissue and shell (N\text{shell}, N\text{tissue}, P\text{shell}, P\text{tissue}, see below). Ingested material is converted to assimilated material using an assimilation efficiency; the balance is deposited as feces. Respiration is a combined function of a temperature-dependent basal rate and a constant fraction of daily assimilation, and is used to consume O\textsubscript{2} and recycle DIN and DIP back to the water column. Oyster-enhanced rates of denitrification (DNF\textsubscript{oy}) are computed using a function of total reef biomass (see below). A constant fraction of N and P deposited in feces is buried (see below).

**Verification of the Exchanges:**

While the reduced spatial resolution of the Harris Creek Model enables fast run times through an online platform, it necessarily loses fine-scale variations in hydrodynamics. Further, the tidal prism approach to computing exchanges uses box area and mean tide range to compute exchanges which are constant over time and not directly controlled by physical processes. To confirm this approach, we used an existing, fine-scale 3D hydrodynamic model of Harris Creek. The Choptank Regional Ocean Modeling System (ChopROMS) (Fig. 4) was used to calculate the volume of water transported across each box boundary within Harris Creek. This 3D numerical model has previously been used.
A model for estimating the TMDL-related benefits of oyster reef restoration

for oyster larval transport predictions in Harris Creek (North et al. 2012). ChopROMS is an open source 3D hydrodynamic model developed by Dr. Wen Long (North et al. 2012). It is based on the Regional Ocean Modeling System (ROMS, http://www.myroms.org/; Shchepetkin et. al 2005), which is a numerical model with a curvilinear orthogonal horizontal grid system and vertical terrain following coordinates. The ChopROMS model is constructed based on a grid system with a dimension of 261x501 and resolution of approximately 120 m - 150 m (Fig. 4). It is forced by observed river discharge, near surface wind, near surface air pressure and temperature, downward short wave radiation, long wave radiation, humidity, and, at the outer boundaries located in the mainstem Bay, tidal and subtidal water level, water temperature, and salinity.

ChopROMS model predictions for June – September, 2010 were stored every 10 minutes to resolve changes in current velocities at tidal time scales (after fourteen test runs of ChopROMS as part of model development and validation to ensure high-quality predictions). These predictions were used to calculate the volume of water flowing into and out of the segments in the Harris Creek Model for comparison to those computed with the tidal prism approach.

Data Sources and Assumptions

The following sections refer to a number of figures showing model forcing data and calibration results. These figures have been compiled at the end of this report in Appendix A.

Estuarine Ecosystem Model:

Delineation of Harris Creek box boundaries and associated watersheds was conducted in ArcGIS. The coastline was obtained from the Chesapeake Bay Program and edited to divide the system into five boxes. Watersheds for each box were delineated manually using the National Hydrography Dataset (NHD, nhd.usgs.gov) high resolution stream lines and National Elevation Dataset (NED, ned.usgs.gov) 2013 1/3 arc-second grid. Mean depths of each box were computed using the NOAA 3 arc-second Coastal Relief Model (www.ngdc.noaa.gov/mgg/coastal/crm.html). The mean tide range (0.41 m, mean high water – mean low water) for computation of tidal prism exchanges was taken as the average of the current tidal datums at the Cambridge (0.49 m) and Poplar Island (0.34 m) NOAA tide stations. Resulting areas, depths, and volumes used in the Harris Creek Model are shown in Table 1.

<table>
<thead>
<tr>
<th>Box</th>
<th>Watershed Area, m²</th>
<th>Open Water Area, m²</th>
<th>Mean Depth, m</th>
<th>Volume, m³</th>
<th>Tidal Prism Volume, m³</th>
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</thead>
<tbody>
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<td>1.80</td>
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<tr>
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<tr>
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<td>11,091,800</td>
<td>2,861,140</td>
<td>0.91</td>
<td>2,616,299</td>
<td>1,173,067</td>
</tr>
</tbody>
</table>
Watershed loads into each spatial element were determined using output for 1985-2005 for the Harris Creek polygon of the CBP Phase V Watershed Model. Monthly loads across all years of freshwater, DIN, DIP, TSS, and organic C were used to compute mean monthly values (Fig. A1). Monthly loads of freshwater to the entire creek were forced directly into the model, converted to a yield of freshwater (per unit area of watershed), and multiplied by the area of each box watershed to compute the input to each box. Material loads (i.e., DIN, DIP, TSS, organic C) were converted to mean concentrations in the inflowing water which were forced into the model and used to compute the load to each box. An average daily value of atmospheric N deposition onto each box was computed from a value of 1 g N m\(^{-2}\) y\(^{-1}\) from Boynton et al. (1995); deposition of P was assumed to be negligible.

Water quality data were compiled from four sources for use in model forcing and calibration (Table 2, Fig. 1). The CBP has conducted approximately monthly sampling of

<table>
<thead>
<tr>
<th>Source</th>
<th>Parameters</th>
<th>Station</th>
<th>Years(^a)</th>
<th>Box</th>
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<td>T, S, DO, TSS, Chl-a, DIN, DIP</td>
<td>EE2.1</td>
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<td>downstream sonde</td>
<td>9/13-present</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>vertical profiler</td>
<td>2012-14</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>upstream sonde</td>
<td>9/13-present</td>
<td>4</td>
</tr>
<tr>
<td>UMCES</td>
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<td>2</td>
<td>2010-12</td>
<td>boundary</td>
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<tr>
<td></td>
<td></td>
<td>3</td>
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<td>20</td>
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<td>2010-11</td>
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<td></td>
<td>HC14</td>
<td>2010-13</td>
<td>5</td>
</tr>
</tbody>
</table>

\(^a\) Data from sources other than the CBP are primarily during warmer months only.
a variety of parameters at station EE2.1 in the lower Choptank River outside the mouth of Harris Creek. The Maryland Department of Natural Resources (MDDNR) operates three high frequency water quality datasondes in the creek. The upper and lower sondes are moored at depths of approximately 3 m; the middle station is a vertical profiler in about 3 m of water from which readings at 1 m were extracted. Values at all depths were used to confirm that stratification is minimal at the site. The monitoring data from the University of Maryland Center for Environmental Science (UMCES) were derived from the TRANSPORT Program and were collected from May through September in 2010, 2011, and 2012 at stations in the lower creek and Choptank River (North unpublished data). Finally, Mr. Drew Koslow (Choptank Riverkeeper, Midshore Riverkeeper Conservancy) provided approximately monthly monitoring data from several stations throughout Harris Creek.

Oyster Sub-Model:
Current default values for the acres of restored reefs in each box are approximate acres planted with juvenile oysters set on oyster shell as of March 2014 based on data provided by the Oyster Recovery Partnership. Current default values for oyster densities were derived from planting densities assuming a 90% mortality rate in year one (Paynter et al. 2013) on the assumption that the oysters of interest would be at least a year old. Current default oyster weights (g dry weight, DW) were computed from recent surveys of individual shell height (mm) on restored reefs (Paytner Lab, University of Maryland, unpublished data) from October 2013 – May 2014, and converted to weight using the equation from Liddel (2008):

\[ g \text{ DW} = 0.00003 \times (\text{shell height})^{2.3512} \]

Default values are provided as placeholders only and in some cases are based on samples from a small subset of sites in Harris Creek that were not randomly selected from the population of restoration sites. Accuracy of the estimated TMDL-related benefits of oyster reef restoration in Harris Creek will depend heavily upon the accuracy of the values entered by the user. Default values will be changed as additional data become available from restored reefs in Harris Creek and the supporting data cited on the model website.

Oyster-enhanced denitrification (\(\mu\text{mol m}^{-2} \text{ h}^{-1}\)) was modeled as a function of total reef biomass (B, g DW m\(^{-2}\)) using an average of regressions in the light and dark from April 2012 (14 °C) in Onancock Creek, VA (Kellogg, unpub. data):

Light: \[ \text{DNF}_{\text{oy}} = 85.701 \ln(B+1) + 358.43 \]

Dark: \[ \text{DNF}_{\text{oy}} = 104.51 \ln(B+1) + 172.43 \]
The intercepts reflect background denitrification in the absence of oysters and were removed as this is simulated separately by the model. Denitrification was scaled to any temperature (T) by multiplying the rates above by the following dimensionless function fit to rates measured in the Choptank River at four temperatures (Kellogg 2013):

\[ f(T) = e^{0.086(T-14)} \]

Denitrification estimates all come from reefs restored using oysters and oyster shell. The impact of the use of alternate substrates on denitrification rates is unknown.

Nitrogen and phosphorus assimilated by oysters was separated into tissue and shell using the following N and P contents expressed as percent of individual dry weight (Kellogg 2013):

- %N\text{tissue}: 9.27
- %P\text{tissue}: 1.26
- %N\text{shell}: 0.21
- %P\text{shell}: 0.04

The relative ratios of these were used to allocate N and P between tissue and shell.

No direct estimates exist for burial of N and P from biodeposits, so we used the rate of 10% from Newell et al. (2005).

**Model Implementation and Calibration**

**Forcing Functions:**

CBP data at station EE2.1 in the lower Choptank River from 1985 to 2012 were interpolated to daily resolution and used to compute mean annual cycles of each parameter to force at the mouth of Harris Creek (Figs. A2, A3). UMCES data at the two stations outside the creek fell mostly within the interannual variability (i.e., ± 2 s.d.) around the CBP mean annual cycles; therefore the CBP cycles were forced into the model to set the boundary conditions.

Since the focus of the model was on simulating mean annual cycles, we developed smooth cosine functions for water temperature and salinity in each box rather than forcing actual measurements (Figs. A4, A5). Functions were fit to pass through the majority of the available measurements; however given the interannual variability in the Chesapeake, especially for salinity, these functions do not capture the relatively fresher conditions that can exist in some years (Fig. A5).

Cosine functions for PAR and photoperiod (fraction of the day that is light) in the Chesapeake region were obtained from Wetzel and Neckles (1986).
Calibration:
Modeled exchanges of water across each box face computed using the tidal prism and 3D ROMS approaches matched well (Fig. A6). While the simplified tidal prism approach misses the high frequency variation in ROMS exchanges, it captures the long-term mean exchanges which is sufficient given the reduced spatial resolution of the Harris Creek Model and focus on simulating mean annual cycles.

Model predictions of chlorophyll-a (Fig. A7), TSS (Fig. A8), and DO (Fig. A9) generally fell within the range of the monitoring data. For chlorophyll-a, the match is particularly good in Box 1. The model appears to fall on the high end of the observations in Boxes 2, 4, and 5, which may be due to the lack of calibration of the benthic microalgal portion of the model, as no data exist to calibrate this state variable which can have a strong influence on phytoplankton dynamics. There are limited TSS data to calibrate the model so the quality of the TSS calibration is unclear; however the model does capture the approximate values in Boxes 1 and 2. Modeled DO matches the MDDNR and UMCEs data well but not the Riverkeeper data. Most of the Riverkeeper data are located at shallow, nearshore sites which may not reflect the average condition within the box as represented by the model, possibly explaining the discrepancy between the model and Riverkeeper data for DO (as well as for chlorophyll-a in Box 5).

Limited data were available to assess simulated individual oyster growth. Liddel (2008) presented seasonal growth data and von Bertalanffy growth functions for oysters in the Choptank River; his results suggest that the initial oyster sizes entered into the default model run (0.73 – 0.98 g DW) should result in growth between 0.62 and 0.80 g DW over the course of a year. With the exception of Box 5, these rates match those estimated with the model (Table 3).

The combined result of these analyses indicates that the model is able to reproduce the mean annual cycling of key water quality variables and oyster growth within the range of available data. This suggests that the model is sufficient for use as a tool to assess the TMDL-related impacts of oyster restoration scenarios within Harris Creek.

<table>
<thead>
<tr>
<th>Box</th>
<th>Growth, g DW y⁻¹</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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</tr>
<tr>
<td>2</td>
<td>0.69</td>
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<td>3</td>
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<tr>
<td>4</td>
<td>0.71</td>
</tr>
<tr>
<td>5</td>
<td>0.34</td>
</tr>
</tbody>
</table>

Table 3. Modeled annual oyster growth using default values for restored acres, density, and oyster size.
Online Interface

A user-friendly interface was developed for the model which is now served online through the VIMS Coastal Systems Ecology and Modeling Program (CSEMP) website. The direct link to the model is:

netsim.vims.edu/netsims/brush/harris_creek_model/index.html

or it can be accessed through the CSEMP online modeling site:

www.vims.edu/research/departments/bio/programs/semp/models/index.php

The online model completes an annual simulation in approximately 55 seconds. As part of this project and several others, we have improved the method by which we serve models online. A new version of the software was purchased in 2013 and extensively tested; the new software allows the user to download model output via their PC clipboard for pasting into a spreadsheet program for analysis. The online interfaces have also been improved with added functionality and model descriptions.

Appendix B provides screen shots and descriptions of each page in the online model. The key user inputs are shown in Fig. 5. The user can enter box-specific values for the acres of restored reefs, restored oyster density, mean oyster weight on the restored reefs, and (optionally) the value of N and P removal (i.e., $/pound). Densities and weights can be entered for any point in time for which the user has data; care needs to be taken when entering densities as the model does not assume mortality over time. As noted above, default values are provided as placeholders. Accuracy of the estimated TMDL-related benefits of oyster reef restoration in Harris Creek will depend heavily upon the accuracy of the values entered by the user.

Fig. 5. Screen shots of the simple, user-friendly interface for altering model parameters.
Future Enhancements

The reduced complexity nature of the Harris Creek Model makes this tool amenable to easy updating as additional data become available. The model will continue to be maintained online through the VIMS Coastal Systems Ecology and Modeling Program and we envision uploading future versions of the model as it is improved through inclusion of new research and monitoring data.

The key factor that would improve the model at this point in time is greater data availability. As noted above, there are currently limited data with which to constrain our denitrification function and seasonal oyster growth, which in turn is used to compute N and P sequestration in tissue and shell. There are no direct estimates of N and P deposition associated with restored reefs in the Chesapeake, or of the rate of burial; values currently employed in the model are rough estimates.

An example of this limitation is illustrated below for estimates of oyster-enhanced denitrification. While the formulation that relates $D_{\text{N}}F_{\text{ov}}$ to oyster biomass is well constrained, the term that scales for temperature is not. The data used to fit that function include two similar values at cooler temperatures in April and November, but two widely different values in the warmer months of June and August. Additionally, none of the data were collected for cold temperatures (e.g., $< 10{\degree C}$), when denitrification is often very low. The standard model run uses a function fit to all data and has a positive y-intercept, predicting denitrification at all temperatures.

To assess the sensitivity of the model to uncertainty in this function, the model was run with the function fit to: a) the current standard function, b) the lower envelope of the data, c) the upper envelope of the data, and d) the standard function but reducing $D_{\text{N}}F_{\text{ov}}$ to zero below 10 $\degree C$. Results are given in Fig. 7 for daily predictions of $D_{\text{N}}F_{\text{ov}}$ in Box 1, and in Table 4 as annual totals in all boxes. The range in

![Fig. 7. Modeled daily denitrification (g N m$^{-2}$ d$^{-1}$) associated with restored reefs in Box 1 using four different versions of the temperature function. See text for details.](image-url)
predicted values indicates the sensitivity of the model to the exact formulation used to predict denitrification. Similar sensitivities exist with other poorly constrained terms in the oyster sub-model. While the model incorporates the best data we have available, reproduces the majority of the available monitoring data, and remains a useful decision-support tool, acquisition and incorporation of new data to resolve these issues will be important for enhancing confidence in the model output.

<table>
<thead>
<tr>
<th>Box</th>
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<th>upper</th>
<th>&gt; 10 °C only</th>
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<td>6.2</td>
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<td>1.1</td>
<td>1.1</td>
<td>1.2</td>
<td>1.0</td>
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</table>

Beyond the availability of data to constrain the oyster sub-model formulations, additional water quality and sediment data would be useful for improving the calibration of the estuarine ecosystem model. Incorporation of more recent high frequency monitoring data from MDDNR will be important for calibration of the phytoplankton (i.e., chl) and dissolved oxygen state variables if these datasets are continued. Even with these data, however, there are no available chlorophyll-a or oxygen data from the main channel of Boxes 3 and 5. Unfortunately there were very limited data available for calibration of TSS and none in Boxes 3-5. Since TSS has a strong effect on simulated oyster filtration and phytoplankton biomass, additional data to constrain the calibration would be an important improvement. The model also simulates water column pools of dissolved inorganic N and P, but no data were available to calibrate these parameters. Finally, benthic microalgae can play a major role in sequestering nutrient releases from the sediments and limiting phytoplankton production in shallow systems such as Harris Creek; however there are no sediment chlorophyll-a data available to calibrate this part of the model.

Regardless of these limitations, the model is able to successfully reproduce the dynamics of water quality and oyster growth in Harris Creek, indicating that it is capable of estimating the TMDL-related benefits of oyster restoration in the system and comparing various scenarios. The model is easily amenable to future updates as new research and monitoring data become available, and the reduced complexity approach makes it readily applicable to other systems in the Chesapeake Bay and on the Eastern Shore.
Outreach Activities

Data from or information about this project have been presented at meetings attended by resource managers, restoration practitioners and researchers. Presentations to date include:

Brush, M.J. and M.L. Kellogg. 2014. A user-friendly, online model for estimating the TMDL-related benefits of oyster reef restoration in Harris Creek, MD. Chesapeake Modeling Symposium 2014, Chesapeake Community Modeling Program, Annapolis, MD.


Literature Cited


Appendix A: Model Inputs and Calibration

Fig. A1. Long-term (1985-2005) mean monthly freshwater inflows to Harris Creek from the CBP Phase V Watershed Model and computed concentrations of DIN, DIP, and TSS in the inflowing water. Error bars on flow depict 2 standard deviations.
Fig. A2. Model boundary conditions. Blue line and shaded region depict the long-term (1985-2012) average annual cycles ± 2 s.d. from CBP station EE2.1. Red (station 2) and green (station 3) lines are UMCES data from all years at stations outside the model domain.
Fig. A3. Model boundary conditions. Blue line and shaded region depict the long-term (1985-2012) average annual cycles ± 2 s.d. from CBP station EE2.1. Red (station 2) and green (station 3) lines are UMCES data from all years at stations outside the model domain.
Fig. A4. Model forcing functions for water temperature (grey lines), fit to data from multiple years from the Riverkeeper (blue), UMCES (red), and MDDNR (purple).
Fig. A5. Model forcing functions for salinity (grey lines), fit to data from multiple years from the Riverkeeper (blue), UMCES (red), and MDDNR (purple).
Fig. A6. Computed volume flows across the downstream boundary of each spatial element during flood tide (inflow, upper) and ebb tide (outflow, lower) from ChopROMS (lines with variability) and tidal prism approach (straight lines).
Fig. A7. Simulated chlorophyll-a (grey) in each spatial element with data from multiple years from the Riverkeeper (blue), UMCES (red), and MDDNR (purple).
Fig. A8. Simulated TSS (grey) in each spatial element with data from multiple years from UMCES (red).
Fig. A9. Simulated DO (grey) in each spatial element with data from multiple years from the Riverkeeper (blue), UMCES (red), and MDDNR (purple).
Appendix B: Online Model

Screen shots of the online model available at: netsim.vims.edu/netsims/brush/harris_creek_model/index.html

Fig. B1. Opening page of the online model, with a brief introduction and contact information. A blue button for “Next Page” in the lower right corner allows the user to navigate through the site. The red button allows the user to skip directly to the scenario analysis page.
Fig. B2. Second page of the online model, with the diagram of the ecosystem model. Buttons for “Next Page” and “Previous Page” in the lower and upper right corners, respectively, allow the user to navigate through the site. The red button takes the user to a page with definitions of all terms (see Fig. B4).
Fig. B3. Third page of the online model, with the diagram of the oyster sub-model. Buttons for “Next Page” and “Previous Page” in the lower and upper right corners, respectively, allow the user to navigate through the site. The red button takes the user to a page with definitions of all terms (see Fig. B4).
Fig. B4. Fourth page of the online model, with definitions of terms found in the model diagrams on Pages 2 (Fig. B2) and 3 (Fig. B3). Buttons return the user to either Page 2 (ecosystem model diagram) or Page 3 (oyster sub-model diagram).
Fig. B5. Scenario analysis page of the online model with user-defined inputs for acreage, density, and oyster weight on restored reefs as well as the economic value (i.e., $/pound) of N and P removal (optional). Buttons below the tables allow the user to run, pause, stop, and resume the model simulation. “Restore” clears all graphs and returns values in these tables to default values. Buttons for “Next Page” and “Previous Page” in the lower and upper right corners, respectively, allow the user to navigate through the site.
Fig. B6. Model output dashboard page. Once the model run is finished, the user can access the output from this page. Blue buttons take the user to graphs for a number of water quality (see Fig. B7) and ecosystem services (see Fig. B8) parameters. Clicking on the red buttons will copy the output to the PC clipboard for pasting into a spreadsheet. Button for “Previous Page” in the upper right corner allows the user to navigate through the site. The button in the lower right corner takes the user back to the scenario analysis page.
Fig. B7. Example output page for simulated water quality parameters over an annual cycle, in this case chlorophyll-a. Additional pages show output for total suspended solids, dissolved oxygen, and secchi depth. The tab in the lower left corner of the graph allows the user to toggle between model boxes (Box 1 is shown). The button in the lower right corner takes the user back to the model output dashboard.
Fig. B8. One of 14 output pages for simulated ecosystem services presented as annual totals, in this case the amount of N denitrified associated with restored reefs. Annual totals are given for Boxes 1 (left) through 5 (right). Other pages show output for volume of water filtered, chlorophyll-a and suspended sediments removed via filtration, N and P sequestered in oyster tissue and shell, N and P buried, total N and P removed due to restored oysters, and the economic value of this N and P removal (if values were entered for $/pound). The button in the lower right corner takes the user back to the model output dashboard.